

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
21 March 2002 (21.03.2002)

PCT

(10) International Publication Number
WO 02/22675 A2

(51) International Patent Classification⁷: **C07K 14/415**

(21) International Application Number: **PCT/US01/28506**

(22) International Filing Date:
14 September 2001 (14.09.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/232,778 15 September 2000 (15.09.2000) US
60/300,183 22 June 2001 (22.06.2001) US

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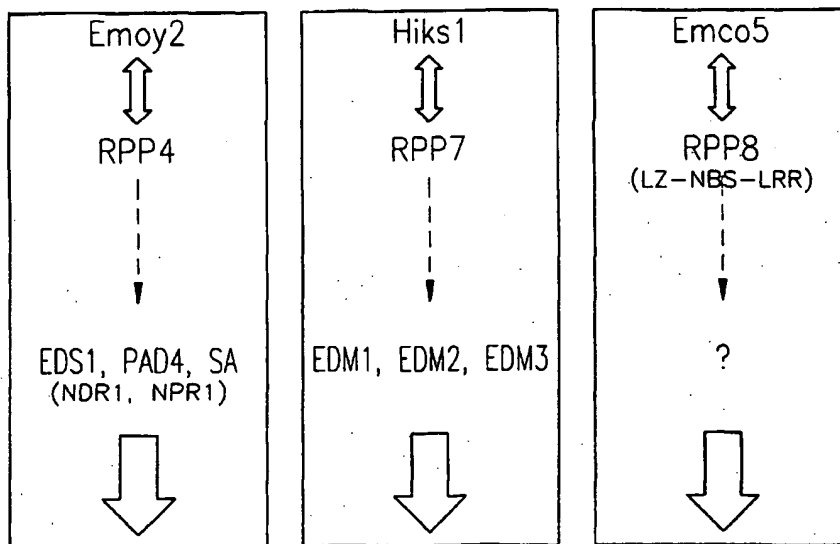
(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,

[Continued on next page]

(54) Title: PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION

RPP-DEPENDENT DEFENSE PATHWAYS



RESISTANCE

(57) Abstract: Methods to identify genes, the expression of which is altered in response to pathogen infection, are provided, as well as the genes identified thereby.

WO 02/22675 A2



CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

— with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION

5

Cross-Reference to Related Applications

This application is a continuation-in-part application of U.S. application Serial No. 60/232,778, filed on September 15, 2000, and of U.S. application Serial No. 60/300,183, filed on June 22, 2001, the disclosures of which are
10 incorporated by reference herein.

Field of the Invention

The present invention generally relates to the field of plant molecular biology, and more specifically to the regulation of gene expression in plants in response to stress, e.g., to pathogen exposure.

15

Background of the Invention

Plants are capable of activating a large array of defense mechanisms in response to pathogen attack. A crucial factor determining the success of these mechanisms is the speed of their activation. Consequently, there is considerable
20 interest in understanding how plants recognize pathogen attack and control expression of defense mechanisms.

Some potential pathogens trigger a very rapid resistance response called gene-for-gene resistance. This occurs when the pathogen carries an avirulence (*avr*) gene that triggers specific recognition by a corresponding host resistance
25 (*R*) gene. *R* gene specificity is generally quite narrow, in most cases only pathogens carrying a particular *avr* gene are recognized. Recognition is thought to be mediated by ligand-receptor binding. *R* genes have been studied extensively in recent years. For a review of *R* genes, see Ellis et al. (1998); Jones et al. (1997); and Ronald (1998).

30 One of the defense mechanisms triggered by gene-for-gene resistance is programmed cell death at the infection site. This is called the hypersensitive response, or HR. Pathogens that induce the HR, or cause cell death by other means, activate a systemic resistance response called systemic acquired resistance (SAR). During SAR, levels of salicylic acid (SA) rise throughout the
35 plant, defense genes such as pathogenesis related (PR) genes are expressed, and the plant becomes more resistant to pathogen attack. SA is a crucial component

of this response. Plants that cannot accumulate SA due to the presence of a transgene that encodes an SA-degrading enzyme (*nahG*), develop a HR in response to challenge by avirulent pathogens, but do not exhibit systemic expression of defense genes and do not develop resistance to subsequent pathogen attack (Ryals et al., 1996). The nature of the systemic signal that triggers SAR is a subject of debate (Shulaev et al., 1995; Vernooji et al., 1994). SA clearly moves from the site of the HR to other parts of the plant, but if this is the signal, it must be effective at extremely low concentration (Willits et al., 1998).

SAR is quite similar to some reactions that occur locally in response to attack by virulent (those that cause disease) or avirulent (those that trigger gene-for-gene resistance) pathogens. In general, activation of defense gene expression occurs more slowly in response to virulent pathogens than in response to avirulent pathogens. Some pathogens trigger expression of defense genes through a different signaling pathway that requires components of the jasmonic acid (JA) and ethylene signaling pathways (Creelman et al., 1997).

One approach to understanding the signal transduction networks that control defense mechanisms is to use genetic methods to identify signaling components and determine their roles within the network. Considerable progress has been made using this approach in *Arabidopsis*-pathogen model systems.

R gene signal transduction

Genes such as *NDR1* and *EDS1*, as well as *DND1* and the lesion-mimic genes, likely act in signal transduction pathways downstream from *R-avr* recognition. *NDR1* and *EDS1* are required for gene-for-gene mediated resistance to avirulent strains of the bacterial pathogen *Pseudomonas syringae* and the oomycete pathogen *Peronospora parasitica*. Curiously, *ndr1* mutants are susceptible to one set of avirulent pathogens, whereas *eds1* mutants are susceptible to a non-overlapping set (Aarts et al., 1998). The five cloned *R* genes that require *EDS1* all belong to the subset of the nucleotide binding site-leucine rich repeat (NBS-LRR) class of *R* genes that contain sequences similar to the cytoplasmic domains of *Drosophila* Toll and mammalian interleukin 1 transmembrane receptors (TIR-NBS-LRR). The two genes that require *NDR1* belong to the leucine-zipper (LZ-NBS-LRR) subclass of NBS-LRR genes. There is another LZ-NBS-LRR gene, *RPP8*, that does not require *EDS1* or *NDR1*, so

the correlation between *R* gene structure and requirement for *EDS1* or *NDR1* is not perfect. Nevertheless, these results show that *R* genes differ in their requirements for downstream factors and that these differences are correlated with *R* gene structural type.

5 *NDR1* encodes a protein with two predicted transmembrane domains (Century et al. 1997). RPM1, which requires *NDR1* to mediate resistance, is membrane-associated, despite the fact that its primary sequence does not include any likely membrane-integral stretches (Boyes et al., 1998). It is possible that part of the function of *NDR1* is to hold *R* proteins close to the membrane. *EDS1*
10 encodes a protein with blocks of homology to triacyl glycerol lipases (Falk et al., 1999). The significance of this homology is not known, but it is tempting to speculate that *EDS1* is involved in synthesis or degradation of a signal molecule. *EDS1* expression is inducible by SA and pathogen infection, suggesting that *EDS1* may be involved in signal amplification (Falk et al., 1999).

15 It has been extremely difficult to isolate mutations in genes other than the *R* genes that are required for gene-for-gene resistance. A selection procedure was devised (McNellis et al., 1998) on the basis of precisely controlled inducible expression of the *avr* gene *avrRpt2* in plants carrying the corresponding resistance gene *RPS2*. Expression of *avrRpt2* in this background is lethal, as it
20 triggers a systemic HR. It is now possible to select for mutants with subtle defects in gene-for-gene signaling by requiring growth on a concentration of inducer slightly higher than the lethal dose.

 Putative plant receptor proteins encoded by *RPP* genes (recognition of *P. parasitica*) mediate specific recognition of *Peronospora* isolates and trigger
25 defense reactions. Recently, McDowell et al. (2000) reported that two members of this class, *RPP7* and *RPP8* (the latter of which encodes a LZ-NBS-LRR type R protein) were not significantly suppressed by mutations in either *EDS1* or *NDR1*, and that *RPP7* resistance was also not compromised by mutations in *EIN2*, *JAR1* or *COI1*, which affect ethylene or jasmonic acid signaling, or in
30 *coil/npr1* or *coil/NahG* backgrounds. The authors suggested that *RPP7* initiates resistance through a novel signaling pathway that is independent of salicylic acid accumulation or jasmonic acid response components.

SA-dependent signaling

SA levels increase locally in response to pathogen attack, and systemically in response to the SAR-inducing signal. SA is necessary and sufficient for activation of PR gene expression and enhanced disease resistance.

- 5 Physiological analyses and characterization of certain lesion-mimic mutants strongly suggest that there is a positive autoregulatory loop affecting SA concentrations (Shirasu et al., 1997; Hunt et al., 1997; Weymann et al., 1995). Several mutants with defects in SA signaling have been characterized. These include *npr1*, in which expression of PR genes in response to SA is blocked;
- 10 *cpr1*, *cpr5*, and *cpr6*, which constitutively express PR genes; the *npr1* suppressor *ssil*; *pad4*, which has a defect in SA accumulation; and *eds5*, which has a defect in PR1 expression.

- Expression of the defense genes PR1, BG2, and PR5 in response to SA treatment requires a gene called NPR1 or NIM1. Mutations in *npr1* abolish
- 15 SAR, and cause enhanced susceptibility to infection by various pathogens (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 1997). NPR1 appears to be a positive regulator of PR gene expression that acts downstream from SA. NPR1 encodes a novel protein that contains ankyrin repeats (which are often involved in protein-protein interactions (Cao et al.,
- 20 1997; Ryals et al., 1997), and that is localized to the nucleus in the presence of SA (Dong et al., 1998). Consequently, it is unlikely that NPR1 acts as a transcription factor to directly control PR gene expression, but its nuclear localization suggests that it may interact with such transcription factors.

- PAD4 appears to act upstream from SA. In *pad4* plants infected with a
- 25 virulent *P. syringae* strain, SA levels, synthesis of the antimicrobial compound camalexin, and PR1 expression are all reduced (Zhou et al., 1998). SA is necessary, but not sufficient, for activation of camalexin synthesis (Zhou et al., 1998; Zhao et al., 1996). The camalexin defect in *pad4* plants is reversible by exogenous SA (Zhou et al., 1998). Mutations in *pad4* do not affect SA levels,
- 30 camalexin synthesis, or PR1 when plants are infected with an avirulent *P. syringae* strain (Zhou et al., 1998). Taken together, these results suggest that PAD4 is required for signal amplification to activate the SA pathway in response to pathogens that do not elicit a strong defense response (Zhou et al., 1998).

JA-dependent signaling

JA signaling affects diverse processes including fruit ripening, pollen development, root growth, and response to wounding (Creelman et al., 1997). The *jarl* and *coil* mutants fail to respond to JA (Feys et al., 1994; Staswick et al., 1992). *COII* has been cloned, and found to encode protein containing leucine-rich repeats and a degenerate F-box motif (Xie et al., 1998). These features are characteristic of proteins that function in complexes that ubiquitinate protein targeted for degradation.

In the past few years it has become apparent that JA plays an important role in regulation of pathogen defenses. For example, the induction of the defensin gene *PDF1.2* after inoculation of *Arabidopsis* with the avirulent pathogen *Alternaria brassicicola* does not require SA or NPR1, but does require ethylene and JA signaling (Penninck et al., 1996).

SA signaling and JA signaling pathways are interconnected in complicated ways. Studies in other systems have shown that SA signaling and JA signaling are mutually inhibitory (Creelman et al., 1997; Harms et al., 1998). However, synthesis of camalexin in response to *P. syringae* infection is blocked in *nahG* (Zhou et al., 1998; Zhao et al., 1996) and *coil* (Glazebrook, 1999) plants, strongly suggesting that camalexin synthesis requires both SA and JA signaling.

Induced systemic resistance (ISR)

Some rhizosphere-associated bacteria promote disease resistance (van Loon et al., 1998). This phenomenon, called ISR, has been studied using *Pseudomonas fluorescens* strain WCS417r to colonize *Arabidopsis* roots (Pieterse et al., 1996). Colonized plants are more resistant to infection by the fungal pathogen *Fusarium oxysporum* f sp *raphani* and *P. syringae* (Pieterse et al., 1996). ISR occurs in *nahG* plants, indicating that it is not a SA-dependent phenomenon (Pieterse et al., 1996). Rather, ISR appears to be JA- and ethylene-dependent. The observation that ethylene can induce ISR in *jarl* mutants led to the hypothesis that ISR requires a JA signal followed by an ethylene signal (Pieterse et al., 1998). No changes in gene expression associated with ISR have been detected (Pieterse et al., 1998), suggesting that it is different from activation of *PDF1.2* expression by *A. brassicicola*.

Curiously, ISR requires *NPR1* (Pieterse et al., 1996). This was unexpected in light of the fact that *NPR1* was previously known to be involved only in SA-dependent processes and ISR is SA-independent. If the SA-dependent signal is received, *NPR1* mediates a resistance response characterized by *PR1* expression, whereas if the ISR signal is received, *NPR1* mediates a different resistance response. It is difficult to imagine how this could occur, unless *NPR1* is interacting with different 'adapter' molecules to mediate the different signals. The ankyrin repeats found in *NPR1* could function in protein-protein interactions between *NPR1* and adapter proteins. Identification of proteins that interact with *NPR1*, and characterization of plants with loss-of-function mutations affecting those proteins, would be very helpful for understanding how *NPR1* acts in each pathway. It would also be worthwhile to determine if the *ssi1* or *cpr6* mutations suppress the ISR defect of *npr1* mutants.

Relevance to disease resistance

Characterization of the effects of various mutations on resistance to different pathogens has revealed that there is considerable variation in the extent to which pathogens are affected by defense mechanisms. SAR is known to confer resistance to a wide array of pathogens, including bacteria, fungi, oomycetes, and viruses. JA signaling is important for limiting the growth of certain fungal pathogens. In *Arabidopsis*, the SA pathway mutants *npr1* and *pad4* show enhanced susceptibility to *P. syringae* and *P. parasitica* (Cao et al., 1994; Delaney et al., 1995; Shah et al., 1997; Zhou et al., 1998; Glazebrook et al., 1997).

Overexpression of rate-limiting defense response regulators may cause the signaling network to respond faster or more strongly to pathogen attack, thereby improving resistance. For example, overexpression of *NPR1* caused increased resistance to *P. syringae* and *P. parasitica* in a dosage dependent manner (Cao et al., 1998). Moreover, *NPR1*-overexpression had no obvious deleterious effects on plant growth, in contrast to mutations that lead to constitutive overexpression of defense responses, which generally cause dwarfism.

Thus, what is needed is the systematic identification of genes useful to confer resistance to pathogens.

Summary of the Invention

The invention provides an isolated nucleic acid molecule (polynucleotide), e.g., DNA, comprising a plant or fungal nucleotide sequence, the expression of which is altered in response to stress, e.g., pathogen infection.

5 For example, the invention provides a nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising at least a portion of a key effector gene(s) responsible for host resistance to particular pathogens. To provide resistance or tolerance to a pathogen in a plant, this sequence may be overexpressed individually, in the sense or antisense orientation, or in

10 combination with other sequences, to confer improved disease resistance or tolerance to a plant relative to a plant that does not comprise and/or express the sequence. The overexpression may be constitutive, or it may be preferable to express the effector gene(s) from an inducible promoter including a promoter which is responsive to external stimuli, such as chemical application, or to

15 pathogen infection, e.g., so as to avoid possible deleterious effects on plant growth. In one embodiment of the invention, the promoter employed to express the nucleotide sequence of the invention may be one that mediates rapid and transient transcription after pathogen infection. Thus, the invention also provides an isolated nucleic acid molecule comprising a plant nucleotide

20 sequence which alters, e.g., increases or decreases, the transcription of plant genes, e.g., open reading frames, in response to stress, e.g., pathogen infection.

As described herein, *Arabidopsis* plants of differing genotypes were infected with different strains of an oomycete, *P. parasitica*. RNA was isolated from each plant/pathogen pair and employed to prepare probes which were hybridized to a gene

25 chip having nucleic acid sequences (probe sets) corresponding to approximately 8,200 *Arabidopsis* genes. Genes were then identified that were upregulated or downregulated in response to infection, including genes that were dependent on *RPP7* or *RPP8*, which act via unconventional signaling cascades and are not dependent on defense regulators such as EDS1, NDR1, PAD4, NPR1, RAR1, PBS3 or salicylic acid (SA). Among the

30 genes showing strong *Peronospora*-induced expression changes, clusters of genes were identified that were specifically upregulated by *RPP7* or *RPP8*, or both. In particular in one analysis, the expression of 184 genes (SEQ ID NOs:1-211 and 792) related to 217 probe sets was upregulated by either *RPP7* or *RPP8*, or both, while in another analysis the expression of genes related to 194 probe sets (SEQ ID NOs:212-399 and 793) was

upregulated by either *RPP7* or *RPP8*, or both. Further, as described below, promoters of genes that were rapidly and transiently transcribed after *P. parasitica* infection and were *RPP7/8*-dependent were significantly enriched with both novel sequence motifs and potential binding sites of known transcription factors. Specifically, the promoters were

5 significantly enriched with two novel sequence motifs (referred to as "motif 1" and "motif 2"), one of which was similar to binding sites for Myb transcription factors, sequence motifs related to WRKY binding sites, and two other novel sequence motifs ("motif 3" and "motif 4"). Moreover, comparisons between expression signatures of wild type plants as well as the *RPP7* loss of function mutants, and *edm1*, *edm2* and

10 *edm3* mutants, allow for predictions regarding the *RPP7* pathway hierarchy.

In addition, more than 200 genes (SEQ ID NOs:75, 214, 228, 301, 339, 400-684, 792-795) were identified that were specifically controlled by the *RPP4*-dependent pathway, which mediates resistance of the *Arabidopsis* ecotype Col-0 to the *Peronospora* isolate Emoy2. According to their response to SA, an important mediator

15 of local and systemic defense responses, and the protein biosynthesis inhibitor cycloheximide (CHX), these genes were further subcategorized into immediate early and secondary response genes. A set of immediate early SA responsive genes (SEQ ID NOs:150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615, and 526) was found to consist exclusively of regulatory genes. Such genes are likely controlled by

20 transcription factors acting closely downstream of SA. One highly conserved motif in the promoters of these immediate early genes was similar to binding sites of WRKY transcription factors (SEQ ID NOs:757-765). Other conserved promoter motifs appeared to be novel and may facilitate the cloning of their cognate transcription factors. A cluster of SA/CHX super-induced genes was found to show elevated expression

25 ground states in the *npr1* mutant (SEQ ID NOs:214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447 and 551) suggesting an NPR1-dependent de-repression mechanism in the control of some SA responsive immediate early genes.

Thus, the invention provides an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence encoding a polypeptide which

30 is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to a pathogen that induces a response mediated by *R* genes, including pathogens such as bacteria, fungi, oomycetes, viruses, nematodes and insects, e.g., aphids (see Hammond-Kosack and Jones (1997), which is specifically incorporated by

reference herein). For example, the plant or fungal nucleotide sequence encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to infection by an oomycete such as *Peronospora*, and is *RPP4*-,
5 *RPP7*-, and/or *RPP8*-dependent. These sequences can be identified by employing an array of nucleic acid samples, e.g., a plurality of oligonucleotides, each plurality corresponding to a different plant gene, on a solid substrate, e.g., a DNA chip, and probes corresponding to nucleic acid from pathogen-infected (e.g., wild-type) plant cells and to nucleic acid from uninfected plant cells or
10 plant cells having a mutation which alters the response to pathogen infection. Thus, genes, the expression of which are altered by pathogen infection, can be systematically identified. Preferably, the nucleotide sequence is from plant DNA, either a dicot or a monocot, which encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by an open reading
15 frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. More preferably, the nucleotide sequence is from plant DNA that is substantially similar to an *Arabidopsis* nucleic acid segment having any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. The term "substantially similar", when used herein with respect to a polypeptide
20 means a polypeptide corresponding to a reference polypeptide, wherein the polypeptide has substantially the same structure and function as the reference polypeptide, e.g., where only changes in amino acid sequence are those which do not affect the polypeptide function. When used for a polypeptide or an amino acid sequence, the percentage of identity between the substantially similar and
25 the reference polypeptide or amino acid sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, up to at least 99%, where the reference polypeptide is an *Arabidopsis* polypeptide encoded by an open reading
30 frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. However, the percent of identity between the substantially similar and the reference polypeptide may be less than 65% as long as the two polypeptides have the same or similar function, e.g., catalyze the same or similar reaction. Another indication that two polypeptides are substantially similar to

each other is that an agent, e.g., an antibody, which specifically binds to one of the polypeptides, specifically binds to the other.

In its broadest sense, the term "substantially similar", when used herein with respect to a nucleotide sequence, means a nucleotide sequence

5 corresponding to a reference nucleotide sequence, wherein the corresponding sequence is from a gene that encodes a polypeptide having substantially the same structure and function as the polypeptide encoded by a gene comprising the reference nucleotide sequence. The term "substantially similar" is specifically intended to include nucleotide sequences wherein the sequence has been

10 modified to optimize expression in particular cells. The percentage of identity between the substantially similar nucleotide sequence and the reference nucleotide sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%,

15 96%, 97%, 98%, up to at least 99%, wherein the reference sequence is preferably any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. Sequence comparisons may be carried out using a Smith-Waterman sequence alignment algorithm (see e.g., Waterman (1995) or <http://www.uto.usc.edu/software/seqaln/index.html>). The localS program, version 1.16, is

20 preferably used with following parameters: match: 1, mismatch penalty: 0.33, open-gap penalty: 2, extended-gap penalty: 2. Further, a nucleotide sequence that is "substantially similar" to a reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C,

25 more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC,

30 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

Hence, the isolated nucleic acid molecules of the invention also include the orthologs of the *Arabidopsis* sequences disclosed herein, i.e., the corresponding nucleic acid molecules in organisms other than *Arabidopsis*,

including, but not limited to, plants other than *Arabidopsis*, preferably cereal plants, e.g., corn, wheat or rice, as well as rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugarbeet, and in fungi. An ortholog is a gene from a different species that
5 encodes a product having the same function as the product encoded by a gene from a reference organism. The encoded ortholog products likely have at least 70% amino acid sequence identity to each other. Hence, the invention includes an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 70% identity to a polypeptide encoded by one or
10 more of the *Arabidopsis* sequences, although it is also envisioned that orthologous genes to those disclosed herein may encode a polypeptide with less than 70%, e.g., less than 65% amino acid sequence identity, but which polypeptide has the same or similar function. Databases such GenBank or one found at <http://bioserver.myongjiac.kr/rjce.html> (for rice) may be employed to
15 identify sequences related to the *Arabidopsis* sequences, e.g., orthologs in cereal crops such as rice. Alternatively, recombinant DNA techniques such as hybridization or PCR may be employed to identify sequences related to the *Arabidopsis* sequences.

Thus, the invention preferably includes an isolated nucleic acid molecule
20 comprising a plant or fungal nucleotide sequence that encodes a polypeptide that has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, amino acid sequence identity to an *Arabidopsis* polypeptide encoded by an open reading
25 frame comprising any one of SEQ ID NOs: 1-684 and 792-795, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795. In one embodiment, the isolated nucleic acid molecule is not SEQ ID NOs: 1-684 and
30 792-795. The invention also provides anti-sense nucleic acid molecules corresponding to the open reading frames or genes identified as responsive to pathogen infection. Also provided are expression cassettes, e.g., recombinant vectors, and host cells, comprising the nucleic acid molecule of the invention in either sense or antisense orientation.

Also provided is an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising a nucleic acid sequence having at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, nucleic acid sequence similarity to an *Arabidopsis* open reading frame comprising any one of SEQ ID NOs: 1-684 and 792-795, the complement thereof, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795.

The nucleic acid molecules of the invention, their encoded polypeptides and compositions thereof, are useful to provide resistance to pathogens and as a diagnostic for the presence or absence of the pathogen by correlating the expression level or pattern of expression of one or more of the nucleic acid molecules of the invention or one or more of the polypeptides encoded thereby. As one embodiment of the invention includes isolated nucleic acid molecules that have increased expression in response to pathogen infection, the invention further provides compositions and methods for enhancing resistance to pathogen infection. The compositions of the invention include plant or fungal nucleotide sequences and the amino acid sequences for the polypeptides or partial-length polypeptides encoded thereby which are useful to provide tolerance or resistance to a plant to a pathogen, preferably by preventing or inhibiting pathogen infection. The resistance or tolerance may be accomplished by decreasing or eliminating expression of a plant gene necessary for pathogen infection and/or replication or by overexpressing a gene product that inhibits pathogen infection and/or replication. Methods of the invention involve stably transforming a plant with one or more of at least a portion of these nucleotide sequences which confer tolerance or resistance operably linked to a promoter capable of driving expression of that nucleotide sequence in a plant cell. By "portion" or "fragment", as it relates to a nucleic acid molecule, sequence or segment of the invention, when it is linked to other sequences for expression, is meant a sequence having at least 80 nucleotides, more preferably at least 150 nucleotides, and still more preferably at least 400 nucleotides. If not employed for expressing, a "portion" or "fragment" means at least 9, preferably 12, more

preferably 15, even more preferably at least 20, consecutive nucleotides, e.g., probes and primers (oligonucleotides), corresponding to the nucleotide sequence of the nucleic acid molecules of the invention. By "resistant" is meant a plant which exhibits substantially no phenotypic changes as a consequence of infection with the pathogen. By "tolerant" is meant a plant which, although it may exhibit some phenotypic changes as a consequence of infection, does not have a substantially decreased reproductive capacity or substantially altered metabolism. Thus, some of the isolated nucleic acid molecules of the invention are useful in a method of combating a pathogen in an agricultural crop. The method comprises introducing to a plant, plant cell, or plant tissue an expression cassette comprising a nucleic acid molecule of the invention so as to yield a transformed differentiated plant, transformed cell or transformed tissue. Transformed cells or tissue can be regenerated to provide a transformed differentiated plant. The transformed differentiated plant preferably expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to pathogen infection relative to a corresponding nontransformed plant. The present invention also provides a transformed plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields under conditions of pathogen infection and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

The invention also includes recombinant nucleic acid molecules which have been modified so as to comprise codons other than those present in the unmodified sequence. The recombinant nucleic acid molecules of the invention include those in which the modified codons specify amino acids that are the same as those specified by the codons in the unmodified sequence, as well as those that specify different amino acids, i.e., they encode a variant polypeptide having one or more amino acid substitutions relative to the polypeptide encoded by the unmodified sequence.

The invention further includes a nucleotide sequence which is complementary to one (hereinafter "test" sequence) which hybridizes under stringent conditions with the nucleic acid molecules of the invention as well as RNA which is encoded by the nucleic acid molecule. When the hybridization is performed under stringent conditions, either the test or nucleic acid molecule of invention is preferably supported, e.g., on a membrane or DNA chip. Thus, either a denatured test or nucleic acid molecule of the invention is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of, e.g., between 55 and 70°C, in double strength citrate buffered saline (SC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon the degree of stringency required such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one-tenth strength SC containing 0.1% SDS.

The present invention also provides a method to identify a gene, the expression of which is altered in response to an external stimulus, e.g., pathogen infection. The method comprises contacting a plurality of samples comprising portions or fragments of isolated nucleic acid molecules with a probe which corresponds to a population of a nucleic acid sequences, the expression of which is altered in response to an external stimulus, so as to form a binary complex. Each sample corresponds to a different gene. Then complex formation is detected or determined. The method may be employed with nucleic acid samples and probes from any organism, e.g., any prokaryotic or eukaryotic organism. Preferably, the nucleic acid sample and probes are from a plant, such as a dicot or monocot. For example, the method comprises contacting a solid substrate comprising a plurality of samples comprising portions or fragments of isolated plant nucleic acid with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from a pathogen infected plant so as to form a complex. Preferred pathogens are those which induce an *R*-gene dependent resistance response. Each individual sample comprises one or more nucleic acid sequences corresponding to a plant gene, e.g., a pool of oligonucleotides corresponding to the same gene or a portion of that gene. The plurality of samples is provided on a DNA chip. A second plurality of samples on a solid substrate, i.e., a DNA chip, each comprising a plurality of samples comprising portions or fragments of

isolated plant nucleic acid is contacted with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from an uninfected or mutant plant or plant cells so as to form a complex. Then complex formation with nucleic acid from infected cells and from uninfected or mutant cells is compared.

5 The invention also provides a method for identifying a plant cell infected with a pathogen, e.g., one that induces a *RPP4*-, *RPP7*- and/or *RPP8*-dependent resistance response. The method comprises contacting nucleic acid obtained from a plant cell suspected of being infected with the pathogen with at least one, preferably at least two, oligonucleotides under conditions effective to amplify at
10 least a portion of a nucleotide sequence in the isolated plant nucleic acid which is substantially similar to at least one of SEQ ID NOs: 1-684 and 792-795, so as to
— yield an amplified product. Then the presence of the amplified product is detected or determined. The presence of the amplified product, e.g., in an amount that is different than the amount of the corresponding amplified product
15 from an uninfected or mutant plant, corresponding to one or more of SEQ ID NOs: 1-684 and 792-795 or an ortholog thereof, is indicative of pathogen infection.

 The invention provides an additional method for identifying a plant cell infected with a pathogen. The method comprises hybridizing a probe selected
20 from SEQ ID NOs: 1-684 and 792-795 to nucleic acid obtained from a plant cell suspected of being infected with a pathogen. The amount of the probe hybridized to nucleic acid obtained from a cell suspected of being infected with a pathogen is compared to hybridization of the probe to nucleic acid isolated from an uninfected or mutant cell. A change in the amount of the hybridized probe in
25 nucleic acid isolated from a cell suspected of being infected by a pathogen relative to the amount of hybridized probe in nucleic acid isolated from an uninfected or mutant cell is indicative of infection.

 Also provided is an isolated nucleic acid molecule comprising a nucleotide sequence that directs transcription, e.g., a promoter, of a linked
30 nucleic acid segment in a host cell, such as a plant cell, wherein transcription is altered, e.g., increased, in response to a pathogen infection. Preferably, the pathogen is *R*-dependent, and more preferably, one that triggers a response that is dependent on *RPP4*, *RPP7* and/or *RPP8*, such as an oomycete (for example, *Peronospora*). It is preferred that the nucleotide sequence is from plant genomic

DNA which has at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, nucleotide sequence identity to a sequence of a promoter from an
5 *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, e.g., SEQ ID NOs: 774-788, or comprising motifs such as one of SEQ ID NOs: 685-773. Thus, the invention also includes orthologs of *Arabidopsis* promoters. Preferably, the nucleotide sequence includes the promoter region from a gene corresponding to SEQ ID NOs: 1-770 and 792-795, which region preferably
10 includes at least one copy of at least one of the following, e.g., a nucleic acid sequence comprising one of SEQ ID NOs: 685-697 ("motif 1"), SEQ ID NOs: 698-709 ("motif 2"), GGT/CCCA ("motif 3"), GNCCAAA ("motif 4"), or SEQ ID NOs: 710-713, 714-756, or 757-773. The promoter sequence is preferably about 25 to 2000, e.g., 50 to 500 or 100 to 1400, nucleotides in length.

15 In one embodiment of the invention, the isolated nucleic acid molecule comprises a plant nucleotide sequence which is the promoter region for any one of SEQ ID NOs: 1-684 and 792-795, or is structurally related to the promoter for SEQ ID NOs: 1-684 and 792-795, i.e., is an orthologous promoter, and is linked to a plant structural gene or open reading frame. Hence, the present invention
20 further provides an expression cassette or a recombinant vector containing the nucleic acid molecule, and the vector may be a plasmid. Such cassettes or vectors, when present in a plant, plant cell or plant tissue result in transcription of the linked nucleic acid segment in the plant, plant tissue or plant cell. Transcription of the linked segment is altered in response to pathogen infection,
25 including *Peronospora* infection. For promoters with motif 1, transcription of linked segments may be altered in response to agents or other stimuli that induce Myb-like transcription factors.

Generally, the promoters of the invention may be employed to express a nucleic acid segment that is operably linked to the promoter, for example, an
30 open reading frame or a portion thereof, an anti-sense construct or a transgene. The open reading frame may be obtained from an insect resistance gene, a bacterial disease resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a

mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a positive selectable marker, a gene affecting plant agronomic characteristics, i.e., yield, standability and the like, or an environment or stress resistance gene, i.e., one or more genes
5 that confer herbicide resistance or tolerance, insect resistance or tolerance, disease resistance or tolerance (viral, bacterial, fungal, oomycete, or nematode), stress tolerance or resistance (as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, salt stress, or oxidative stress), increased yields, food content and makeup, physical appearance, male
10 sterility, drydown, standability, prolificacy, starch properties or quantity, oil quantity and quality, amino acid or protein composition, and the like.

— Preferably, the promoters of the invention include a consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743,
15 250 to about 743, 400 to about 743, 600 to about 743, of the promoter sequences from genes comprising any one of SEQ ID NOs:685-788, 714-756, and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

In a particular embodiment of the invention said consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500,
20 contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, has at least 75%, preferably 80%, more preferably 90% and most preferably 95% sequence identity with a corresponding consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40
25 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs:685-788, 714-756, and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

The expression cassettes or vectors of the invention may optionally
30 include other regulatory sequences, e.g., transcription terminator sequences, introns and/or enhancers, and may be contained in a host cell. The expression cassette or vector may augment the genome of a transformed plant or may be maintained extrachromosomally. The expression cassette or vector may further have a Ti plasmid and be contained in an *Agrobacterium tumefaciens* cell; it may

be carried on a microparticle, wherein the microparticle is suitable for ballistic transformation of a plant cell; or it may be contained in a plant cell protoplast. Further, the expression cassette can be contained in a plant, plant cell or plant tissue from a dicot or a monocot. In particular, the plant may be a cereal plant.

5 The present invention further provides a method of augmenting a plant genome by contacting plant cells with an expression cassette or vector of the invention, i.e., one having a nucleotide sequence that directs transcription of a linked nucleic acid segment in a plant cell, wherein transcription of the linked segment is altered in response to a pathogen such as an oomycete, e.g.,
10 *Peronospora*, infection, and wherein the nucleic sequence is from plant DNA that has at least 65%, and more preferably at least 70%, identity to the sequence of a promoter from an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, so as to yield transformed plant cells; and regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the
15 differentiated transformed plant expresses the linked fragment in the cells of the plant in response to infection. The present invention also provides a plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in
20 which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and
25 probes.

The invention also provides a method of plant breeding, e.g., to prepare a crossed fertile transgenic plant. The method comprises crossing a fertile transgenic plant comprising a particular nucleic acid molecule of the invention with itself or with a second plant, e.g., one lacking the particular nucleic acid
30 molecule, to prepare the seed of a crossed fertile transgenic plant comprising the particular nucleic acid molecule. The seed is then planted to obtain a crossed fertile transgenic plant. The plant may be a monocot or a dicot. In a particular embodiment, the plant is a cereal plant.

The crossed fertile transgenic plant may have the particular nucleic acid molecule inherited through a female parent or through a male parent. The second plant may be an inbred plant. The crossed fertile transgenic may be a hybrid. Also included within the present invention are seeds of any of these
5 crossed fertile transgenic plants.

The present invention also provides a method to identify a nucleotide sequence that directs transcription of nucleic acid in the genome of a plant cell in response to pathogen exposure, by contacting a probe comprising plant nucleic acid, e.g., cRNA, isolated from tissues of a plant contacted with the pathogen,
10 with a plurality of isolated nucleic acid samples on a plurality of solid substrates, wherein each sample is a plurality of oligonucleotides corresponding to at least a portion of a plant gene, so as to form a complex between at least a portion of the probe and a nucleic acid sample(s) having sequences that are structurally related to the sequences in the probe. Then complex formation is determined or
15 detected to determine which samples represent genes comprising promoters that are responsive to infection with the pathogen. The probe and/or samples may be nucleic acid from a dicot or from a monocot.

A method to shuffle the nucleic acid molecules of the invention is provided. This method involves fragmentation of a (parent) nucleic acid
20 molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-684 and 792-795, the ortholog thereof, or the corresponding gene thereof, followed by religation. This method allows for the production of polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule. Accordingly, the invention provides cells and transgenic plants
25 containing nucleotide sequences produced through shuffling that encode polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule.

A computer readable medium containing the nucleic acid sequences of the invention as well as methods of use for the computer readable medium are
30 provided. This medium allows a nucleic acid molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795 to be used as a reference sequence to search against databases. This medium also allows for computer-based manipulation of a nucleic acid sequence

corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795, and the corresponding gene or polypeptide encoded by the nucleic acid sequence.

5

Brief Description of the Figures

Figure 1 depicts *RPP*-dependent defense pathways.

Figure 2 depicts nucleotide sequences including the promoter region and motifs therein for genes, the expression of which is altered in response to pathogen infection (SEQ ID NOs: 774-788).

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Figure 3 is a schematic of the overlap in genes that are induced early after *P. parasitica* infection and in a *RPP8*-specific manner, genes that are induced late after infection and in a *RPP8*-specific manner, and genes induced early and late after infection in a *RPP7*-specific manner.

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Figure 4 shows a schematic of *RPP4*-pathway, *RPP7*-pathway and *RPP8*-upregulated transcription factor genes.

Detailed Description of the Invention

Definitions

20

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base which is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated.

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Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzner et al., 1991; Ohtsuka et al., 1985; Rossolini et al., 1994). A "nucleic acid fragment" is a fraction of a given nucleic acid molecule. In higher plants, deoxyribonucleic

acid (DNA) is the genetic material while ribonucleic acid (RNA) is involved in the transfer of information contained within DNA into proteins. The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. The terms "nucleic acid", "nucleic acid molecule", "nucleic acid fragment" or "nucleic acid sequence or segment" may also be used interchangeably with gene, cDNA, DNA and RNA encoded by a gene.

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or an "isolated" or "purified" polypeptide is a DNA molecule or polypeptide that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or polypeptide may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In one embodiment, an "isolated" nucleic acid is free of sequences that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein or polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention, or biologically active portion thereof, is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein-of-interest chemicals. Fragments and variants of the disclosed nucleotide sequences and proteins or partial-length proteins encoded thereby are also encompassed by the present invention. By "fragment" or "portion" is meant a full length or less than

full length of the nucleotide sequence encoding, or the amino acid sequence of, a polypeptide or protein. Alternatively, fragments or portions of a nucleotide sequence that are useful as hybridization probes generally do not encode fragment proteins retaining biological activity. Thus, fragments or portions of a nucleotide sequence may range from at least about 9 nucleotides, about 12 nucleotides, about 20 nucleotides, about 50 nucleotides, about 100 nucleotides or more.

The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. For example, gene refers to a nucleic acid fragment that expresses mRNA, functional RNA, or specific protein, including regulatory sequences. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

"Naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a protein or nucleotide sequence present in an organism (including a virus), which can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

A "marker gene" encodes a selectable or screenable trait.

"Selectable marker" is a gene whose expression in a cell gives the cell a selective advantage. The selective advantage possessed by the cells transformed with the selectable marker gene may be due to their ability to grow in the presence of a negative selective agent, such as an antibiotic or a herbicide, compared to the growth of non-transformed cells. The selective advantage possessed by the transformed cells, compared to non-transformed cells, may also be due to their enhanced or novel capacity to utilize an added compound as a nutrient, growth factor or energy source. Selectable marker gene also refers to a gene or a combination of genes whose expression in a cell gives the cell both a negative and/or a positive selective advantage.

The term "chimeric" refers to any gene or DNA that contains 1) DNA

sequences, including regulatory and coding sequences, that are not found together in nature, or 2) sequences encoding parts of proteins not naturally adjoined, or 3) parts of promoters that are not naturally adjoined. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are
5 derived from different sources, or comprise regulatory sequences and coding sequences derived from the same source, but arranged in a manner different from that found in nature.

A "transgene" refers to a gene that has been introduced into the genome by transformation and is stably maintained. Transgenes may include, for
10 example, DNA that is either heterologous or homologous to the DNA of a particular plant to be transformed. Additionally, transgenes may comprise native genes inserted into a non-native organism, or chimeric genes. The term "endogenous gene" refers to a native gene in its natural location in the genome of an organism. A "foreign" gene refers to a gene not normally found in the host
15 organism but that is introduced by gene transfer.

The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

By "variants" is intended substantially similar sequences. For nucleotide sequences, variants include those sequences that, because of the degeneracy of
20 the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those
25 generated, for example, by using site-directed mutagenesis which encode the native protein, as well as those that encode a polypeptide having amino acid substitutions. Generally, nucleotide sequence variants of the invention will have at least 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g.,
30 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98%, sequence identity to the native (endogenous) nucleotide sequence.

"DNA shuffling" is a method to introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The

DNA molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA preferably encodes a variant polypeptide modified with respect to the polypeptide encoded by the template DNA, and may
5 have an altered biological activity with respect to the polypeptide encoded by the template DNA.

The nucleic acid molecules of the invention can be optimized for enhanced expression in plants of interest. See, for example, EPA035472; WO91/16432; Perlak et al., 1991; and Murray et al., 1989. In this manner, the
10 genes or gene fragments can be synthesized utilizing plant-preferred codons. See, for example, Campbell and Gowri, 1990 for a discussion of host-preferred codon usage. Thus, the nucleotide sequences can be optimized for expression in any plant. It is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may
15 also be used. Variant nucleotide sequences and proteins also encompass sequences and protein derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different coding sequences can be manipulated to create a new polypeptide possessing the desired properties. In this manner, libraries of recombinant polynucleotides are
20 generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer, 1994; Stemmer, 1994; Cramer et al., 1997; Moore et al., 1997; Zhang et al., 1997; Cramer et al., 1998; and
25 U.S. Patent Nos. 5,605,793 and 5,837,458.

"Conservatively modified variations" of a particular nucleic acid sequence refers to those nucleic acid sequences that encode identical or essentially identical amino acid sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences.
30 Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the

encoded protein. Such nucleic acid variations are "silent variations" which are one species of "conservatively modified variations." Every nucleic acid sequence described herein which encodes a polypeptide also describes every possible silent variation, except where otherwise noted. One of skill will
5 recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each "silent variation" of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

"Recombinant DNA molecule" is a combination of DNA sequences that
10 are joined together using recombinant DNA technology and procedures used to join together DNA sequences as described, for example, in Sambrook et al., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (1989).

The terms "heterologous DNA sequence," "exogenous DNA segment" or "heterologous nucleic acid," each refer to a sequence that originates from a
15 source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the
20 terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" DNA sequence is a DNA sequence that is naturally
25 associated with a host cell into which it is introduced.

"Wild-type" refers to the normal gene, or organism found in nature without any known mutation.

"Genome" refers to the complete genetic material of an organism.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or
30 *Agrobacterium* binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

Specifically included are shuttle vectors by which is meant a DNA vehicle capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eukaryotic (e.g. higher plant, mammalian, yeast or fungal cells).

5 "Cloning vectors" typically contain one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector. Marker genes typically
10 include genes that provide tetracycline resistance, hygromycin resistance or ampicillin resistance.

"Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of
15 interest which is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the
20 nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. The expression of the nucleotide sequence in the expression cassette may be under
25 the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, the promoter can also be specific to a particular tissue or organ or stage of development.

Such expression cassettes will comprise the transcriptional initiation
30 region of the invention linked to a nucleotide sequence of interest. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene of interest to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

The transcriptional cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau et al., 1991; Proudfoot, 1991; Sanfacon et al., 1991; Mogen et al., 1990; Munroe et al., 1990; Ballas et al., 1989; Joshi et al., 1987.

An oligonucleotide corresponding to a nucleic acid molecule of the invention may be about 30 or fewer nucleotides in length (e.g., 9, 12, 15, 18, 20, 21 or 24, or any number between 9 and 30). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16-24 nucleotides in length may be preferred. Those skilled in the art are well versed in the design of primers for use processes such as PCR. If required, probing can be done with entire restriction fragments of the gene disclosed herein which may be 100's or even 1000's of nucleotides in length.

"Coding sequence" refers to a DNA or RNA sequence that codes for a specific amino acid sequence and excludes the non-coding sequences. It may constitute an "uninterrupted coding sequence", i.e., lacking an intron, such as in a cDNA or it may include one or more introns bounded by appropriate splice junctions. An "intron" is a sequence of RNA which is contained in the primary transcript but which is removed through cleavage and re-ligation of the RNA within the cell to create the mature mRNA that can be translated into a protein.

The terms "open reading frame" and "ORF" refer to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence. The terms "initiation codon" and "termination codon" refer to a unit of three adjacent nucleotides ('codon') in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation).

A "functional RNA" refers to an antisense RNA, ribozyme, or other RNA that is not translated.

The term "RNA transcript" refers to the product resulting from RNA polymerase catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without introns and that can be translated into protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA.

"Regulatory sequences" and "suitable regulatory sequences" each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, promoters, translation leader sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. As is noted above, the term "suitable regulatory sequences" is not limited to promoters. However, some suitable regulatory sequences useful in the present invention will include, but are not limited to constitutive plant promoters, plant tissue-specific promoters, plant development specific promoters, inducible plant promoters and viral promoters.

"5' non-coding sequence" refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency (Turner et al., 1995).

"3' non-coding sequence" refers to nucleotide sequences located 3' (downstream) to a coding sequence and include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al., 1989.

The term "translation leader sequence" refers to that DNA sequence portion of a gene between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency.

The term "mature" protein refers to a post-translationally processed polypeptide without its signal peptide. "Precursor" protein refers to the primary product of translation of an mRNA. "Signal peptide" refers to the amino terminal extension of a polypeptide, which is translated in conjunction with the polypeptide forming a precursor peptide and which is required for its entrance into the secretory pathway. The term "signal sequence" refers to a nucleotide sequence that encodes the signal peptide.

The term "intracellular localization sequence" or "signal sequence" refers to a nucleotide sequence that encodes an intracellular targeting signal. An "intracellular targeting signal" is an amino acid sequence that is translated in conjunction with a protein and directs it to a particular sub-cellular compartment. "Endoplasmic reticulum (ER) stop transit signal" refers to a carboxy-terminal extension of a polypeptide, which is translated in conjunction with the polypeptide and causes a protein that enters the secretory pathway to be retained in the ER. "ER stop transit sequence" refers to a nucleotide sequence that encodes the ER targeting signal. Other intracellular targeting sequences encode targeting signals active in seeds and/or leaves and vacuolar targeting signals.

"Promoter" refers to a nucleotide sequence, usually upstream (5') to its coding sequence, which controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription. "Promoter" includes a minimal promoter that is a short DNA sequence comprised of a TATA- box and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. "Promoter" also refers to a nucleotide sequence that includes a minimal promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence which can stimulate promoter activity and may be an innate

element of the promoter or a heterologous element inserted to enhance the level or tissue specificity of a promoter. It is capable of operating in both orientations (normal or flipped), and is capable of functioning even when moved either upstream or downstream from the promoter. Both enhancers and other upstream promoter elements bind sequence-specific DNA-binding proteins that mediate their effects. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even be comprised of synthetic DNA segments. A promoter may also contain DNA sequences that are involved in the binding of protein factors which control the effectiveness of transcription initiation in response to physiological or developmental conditions.

The "initiation site" is the position surrounding the first nucleotide that is part of the transcribed sequence, which is also defined as position +1. With respect to this site all other sequences of the gene and its controlling regions are numbered. Downstream sequences (i.e. further protein encoding sequences in the 3' direction) are denominated positive, while upstream sequences (mostly of the controlling regions in the 5' direction) are denominated negative.

Promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation are referred to as "minimal or core promoters." In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription. A "minimal or core promoter" thus consists only of all basal elements needed for transcription initiation, e.g., a TATA box and/or an initiator.

"Constitutive expression" refers to expression using a constitutive or regulated promoter. "Conditional" and "regulated expression" refer to expression controlled by a regulated promoter.

"Constitutive promoter" refers to a promoter that is able to express the gene that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant. Each of the transcription-activating elements do not exhibit an absolute tissue-specificity, but mediate transcriptional activation in most plant parts at a level of $\geq 1\%$ of the level reached in the part of the plant in which transcription is most active.

"Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and

include both tissue-specific and inducible promoters. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. New promoters of various types useful in plant cells are constantly being discovered, numerous examples may be found in the compilation by Okamuro et al., 1989. Since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of different lengths may have identical promoter activity.

Typical regulated promoters useful in plants include but are not limited to safener-inducible promoters, promoters derived from the tetracycline-inducible system, promoters derived from salicylate-inducible systems, promoters derived from alcohol-inducible systems, promoters derived from glucocorticoid-inducible system, promoters derived from pathogen-inducible systems, and promoters derived from ecdysome-inducible systems.

"Tissue-specific promoter" refers to regulated promoters that are not expressed in all plant cells but only in one or more cell types in specific organs (such as leaves or seeds), specific tissues (such as embryo or cotyledon), or specific cell types (such as leaf parenchyma or seed storage cells). These also include promoters that are temporally regulated, such as in early or late embryogenesis, during fruit ripening in developing seeds or fruit, in fully differentiated leaf, or at the onset of senescence.

"Inducible promoter" refers to those regulated promoters that can be turned on in one or more cell types by an external stimulus, such as a chemical, light, hormone, stress, or a pathogen.

"Operably-linked" refers to the association of nucleic acid sequences on single nucleic acid fragment so that the function of one is affected by the other. For example, a regulatory DNA sequence is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (i.e., that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can be operably-linked to regulatory sequences in sense or antisense orientation.

"Expression" refers to the transcription and/or translation of an endogenous gene or a transgene in plants. For example, in the case of antisense constructs, expression may refer to the transcription of the antisense DNA only. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA. Expression may also refer to the production of protein.

"Altered levels" refers to the level of expression in transgenic cells or organisms that differs from that of normal or untransformed cells or organisms.

"Overexpression" refers to the level of expression in transgenic cells or organisms that exceeds levels of expression in normal or untransformed cells or organisms.

"Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of protein from an endogenous gene or a transgene.

"Co-suppression" and "transwitch" each refer to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar transgene or endogenous genes (U.S. Patent No. 5,231,020).

"Gene silencing" refers to homology-dependent suppression of viral genes, transgenes, or endogenous nuclear genes. Gene silencing may be transcriptional, when the suppression is due to decreased transcription of the affected genes, or post-transcriptional, when the suppression is due to increased turnover (degradation) of RNA species homologous to the affected genes. (English et al., 1996). Gene silencing includes virus-induced gene silencing (Ruiz et al., 1998).

"Silencing suppressor" gene refers to a gene whose expression leads to counteracting gene silencing and enhanced expression of silenced genes. Silencing suppressor genes may be of plant, non-plant, or viral origin. Examples include, but are not limited to HC-Pro, P1-HC-Pro, and 2b proteins. Other examples include one or more genes in TGMV-B genome.

"Transcription stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as polyadenylation signal sequences, capable of terminating transcription. Examples include the 3' non-regulatory regions of genes encoding nopaline synthase and the small subunit of ribulose biphosphate carboxylase.

"Translation stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as one or more termination codons in all three frames, capable of terminating translation. Insertion of a translation stop fragment adjacent to or near the initiation codon at the 5' end of the coding
5 sequence will result in no translation or improper translation. Excision of the translation stop fragment by site-specific recombination will leave a site-specific sequence in the coding sequence that does not interfere with proper translation using the initiation codon.

The terms "*cis*-acting sequence" and "*cis*-acting element" refer to DNA or
10 RNA sequences whose functions require them to be on the same molecule. An example of a *cis*-acting sequence on the replicon is the viral replication origin.

The terms "*trans*-acting sequence" and "*trans*-acting element" refer to DNA or RNA sequences whose function does not require them to be on the same molecule.

15 "Chromosomally-integrated" refers to the integration of a foreign gene or DNA construct into the host DNA by covalent bonds. Where genes are not "chromosomally integrated" they may be "transiently expressed." Transient expression of a gene refers to the expression of a gene that is not integrated into the host chromosome but functions independently, either as part of an
20 autonomously replicating plasmid or expression cassette, for example, or as part of another biological system such as a virus.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence
25 identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full length cDNA or gene sequence, or the complete cDNA or gene sequence.

30 (b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller, 1988; the local homology algorithm of Smith et al., 1981; the homology alignment algorithm of Needleman and Wunsch, 1970; the search-for-similarity-method of Pearson and Lipman, 1988; the algorithm of Karlin and Altschul, 1990, modified as in Karlin and Altschul, 1993.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al., 1988; Higgins et al., 1989; Corpet et al., 1988; Huang et al., 1992; and Pearson et al., 1994. The ALIGN program is based on the algorithm of Myers and Miller, *supra*. The BLAST programs of Altschul et al., 1990, are based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., 1990). These initial neighborhood word hits act as seeds for initiating searches to find

longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al., 1997. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al., *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g. BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989). See <http://www.ncbi.nlm.nih.gov>. Alignment may also be performed manually by inspection.

For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein is preferably made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By

5 "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

(c) As used herein, "sequence identity" or "identity" in the context of two
10 nucleic acid or polypeptide sequences makes reference to a specified percentage of residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window, as measured by sequence comparison algorithms or by visual inspection. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions
15 which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted
20 upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity.
25 Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

30 (d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal

alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, and most preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 70%, more preferably at least 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions (see below). Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%,

75%, 76%, 77%, 78%, or 79%, preferably 80%, 81%, 82%, 83%, 84%, 85%,
86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or
94%, or even more preferably, 95%, 96%, 97%, 98% or 99%, sequence identity
to the reference sequence over a specified comparison window. Preferably,
5 optimal alignment is conducted using the homology alignment algorithm of
Needleman and Wunsch, 1970. An indication that two peptide sequences are
substantially identical is that one peptide is immunologically reactive with
antibodies raised against the second peptide. Thus, a peptide is substantially
identical to a second peptide, for example, where the two peptides differ only by
10 a conservative substitution.

For sequence comparison, typically one sequence acts as a reference
sequence to which test sequences are compared. When using a sequence
comparison algorithm, test and reference sequences are input into a computer,
subsequence coordinates are designated if necessary, and sequence algorithm
15 program parameters are designated. The sequence comparison algorithm then
calculates the percent sequence identity for the test sequence(s) relative to the
reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are
substantially identical is that the two molecules hybridize to each other under
20 stringent conditions. The phrase "hybridizing specifically to" refers to the
binding, duplexing, or hybridizing of a molecule only to a particular nucleotide
sequence under stringent conditions when that sequence is present in a complex
mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to
complementary hybridization between a probe nucleic acid and a target nucleic
25 acid and embraces minor mismatches that can be accommodated by reducing the
stringency of the hybridization media to achieve the desired detection of the
target nucleic acid sequence.

"Stringent hybridization conditions" and "stringent hybridization wash
conditions" in the context of nucleic acid hybridization experiments such as
30 Southern and Northern hybridizations are sequence dependent, and are different
under different environmental parameters. Longer sequences hybridize
specifically at higher temperatures. The T_m is the temperature (under defined
ionic strength and pH) at which 50% of the target sequence hybridizes to a
perfectly matched probe. Specificity is typically the function of post-

hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, 1984; $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with >90% identity are sought, the T_m can be decreased 10°C . Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

An example of highly stringent wash conditions is 0.15 M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2X SSC wash at 65°C for 15 minutes (see, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1X SSC at 45°C for 15 minutes.

An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6X SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, more preferably about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C and at least about 60°C for long probes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2X (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.

The following are examples of sets of hybridization/wash conditions that may be used to clone orthologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5

M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with
5 washing in 0.1X SSC, 0.1% SDS at 65°C.

By "variant" polypeptide is intended a polypeptide derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native
10 protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

Thus, the polypeptides of the invention may be altered in various ways
15 including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the polypeptides can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel, 1985; Kunkel et al., 1987; U.
20 S. Patent No. 4,873,192; Walker and Gaastra, 1983, and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff et al., 1978, herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar
25 properties, are preferred.

Thus, the genes and nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant forms. Likewise, the polypeptides of the invention encompass both naturally occurring proteins as well as variations and modified forms thereof. Such variants will continue to
30 possess the desired activity. The deletions, insertions, and substitutions of the polypeptide sequence encompassed herein are not expected to produce radical changes in the characteristics of the polypeptide. However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of

doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays.

Individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%,
5 more typically less than 1%) in an encoded sequence are "conservatively modified variations," where the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative
10 substitutions for one another: Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I); Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine (N), Glutamine (Q). See also, Creighton, 1984. In addition,
15 individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also "conservatively modified variations."

"Production tissue" refers to mature, harvestable tissue consisting of non-dividing, terminally-differentiated cells. It excludes young, growing tissue
20 consisting of germline, meristematic, and not-fully-differentiated cells.

"Germline cells" refer to cells that are destined to be gametes and whose genetic material is heritable.

The word "plant" refers to any plant, particularly to seed plant, and "plant cell" is a structural and physiological unit of the plant, which comprises a cell
25 wall but may also refer to a protoplast. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

"Plant tissue" includes differentiated and undifferentiated tissues or plants, including but not limited to roots, stems, shoots, leaves, pollen, seeds,
30 tumor tissue and various forms of cells and culture such as single cells, protoplast, embryos, and callus tissue. The plant tissue may be in plants or in organ, tissue or cell culture.

The term "altered plant trait" means any phenotypic or genotypic change in a transgenic plant relative to the wild-type or non-transgenic plant host.

The term "transformation" refers to the transfer of a nucleic acid fragment into the genome of a host cell, resulting in genetically stable inheritance. Host cells containing the transformed nucleic acid fragments are referred to as "transgenic" cells, and organisms comprising transgenic cells are referred to as "transgenic organisms". Examples of methods of transformation of plants and plant cells include *Agrobacterium*-mediated transformation (De Blaere et al., 1987) and particle bombardment technology (Klein et al., 1987; U.S. Patent No. 4,945,050). Whole plants may be regenerated from transgenic cells by methods well known to the skilled artisan (see, for example, Fromm et al., 1990).

"Transformed," "transgenic," and "recombinant" refer to a host cell or organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome generally known in the art and are disclosed in Sambrook et al., 1989. See also Innis et al., 1995; and Gelfand, 1995; and Innis and Gelfand, 1999. Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially mismatched primers, and the like. For example, "transformed," "transformant," and "transgenic" plants or calli have been through the transformation process and contain a foreign gene integrated into their chromosome. The term "untransformed" refers to normal plants that have not been through the transformation process.

A "transgenic plant" is a plant having one or more plant cells that contain an expression vector.

"Transiently transformed" refers to cells in which transgenes and foreign DNA have been introduced (for example, by such methods as *Agrobacterium*-mediated transformation or biolistic bombardment), but not selected for stable maintenance.

"Stably transformed" refers to cells that have been selected and regenerated on a selection media following transformation.

"Transient expression" refers to transgene expression in cells, e.g., after transformation with recombinant virus or by such methods as *Agrobacterium*-mediated transformation, electroporation, or biolistic bombardment, but not selected for its stable maintenance.

"Genetically stable" and "heritable" refer to chromosomally-integrated genetic elements that are stably maintained in the plant and stably inherited by progeny through successive generations.

5 "Primary transformant" and "T0 generation" refer to transgenic plants that are of the same genetic generation as the tissue which was initially transformed (i.e., not having gone through meiosis and fertilization since transformation).

"Secondary transformants" and the "T1, T2, T3, etc. generations" refer to transgenic plants derived from primary transformants through one or more meiotic and fertilization cycles. They may be derived by self-fertilization of
10 primary or secondary transformants or crosses of primary or secondary transformants with other transformed or untransformed plants.

"Significant increase" is an increase that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater.

15 "Significantly less" means that the decrease is larger than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater.

I. The Nucleic Acid Molecules of the Invention and Polypeptide Encoded

20 Thereby

This invention relates to isolated plant, e.g., *Arabidopsis* and rice, nucleic acid molecules, sequences and segments (fragments), the expression of which is altered in response to pathogen infection, as well as the endogenous plant promoters for those expressed molecules, sequences or segments. However, the
25 expression of these genes may also be altered in response to non-pathogens, e.g., in response to environmental stimuli. The nucleic acid molecules can be used in pathogen control strategies, e.g., by overexpressing nucleic acid molecules which can confer tolerance to a cell, or by altering the expression of host genes which are required for pathogen infection, e.g., by "knocking out" the expression of at
30 least one genomic copy of the gene. Plants having genetic disruptions in host genes may be less susceptible to infection, e.g., due to a decrease or absence of a host protein needed for infection, or, alternatively, hypersusceptible to infection. Plants that are hypersusceptible to infection may be useful to prepare transgenic

plants as the expression of the gene(s) which was disrupted may be related to gene silencing.

- Preferred sources for the nucleic acid molecules of the invention include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.),
- oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Wolffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wolffella* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*, *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*).
- Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt, *Biosystematic Investigation on the Family of Duckweeds: The family of*

Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula,

Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia.

- Other vegetable sources (and databases to identify orthologs of the invention) for the nucleic acid sequences of the invention include those are shown in Table 1.

Table 1

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber		http://www.cucurbit.org/
	<i>Cucumis melo</i>	Melon		http://genome.cornell.edu/cgc/
	<i>Citrullus lanatus</i>	Watermelon		
	<i>Cucurbita pepo</i>	Squash – summer		
	<i>Cucurbita maxima</i>	Squash - winter		
	<i>Cucurbita moschata</i>	Pumpkin /butternut		
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	<ul style="list-style-type: none"> 15x BAC on variety Heinz 1706 order from Clemson Genome center (www.genome.clemson.edu) 11.6x BAC of L. cheesmanii (originates from J. Giovannoni) available from Clemson genome center (www.genome.clemson.edu) EST collection 	genome.cornell.edu/solgenes http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=solgenes http://genome.cornell.edu/tgc/ http://tgrc.ucdavis.edu/

			<p>from TIGR (www.tigr.org/tb/lgi/index.html)</p> <ul style="list-style-type: none"> • EST collection from Clemson Genome Center (www.genome.clemson.edu) • TAG 99:254-271, 1999 (esculentum x pennelli) • TAG 89:1007-1013, 1994 (peruvianum) • Plant Cell Reports 12:293-297, 1993 (RAPDs) • Genetics 132:1141-1160, 1992 (potato x tomato) • Genetics 120:1095-1105, 1988 (RFLP potato and tomato) • Genetics 115:387-393, 1986 (esculentum x pennelli isozyme and cDNAs) 	
	<i>Capsicum annuum</i>	Pepper		http://neptune.netimages.com/~chile/science.html
	<i>Capsicum frutescens</i>	Chile pepper		
	<i>Solanum melongena</i>	Eggplant		
	(<i>Nicotiana tabacum</i>)	(Tobacco)		
	(<i>Solanum tuberosum</i>)	(Potato)		
	(<i>Petunia x hybrida hort. ex E. Vilm.</i>)	(Petunia)	4x BAC of <i>Petunia hybrida</i> 7984 available from	

			Clemson genome center (www.genome.clemson.edu)	
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Brassicaceae	<i>Brassica oleracea</i> L. var. <i>italica</i>	Broccoli		http://res.agr.ca/ecorc/cwmt/crucifer/traits/index.htm http://geneous.cit.cornell.edu/cabbage/aboutcab.html
	<i>Brassica oleracea</i> L. var. <i>capitata</i>	Cabbage		
	<i>Brassica rapa</i>	Chinese Cabbage		
	<i>Brassica oleracea</i> L. var. <i>botrytis</i>	Cauliflower		
	<i>Raphanus sativus</i> var. <i>niger</i>	Daikon		
	(<i>Brassica napus</i>)	(Oilseed rape)		http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb
		Arabidopsis	12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=agr
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Umbelliferae	<i>Daucus carota</i>	Carrot		
Compositae	<i>Lactuca sativa</i>	Lettuce		
	<i>Helianthus annuus</i>	(Sunflower)		
Total				
Chenopodiaceae	<i>Spinacia oleracea</i>	Spinach		
	(<i>Beta vulgaris</i>)	(Sugar Beet)		
Total				

Leguminosae	<i>Phaseolus vulgaris</i>	Bean	4.3x BAC available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=beanges
	<i>Pisum sativum</i>	Pea		
	(<i>Glycine max</i>)	(Soybean)	7.5x and 7.9x BACs available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase
Total			http://www.nal.usda.gov/pgdic/Map_projects/	
Gramineae	<i>Zea mays</i>	Sweet Corn	Novartis BACs for Mo17 and B73 have been donated to Clemson Genome Center (www.genome.clemson.edu)	
	(<i>Zea mays</i>)	(Field Corn)		http://www.agron.missouri.edu/mnl/
Total			http://www.nal.usda.gov/pgdic/Map_projects/	
Liliaceae	<i>Allium cepa</i>	Onion		
		Leek		
		(Garlic)		
		(Asparagus)		
Total			http://www.nal.usda.gov/pgdic/Map_projects/	

Preferred forage and turf grass nucleic acid sources for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop. Preferably, the nucleic acid sources are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.), and even more preferably corn and soybean.

According to one embodiment, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence obtained or obtainable

from any plant gene which encodes a polypeptide having at least 70% amino acid sequence identity to a polypeptide encoded by SEQ ID NOs. 1-684 or 789-795, or a promoter for said gene. Thus, based on the *Arabidopsis* nucleic acid sequences of the present invention, orthologs of those sequences may be identified or isolated from the genome of any desired organism, preferably from another plant, according to well known techniques based on their sequence similarity to the *Arabidopsis* coding sequences, e.g., hybridization, PCR or computer generated sequence comparisons. For example, all or a portion of a particular *Arabidopsis* sequence is used as a probe that selectively hybridizes to other gene sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen source organism. Further, suitable genomic and cDNA libraries may be prepared from any cell or tissue of an organism. Such techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g., Sambrook et al., 1989) and amplification by PCR using oligonucleotide primers preferably corresponding to sequence domains conserved among related polypeptide or subsequences of the nucleotide sequences provided herein (see, e.g., Innis et al., 1990). These methods are particularly well suited to the isolation of gene sequences from organisms closely related to the organism from which the probe sequence is derived. The application of these methods using the *Arabidopsis* coding sequences as probes is well suited for the isolation of gene sequences from any source organism, preferably other plant species. In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art as discussed hereinabove.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P , or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the

sequence of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook et al., 1989. In general, sequences that hybridize to the sequences disclosed herein will have at least 40% to 50%, about
5 60% to 70% and even about 80% 85%, 90%, 95% to 98% or more identity with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

The nucleic acid molecules of the invention can also be identified by, for
10 example, a search of known databases for genes encoding polypeptides having a specified amino acid sequence identity. Methods of alignment of sequences for comparison are well known in the art and are described hereinabove.

II. Expression Cassettes of the Invention

15 The present invention also encompasses expression cassettes, preferably in the form of a recombinant vectors comprising the nucleic acid sequences of the invention. In such vectors, the expression cassette comprises regulatory elements for expression of the nucleotide sequences in a host cell capable of expressing the nucleotide sequences. Such regulatory elements usually comprise
20 promoter and termination signals and preferably also comprise elements allowing efficient translation of polypeptides encoded by the nucleic acid sequences of the present invention. For efficient initiation of translation, sequences adjacent to the initiating methionine may require modification. For example, they can be modified by the inclusion of sequences known to be
25 effective in plants. Joshi (1987) has suggested an appropriate consensus for plants and Clontech suggests a further consensus translation initiator (1993/1994 catalog, page 210). These consensus are suitable for use with the nucleotide sequences of this invention. The sequences are incorporated into constructions comprising the nucleotide sequences, up to and including the ATG (whilst
30 leaving the second amino acid unmodified), or alternatively up to and including the GTC subsequent to the ATG (with the possibility of modifying the second amino acid of the transgene).

Vectors comprising the nucleic acid sequences are usually capable of replication in particular host cells, e.g., as extrachromosomal molecules, and are

therefore used to amplify the nucleic acid sequences of this invention in the host cells. In a preferred embodiment, host cells for such vectors are plant cells.

A. Promoters and Enhancers

Expression of the nucleotide sequences in transgenic plants is driven by
5 promoters shown to be functional in plants. The choice of promoter will vary
depending on the temporal and spatial requirements for expression, and also
depending on the target species. In many cases, expression in multiple tissues is
desirable. Although many promoters from dicotyledons have been shown to be
operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters
10 are selected for expression in dicotyledons, and monocotyledonous promoters for
expression in monocotyledons. However, there is no restriction to the
provenance of selected promoters; it is sufficient that they are operational in
driving the expression of the nucleotide sequences in the desired cell.

These promoters include, but are not limited to, constitutive, inducible,
15 temporally regulated, developmentally regulated, chemically regulated, stress-
responsive, tissue-preferred and tissue-specific promoters. Promoter sequences
are known to be strong or weak. A strong promoter provides for a high level of
gene expression, whereas a weak promoter provides for a very low level of gene
expression. An inducible promoter is a promoter that provides for the turning on
20 and off of gene expression in response to an exogenously added agent, or to an
environmental or developmental stimulus. A bacterial promoter such as the P_{tac}
promoter can be induced to varying levels of gene expression depending on the
level of isothiopyrogalactoside added to the transformed bacterial cells. An
isolated promoter sequence that is a strong promoter for heterologous nucleic
25 acid is advantageous because it provides for a sufficient level of gene expression
to allow for easy detection and selection of transformed cells and provides for a
high level of gene expression when desired.

Preferred promoters that are expressed constitutively include promoters
from genes encoding actin or ubiquitin and the CaMV 35S and 19S promoters.
30 The nucleotide sequences of this invention can also be expressed under the
regulation of promoters that are chemically regulated. This enables the nucleic
acid sequence or encoded polypeptide to be synthesized only when the crop
plants are treated with the inducing chemicals. Preferred technology for
chemical induction of gene expression is detailed in the published application EP

0 332 104 (to Ciba-Geigy) and U.S. Patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

Tissue-specific or tissue-preferential promoters useful in the present invention. Also useful are promoters which confer seed-specific expression, such as those disclosed by Schernthaner et al., 1988; anther (tapetal) specific promoter B6 (Huffman et al.); and pistil-specific promoters such as a modified S13 promoter (Dzelkalns et al., 1993).

Preferred tissue specific expression patterns include green tissue-specific, root-specific, stem-specific, and flower-specific. Promoters suitable for expression in green tissue include many which regulate genes involved in photosynthesis and many of these have been cloned from both monocotyledons and dicotyledons. A preferred promoter is the maize PEPC promoter from the phosphoenol carboxylase gene (Hudspeth & Grula, 1989). A preferred promoter for root-specific expression is that described by de Framond (1991; EP 0 452 269 to Ciba-Geigy). A preferred stem specific promoter is that described in U.S. Patent No. 5,625,136 (to Ciba-Geigy) and which drives expression of the maize *trpA* gene.

Other promoters which direct specific or enhanced expression in certain plant tissues will be known to those of skill in the art in light of the present disclosure. These include, for example, the *rbcS* promoter, specific for green tissue; the *ocs*, *nos*, and *mas* promoters which have higher activity in roots or wounded leaf tissue; a truncated (-90 to +8) 35S promoter which directs enhanced expression in roots, an tubulin gene that directs expression in roots and promoters derived from zein storage protein genes which direct expression in endosperm. It is particularly contemplated that one may advantageously use the 16 bp *ocs* enhancer element from the octopine synthase (*ocs*) gene (Bonchez et al., 1989), especially when present in multiple copies, to achieve enhanced expression in roots.

Preferred plant promoters include, but are not limited to, a promoter such as the CaMV 35S promoter, an enhanced 35S promoter or others such as CaMV 19S, *nos*, *Adh1*, sucrose synthase, α -tubulin, ubiquitin, actin, *cab*, PEPCase or those associated with the R gene complex. Further suitable promoters include the U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein

protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a 27 kD zein protein, the A20 promoter from the gene encoding a 19 kD -zein protein, inducible promoters, such as the light inducible promoter derived from the pea *rbcS* gene and the actin promoter from rice; seed specific promoters, such as the phaseolin promoter from beans, may also be used. Other promoters useful in the practice of the invention are known to those of skill in the art.

Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990,) corn alcohol dehydrogenase 1 (Vogel et al., 1992; Dennis et al., 1984), corn light harvesting complex (Simpson, 1985; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985; Rochester et al., 1986), pea small subunit RuBP carboxylase (Poulsen et al., 1986; Cashmore et al., 1983), Ti plasmid mannopine synthase (Langridge et al., 1989), Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991), α -tubulin, cab (Sullivan et al., 1989), PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters (Chandler et al., 1989), and chalcone synthase promoters (Franken et al., 1991).

Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

Several tissue-specific regulated genes and/or promoters have been reported in plants. These include genes encoding the seed storage proteins (such as napin, cruciferin, beta-conglycinin, and phaseolin) zein or oil body proteins (such as oleosin), or genes involved in fatty acid biosynthesis (including acyl carrier protein, stearyl-ACP desaturase, and fatty acid desaturases (fad 2-1)), and other genes expressed during embryo development (such as Bce4, see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific

expression is the pea vicilin promoter (Czako et al., 1992. (See also U.S. Pat. No. 5,625,136, herein incorporated by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from Arabidopsis (Gan et al., 1995, 270 (5244), 1986-8).

A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. 4,943,674, the disclosure of which is hereby incorporated by reference. cDNA clones that are preferentially expressed in cotton fiber have been isolated (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in U.S. Patent No. 4,535,060, U.S. Patent No. 4,769,061, U.S. Patent No. 4,801,590, and U.S. Patent No. 5,107,065, which disclosures are incorporated herein by reference.

Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an example of a developmentally-regulated fiber cell protein is E6 (John et al., 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

The tissue-specificity of some "tissue-specific" promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with "leaky" expression by a combination of different tissue-specific promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379). Several inducible promoters ("gene switches") have been reported. Many are described in the review by Gatz (1996 and 1997). These include tetracycline repressor system, *Lac* repressor system, copper-inducible systems, salicylate-inducible systems (such as the PR1a system), glucocorticoid- (Aoyama, 1997) and ecdysone-inducible systems. Also included are the benzene sulphonamide- (U.S. Patent No. 5,364,780) and alcohol- (WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters. Other studies have focused on genes inducibly regulated in response to

environmental stress or stimuli such as increased salinity, drought, pathogen and wounding. (Graham et al., 1985; Graham et al., 1985, Smith et al., 1986).

Accumulation of metallocarboxypeptidase-inhibitor protein has been reported in leaves of wounded potato plants (Graham et al., 1981). Other plant genes have
5 been reported to be induced methyl jasmonate, elicitors, heat-shock, anaerobic stress, or herbicide safeners.

Frequently it is desirable to have continuous or inducible expression of a DNA sequence throughout the cells of an organism in a tissue-independent manner. For example, increased resistance of a plant to infection by soil- and air
10 borne pathogens might be accomplished by genetic manipulation of the plant's genome to comprise a continuous promoter operably linked to a heterologous or -homologous pathogen-resistance gene such that pathogen-resistance proteins are continuously expressed throughout the plant's tissues.

Alternatively, it might be desirable to inhibit expression of a native DNA
15 sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive expression of the antisense sequence produces an RNA transcript that interferes with translation of the
20 mRNA of the native DNA sequence.

Other elements include those that can be regulated by endogenous or exogenous agents, e.g., by DNA binding proteins such as zinc finger proteins, including naturally occurring zinc finger proteins or chimeric zinc finger proteins (see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO
25 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311) or myb-like transcription factors. For example, a chimeric zinc finger protein may include amino acid sequences which bind to a specific DNA sequence (the zinc finger) and amino acid sequences that activate (e.g., GAL 4 sequences) or repress the transcription of the sequences linked to the specific
30 DNA sequence.

B. 5' and 3' Sequences

In addition to promoters, a variety of 3' transcriptional terminators are also available for use in the present invention. Transcriptional terminators are responsible for the termination of transcription and correct mRNA

polyadenylation. The 3' nontranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the tml terminator, the nopaline synthase terminator, the pea rbcS E9' terminator, the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato, although other 3' elements known to those of skill in the art can also be employed.

The 5' regulatory region of the expression cassette may also include other enhancing sequences. Numerous sequences have been found to enhance gene expression in transgenic plants. These include sequences which have been shown to enhance expression such as intron sequences (e.g., from *Adh1*, *bronzel* or the sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other leaders known in the art include but are not limited to: Picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5 noncoding region) (Elroy-Stein et al., 1989); Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison et al., 1986); MDMV leader (Maize Dwarf Mosaic Virus); Human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak et al., 1991); Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling et al., 1987; Tobacco mosaic virus leader (TMV), (Gallie et al., 1989; and Maize Chlorotic Mottle Virus leader (MCMV) (Lommel et al., 1991. See also, Della-Cioppa et al., 1987.

C. Targeting Sequences

It may be preferable to target expression of the nucleotide sequences of the present invention to different cellular localizations in the plant. In some cases, localization in the cytosol may be desirable, whereas in other cases, localization in some subcellular organelle, e.g., the nucleus, may be preferred. Subcellular

localization of transgene encoded enzymes is undertaken using techniques well known in the art. Typically, the DNA encoding the target peptide from a known organelle-targeted gene product is manipulated and fused upstream of the nucleotide sequence. Many such target sequences are known for the chloroplast and their functioning in heterologous constructions has been shown. The expression of the nucleotide sequences of the present invention is also targeted to the endoplasmic reticulum or to the vacuoles of the host cells. Techniques to achieve this are well-known in the art.

D. Marker Genes

10 In order to improve the ability to identify transformants, one may desire to employ a selectable or screenable marker gene as, or in addition to, the preselected nucleic acid sequence or segment. "Marker genes" are genes that impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker.

15 Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can 'select' for by chemical means, i.e., through the use of a selective agent (e.g., a herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing, i.e., by 'screening' (e.g., the R-locus trait). Of course, many examples of suitable

20 marker genes are known to the art and can be employed in the practice of the invention.

Included within the terms selectable or screenable marker genes are also genes which encode a "secretable marker" whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include

25 markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected by their catalytic activity. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA; small active enzymes detectable in extracellular solution (e.g., α -amylase, β -lactamase, phosphinothricin

30 acetyltransferase); and proteins that are inserted or trapped in the cell wall (e.g., proteins that include a leader sequence such as that found in the expression unit of extensin or tobacco PR-S).

With regard to selectable secretable markers, the use of a gene that encodes a polypeptide that becomes sequestered in the cell wall, and which polypeptide

includes a unique epitope is considered to be particularly advantageous. Such a secreted antigen marker would ideally employ an epitope sequence that would provide low background in plant tissue, a promoter-leader sequence that would impart efficient expression and targeting across the plasma membrane, and
5 would produce protein that is bound in the cell wall and yet accessible to antibodies. A normally secreted wall protein modified to include a unique epitope would satisfy all such requirements.

Elements of the present disclosure are exemplified in detail through the use of particular marker genes. However in light of this disclosure, numerous other
10 possible selectable and/or screenable marker genes will be apparent to those of skill in the art in addition to the one set forth herein below. Therefore, it will be understood that the following discussion is exemplary rather than exhaustive. In light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the present invention renders possible the
15 introduction of any gene, including marker genes, into a recipient cell to generate a transformed plant cell, e.g., a monocot cell.

Possible selectable markers for use in connection with the present invention include, but are not limited to, a *neo* gene, which codes for kanamycin resistance and can be selected for using kanamycin, G418, a gene encoding
20 resistance to bleomycin, and the like; a *bar* gene which codes for bialaphos resistance; a gene which encodes an altered EPSP synthase protein thus conferring glyphosate resistance; a nitrilase gene such as *bxn* from *Klebsiella ozaenae* which confers resistance to bromoxynil; a mutant acetolactate synthase gene (ALS) which confers resistance to imidazolinone, sulfonylurea or other
25 ALS-inhibiting chemicals (European Patent Application 154,204, 1985); a methotrexate-resistant DHFR gene; a dalapon dehalogenase gene that confers resistance to the herbicide dalapon; or a mutated anthranilate synthase gene that confers resistance to 5-methyl tryptophan. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a
30 suitable chloroplast transit peptide, CTP (European Patent Application 0 218 571, 1987).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the *bar* gene from *Streptomyces*

hygroscopicus or the *pat* gene from *Streptomyces viridochromogenes* (U.S. Patent No. 5,550,318). The enzyme phosphinothricin acetyltransferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, causing rapid accumulation of ammonia and cell death. The success in using this selective system in conjunction with monocots was particularly surprising because of the major difficulties which have been reported in transformation of cereals.

Screenable markers that may be employed include, but are not limited to, a β -glucuronidase or *uidA* gene (GUS) which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues; a β -lactamase gene, which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a *xy/E* gene which encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene; a tyrosinase gene which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to form the easily detectable compound melanin; a β -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene, which allows for bioluminescence detection; or an aequorin gene, which may be employed in calcium-sensitive bioluminescence detection, or a green fluorescent protein.

Genes from the maize R gene complex are contemplated to be particularly useful as screenable markers. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. Maize strains can have one, or as many as four, R alleles which combine to regulate pigmentation in a developmental and tissue specific manner. A gene from the R gene complex was applied to maize transformation, because the expression of this gene in transformed cells does not harm the cells. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line carries dominant alleles for genes encoding the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2), but carries a recessive allele at the R locus, transformation of any cell from that line with R will result in red pigment formation. Exemplary lines include Wisconsin 22

which contains the rg-Stadler allele and TR112, a K55 derivative which is r-g, b, Pl. Alternatively any genotype of maize can be utilized if the C1 and R alleles are introduced together.

A further screenable marker contemplated for use in the present invention is firefly luciferase, encoded by the *lux* gene. The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation counting, fluorescent spectrophotometry, low-light video cameras, photon counting cameras or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening.

E. Other Sequences

A vector of the invention can also further comprise plasmid DNA. Plasmid vectors include additional DNA sequences that provide for easy selection, amplification, and transformation of the expression cassette in prokaryotic and eukaryotic cells, e.g., pUC-derived vectors such as pUC8, pUC9, pUC18, pUC19, pUC23, pUC119, and pUC120, pSK-derived vectors, pGEM-derived vectors, pSP-derived vectors, or pBS-derived vectors. The additional DNA sequences include origins of replication to provide for autonomous replication of the vector, additional selectable marker genes, preferably encoding antibiotic or herbicide resistance, unique multiple cloning sites providing for multiple sites to insert DNA sequences or genes encoded in the expression cassette, and sequences that enhance transformation of prokaryotic and eukaryotic cells.

Another vector that is useful for expression in both plant and prokaryotic cells is the binary Ti plasmid (as disclosed in Schilperoort et al., U.S. Patent No. 4,940,838) as exemplified by vector pGA582. This binary Ti plasmid vector has been previously characterized by An, cited *supra*. This binary Ti vector can be replicated in prokaryotic bacteria such as *E. coli* and *Agrobacterium*. The *Agrobacterium* plasmid vectors can be used to transfer the expression cassette to dicot plant cells, and under certain conditions to monocot cells, such as rice cells. The binary Ti vectors preferably include the nopaline T DNA right and left borders to provide for efficient plant cell transformation, a selectable marker gene, unique multiple cloning sites in the T border regions, the *co/E1* replication of origin and a wide host range replicon. The binary Ti vectors carrying an

expression cassette of the invention can be used to transform both prokaryotic and eukaryotic cells, but is preferably used to transform dicot plant cells.

Virtually any DNA may be used for delivery to recipient cells to ultimately produce fertile transgenic plants in accordance with the present invention. For example, DNA segments in the form of vectors and plasmids, or linear DNA fragments, in some instance containing only the DNA element to be expressed in the plant, and the like, may be employed.

Vectors, plasmids, cosmids, YACs (yeast artificial chromosomes) and DNA segments for use in transforming such cells will, of course, generally comprise the cDNA, gene or genes which one desires to introduce into the cells. These DNA constructs can further include structures such as promoters, enhancers, polylinkers, or even regulatory genes as desired. The DNA segment or gene chosen for cellular introduction will often encode a protein which will be expressed in the resultant recombinant cells, such as will result in a screenable or selectable trait and/or which will impart an improved phenotype to the regenerated plant. However, this may not always be the case, and the present invention also encompasses transgenic plants incorporating non-expressed transgenes.

20 III. Transformation

The expression cassettes of the present invention can be introduced into a host cell, e.g., a plant cell, in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of cell, e.g., monocotyledonous or dicotyledonous, targeted for transformation. Vectors which may be used to transform plant tissue with the expression cassettes of the present invention include both *Agrobacterium* vectors and ballistic vectors, as well as vectors suitable for DNA-mediated transformation, e.g., direct uptake or via electroporation. However, cells other than plant cells may be transformed with the expression cassettes of the invention.

Suitable methods of transforming plant cells include, but are not limited to, microinjection (Crossway et al., 1986), direct DNA transfer to plant cells by PEG precipitation; liposomes; electroporation (Riggs et al., 1986, *Agrobacterium*-mediated transformation (Hinchey et al., 1988), direct gene transfer (Paszkowski et al., 1984), and ballistic particle acceleration using

devices available from Agracetus, Inc., Madison, Wis. and BioRad, Hercules, Calif. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al., 1988). Also see, Weissinger et al., 1988; Sanford et al., 1987 (onion); Christou et al., 1988 (soybean); McCabe et al., 1988 (soybean); Datta et al., 1990 (rice); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Fromm et al., 1990 (maize); and Gordon-Kamm et al., 1990 (maize); Svab et al., 1990 (tobacco chloroplast); Koziel et al., 1993 (maize); Shimamoto et al., 1989 (rice); Christou et al., 1991 (rice); European Patent Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., 1993 (wheat); Weeks et al., 1993 (wheat).

In one embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al., 1994.

The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate orthologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for transformation (Svab et al., 1990; Staub et al., 1992). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub et al., 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial *aadA* gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3'-adenyltransferase (Svab et al., 1993). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a

homoplastidic state. Plastid expression, in which genes are inserted by orthologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplastic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

Agrobacterium tumefaciens cells containing a vector comprising an expression cassette of the present invention, wherein the vector comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an *Agrobacterium tumefaciens* as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell. Numerous *Agrobacterium* vector systems useful in carrying out the present invention are known. For example, U.S. Pat. No. 4,459,355 discloses a method for transforming susceptible plants, including dicots, with an *Agrobacterium* strain containing the Ti plasmid. The transformation of woody plants with an *Agrobacterium* vector is disclosed in U.S. Patent No. 4,795,855. Further, U.S. Patent No. 4,940,838 to Schilperoort et al. discloses a binary *Agrobacterium* vector (i.e., one in which the *Agrobacterium* contains one plasmid having the vir region of a Ti plasmid but no T region, and a second plasmid having a T region but no vir region) useful in carrying out the present invention.

It is particularly preferred to use the binary type vectors of Ti and Ri plasmids of *Agrobacterium spp.* Ti-derived vectors transform a wide variety of higher plants, including monocotyledonous and dicotyledonous plants, such as soybean, cotton, rape, tobacco, and rice (Pacciotti et al., 1985; Byrne et al., 1987; Sukhapinda et al., 1987; Lorz et al., 1985; Potrykus, 1985; Park et al., 1985; Hiei et al., 1994. The use of T-DNA to transform plant cells has received extensive study and is amply described (EP 120516; Hoekema, 1985; Knauf, et al., 1983; and An. et al., 1985. For introduction into plants, the nucleotide sequences of the invention can be inserted into binary vectors as described in the examples.

Transformation of plants can be undertaken with a single DNA molecule or multiple DNA molecules (i.e., co-transformation), and both these techniques are suitable for use with the expression cassettes of the present invention.

Numerous transformation vectors are available for plant transformation, and the expression cassettes of this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation.

Preferred plant cells for transformation include, but are not limited to, cells from plant such as corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wofsiella* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*, *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*).

- Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt,
- 5 Biosystematic Investigation on the Family of Duckweeds: The family of *Lemnaceae* - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis*
 - 10 such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and
 - 15 chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*);
 - 20 redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils,
 - 25 chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula,
 - 30 blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry,

nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens,

5 Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Other vegetables are in Table 1.

10 Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

Preferably, plants of the present invention are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean,

15 barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, and the like), and even more preferably rice, corn and soybean.

In a preferred embodiment, the host cells are monocot or dicot cells, including, but are not limited to, wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince,

20 cherry, apricot, pepper, melon, lettuce, cauliflower, *Brassica*, e.g., broccoli, cabbage, brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry,

25 chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut, nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g.,

30 lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia,

Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. More preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be
5 regenerated into a transgenic plant.

Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term "organogenesis," as used herein, means a process by which shoots and roots are developed sequentially from meristematic centers; the
10 term "embryogenesis," as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen,
15 embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem).

The choice of plant tissue source for transformation will depend on the nature of the host plant and the transformation protocol. Useful tissue sources
20 include callus, suspension culture cells, protoplasts, leaf segments, stem segments, tassels, pollen, embryos, hypocotyls, tuber segments, meristematic regions, and the like. The tissue source is selected and transformed so that it retains the ability to regenerate whole, fertile plants following transformation, i.e., contains totipotent cells. Type I or Type II embryonic maize callus and
25 immature embryos are preferred *Zea mays* tissue sources. Selection of tissue sources for transformation of monocots is described in detail in U.S. Application Serial No. 08/112,245 and PCT publication WO 95/06128 (incorporated herein by reference).

For certain plant species, different antibiotic or herbicide selection markers
30 may be preferred. Selection markers used routinely in transformation include the nptII gene which confers resistance to kanamycin and related antibiotics (Messing & Vierra, 1982); Bevan et al., 1983), the *bar* gene which confers resistance to the herbicide phosphinothricin (White et al., 1990, Spencer et al., 1990), the *hph* gene which confers resistance to the antibiotic hygromycin

(Blochinger & Diggelmann), and the *dhfr* gene, which confers resistance to methotrexate (Bourouis et al., 1983).

Thus, the present invention also provides a transformed (transgenic) plant cell, *in planta* or *ex planta*, including, but not limited to, a transformed plant cell

5 from plants such as corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet

10 (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos*

15 *nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond

20 (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus

25 *Woffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wofieldia* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*,

30 *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*). Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt,

Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens,

Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia, as well
 5 as from vegetables including those described in Table 1.

In a preferred embodiment, the transformed cells, include, but are not limited to, transformed wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince, cherry, apricot, pepper, melon, lettuce, cauliflower, *Brassica*, e.g., broccoli, cabbage,
 10 brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry, chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut,
 15 nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field
 20 bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia, Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura,
 25 Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. Preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be regenerated into a transgenic plant.

30 IV. Identification of Transgenic Plants

To confirm the presence of the preselected nucleic acid segment(s) or "transgene(s)" in the regenerating plants, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays well known to those of skill in the art, such as Southern and Northern blotting, *in situ*

hybridization and nucleic acid-based amplification methods such as PCR or RT-PCR; "biochemical" assays, such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant, e.g., for disease or pest resistance.

DNA may be isolated from cell lines or any plant parts to determine the presence of the preselected nucleic acid segment through the use of techniques well known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

The presence of nucleic acid elements introduced through the methods of this invention may be determined by polymerase chain reaction (PCR). Using this technique discrete fragments of nucleic acid are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a preselected nucleic acid segment is present in a stable transformant, but does not prove integration of the introduced preselected nucleic acid segment into the host cell genome. In addition, it is not possible using PCR techniques to determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that using PCR techniques it would be possible to clone fragments of the host genomic DNA adjacent to an introduced preselected DNA segment.

Positive proof of DNA integration into the host genome and the independent identities of transformants may be determined using the technique of Southern hybridization. Using this technique specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition it is possible through Southern hybridization to demonstrate the presence of introduced preselected DNA segments in high molecular weight DNA, i.e., confirm that the introduced preselected DNA segment has been integrated into the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR, e.g., the presence of a preselected DNA segment, but also demonstrates integration into the genome and characterizes each individual transformant.

It is contemplated that using the techniques of dot or slot blot hybridization which are modifications of Southern hybridization techniques one could obtain the same information that is derived from PCR, e.g., the presence of a preselected DNA segment.

5 Both PCR and Southern hybridization techniques can be used to demonstrate transmission of a preselected DNA segment to progeny. In most instances the characteristic Southern hybridization pattern for a given transformant will segregate in progeny as one or more Mendelian genes (Spencer et al., 1992); Laursen et al., 1994) indicating stable inheritance of the gene. The
10 nonchimeric nature of the callus and the parental transformants (R_0) was suggested by germline transmission and the identical Southern blot hybridization patterns and intensities of the transforming DNA in callus, R_0 plants and R_1 progeny that segregated for the transformed gene.

Whereas DNA analysis techniques may be conducted using DNA isolated
15 from any part of a plant, RNA may only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used for detection and quantitation of RNA produced from introduced preselected DNA segments. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes
20 such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information
25 about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

While Southern blotting and PCR may be used to detect the preselected
30 DNA segment in question, they do not provide information as to whether the preselected DNA segment is being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced preselected DNA segments or evaluating the phenotypic changes brought about by their expression.

Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or
5 denaturing gel electrophoresis or isoelectric focussing, or by chromatographic techniques such as ion exchange or gel exclusion chromatography. The unique structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations of approaches may be employed with even greater specificity such as Western
10 blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid sequencing following purification. Although these are among the most commonly employed, other procedures may be additionally
15 used.

Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and quantifying the loss of substrates or the
20 generation of products of the reactions by physical or chemical procedures. Examples are as varied as the enzyme to be analyzed.

Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical
25 composition, morphology, or physiological properties of the plant. Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays.

30 V. Utility

Once an expression cassette of the invention has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. Particularly preferred plants of the invention

include the agronomically important crops listed above. The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction and can thus be maintained and propagated in progeny plants. The present invention also relates to a transgenic plant cell, tissue, organ, seed or plant part obtained from the transgenic plant. Also included within the invention are transgenic descendants of the plant as well as transgenic plant cells, tissues, organs, seeds and plant parts obtained from the descendants.

Preferably, the expression cassette in the transgenic plant is sexually transmitted. In one preferred embodiment, the coding sequence is sexually transmitted through a complete normal sexual cycle of the R0 plant to the R1 generation. Additionally preferred, the expression cassette is expressed in the cells, tissues, seeds or plant of a transgenic plant in an amount that is different than the amount in the cells, tissues, seeds or plant of a plant which only differs in that the expression cassette is absent.

The transgenic plants produced herein are thus expected to be useful for a variety of commercial and research purposes. Transgenic plants can be created for use in traditional agriculture to possess traits beneficial to the grower (e.g., agronomic traits such as resistance to water deficit, pest resistance, herbicide resistance or increased yield), beneficial to the consumer of the grain harvested from the plant (e.g., improved nutritive content in human food or animal feed), or beneficial to the food processor (e.g., improved processing traits). In such uses, the plants are generally grown for the use of their grain in human or animal foods. However, other parts of the plants, including stalks, husks, vegetative parts, and the like, may also have utility, including use as part of animal silage or for ornamental purposes. Often, chemical constituents (e.g., oils or starches) of maize and other crops are extracted for foods or industrial use and transgenic plants may be created which have enhanced or modified levels of such components.

Transgenic plants may also find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements

encoded by the expression cassette may be transferred, e.g., from maize cells to cells of other species, e.g., by protoplast fusion.

The transgenic plants may have many uses in research or breeding, including creation of new mutant plants through insertional mutagenesis, in order
5 to identify beneficial mutants that might later be created by traditional mutation and selection. An example would be the introduction of a recombinant DNA sequence encoding a transposable element that may be used for generating genetic variation. The methods of the invention may also be used to create plants having unique "signature sequences" or other marker sequences which can
10 be used to identify proprietary lines or varieties.

Thus, the transgenic plants and seeds according to the invention can be used in plant breeding which aims at the development of plants with improved properties conferred by the expression cassette, such as tolerance of viruses or other pests, or other stresses. The various breeding steps are characterized by
15 well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate descendant plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding,
20 variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain
25 properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can
30 be obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

VI. A Computer Readable Medium

The invention also provides a computer readable medium having stored thereon a data structure containing nucleic acid sequences having at least 70% sequence identity to a nucleic acid sequence selected from those listed in SEQ ID Nos: 1-795 as well as complementary, ortholog, and variant sequences thereof. Storage and use of nucleic acid sequences on a computer readable medium is well known in the art. (See for example U.S. Patent Nos. 6,023,659; 5,867,402; 5,795,716) Examples of such medium include, but are not limited to, magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory. Accordingly, the nucleic acid sequences contained on the computer readable medium may be compared through use of a module that receives the sequence information and compares it to other sequence information. Examples of other sequences to which the nucleic acid sequences of the invention may be compared include those maintained by the National Center for Biotechnology Information (NCBI)(<http://www.ncbi.nlm.nih.gov/>) and the Swiss Protein Data Bank. A computer is an example of such a module that can read and compare nucleic acid sequence information. Accordingly, the invention also provides the method of comparing a nucleic acid sequence of the invention to another sequence. For example, a sequence of the invention may be submitted to the NCBI for a Blast search as described herein where the sequence is compared to sequence information contained within the NCBI database and a comparison is returned. The invention also provides nucleic acid sequence information in a computer readable medium that allows the encoded polypeptide to be optimized for a desired property. Examples of such properties include, but are not limited to, increased or decreased: thermal stability, chemical stability, hydrophylicity, hydrophobicity, and the like. Methods for the use of computers to model polypeptides and polynucleotides having altered activities are well known in the art and have been reviewed. (Lesyng et al., 1993; Surles et al., 1994; Koehl et al., 1996; Rossi et al., 2001).

The invention will be further described by the following examples which is not intended to limit the scope of the invention.

Example 1**GeneChip Standard Protocol****Quantitation of total RNA**

Total RNA from plant tissue is extracted and quantified.

- 5 1. Quantify total RNA using GeneQuant
 1OD₂₆₀=40 mg RNA/ml; A260/A280=1.9 to about 2.1
2. Run gel to check the integrity and purity of the extracted RNA

Synthesis of double-stranded cDNA

- 10 Gibco/BRL SuperScript Choice System for cDNA Synthesis (Cat#1B090-019)

was employed to prepare cDNAs. T7-(dT)₂₄ oligonucleotides were prepared

and purified by HPLC. (5'-

- 15 GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-(dT)₂₄-3'(SEQ ID NO:800).

Step 1. Primer hybridization:

Incubate at 70°C for 10 minutes

Quick spin and put on ice briefly

- 20 **Step 2. Temperature adjustment:**

I Incubate at 42°C for 2 minutes

Step 3. First strand synthesis:

DEPC-water- 1 µl

RNA (10 µg final)-10 µl

- 25 T7=(dT)₂₄ Primer (100 pmol final)-1 µl pmol

5X 1st strand cDNA buffer-4 µl

0.1M DTT (10 mM final)- 2 µl

10 mM dNTP mix (500 µM final)-1 µl

Superscript II RT 200 U/µl- 1 µl

- 30 Total of 20 µl

Mix well

Incubate at 42°C for 1 hour

Step 4. Second strand synthesis:

Place reactions on ice, quick spin

- DEPC-water- 91 μ l
 5X 2nd strand cDNA buffer- 30 μ l
 mM dNTP mix (250 mM final) - 3 μ l
E. coli DNA ligase (10 U/ μ l)-1 μ l
 5 *E. coli* DNA polymerase 1-10 U/ μ l- 4 μ l
 RnaseH 2U/ μ l -1 μ l
 T4 DNA polymerase 5 U/ μ l-2 μ l
 0.5 M EDTA (0.5 M final)--10 μ l
 Total 162 μ l
 10 Mix/spin down/incubate 16°C for 2 hours

Step 5. Completing the reaction:

Incubate at 16°C for 5 minutes

Purification of double stranded cDNA

- 15 1. Centrifuge PLG (Phase Lock Gel, Eppendorf 5 Prime, Inc., PI-188233)
 at 14,000X, transfer 162 μ l of cDNA to PLG
 2. Add 162 μ l of Phenol:Chloroform:Isoamyl alcohol (pH 8.0), centrifuge
 2 minutes
 3. Transfer the supernatant to a fresh 1.5 ml tube, add
 20 Glycogen (5 mg/ml) 2
 0.5 M NH₄OAc (0.75xVol) 120
 ETOH (2.5xVol, -20 °C) 400
 4. Mix well and centrifuge at 14,000X for 20 minutes
 5. Remove supernatant, add 0.5 ml 80% EtOH (-20°C)
 25 6. Centrifuge for 5 minutes, air dry or by speed vac for 5-10 minutes
 7. Add 44 μ l DEPC H₂O

Analyze of quantity and size distribution of cDNA

Run a gel using 1 μ l of the double-stranded synthesis product

30 Synthesis of biotinylated cRNA

(use Enzo BioArray High Yield RNA Transcript Labeling Kit Cat#900182)

Purified cDNA	22 μ l
10X Hy buffer	4 μ l
10X biotin ribonucleotides	4 μ l

10X DTT	4 μ l
10X Rnase inhibitor mix	4 μ l
20X T7 RNA polymerase	2 μ l
Total	40 μ l

- 5 Centrifuge 5 seconds, and incubate for 4 hours at 37°C
Gently mix every 30-45 minutes

Purification and quantification of cRNA

(use Qiagen Rneasy Mini kit Cat# 74103)

- 10 Determine concentration and dilute to 1 μ g/ μ l concentration

Fragmentation of cRNA

cRNA (1 μ g/ μ l)	15 μ l
5X Fragmentation Buffer*	6 μ l
DEPC H ₂ O	9 μ l
	30 μ l

*5x Fragmentation Buffer

1M Tris (pH8.1)	4.0 ml
MgOAc	0.64 g
KOAc	0.98 g
DEPC H ₂ O	
Total	20 ml
Filter Sterilize	

25

Array wash and staining

Stringent Wash Buffer**

Non-Stringent Wash Buffer***

SAPE Stain****

- 30 Antibody Stain*****

Wash on fluidics station using the appropriate antibody amplification protocol

**Stringent Buffer: 12X MES 83.3 ml, 5 M NaCl 5.2 ml, 10% Tween 1.0 ml, H₂O 910 ml,

Filter Sterilize

***Non-Stringent Buffer: 20X SSPE 300 ml, 10% Tween 1.0 ml, H₂O 698 ml,
Filter Sterilize, Antifoam 1.0.

****SAPE stain: 2X Stain Buffer 600 µl, BSA 48 µl, SAPE 12µl, H₂O 540 µl.

5 *****Antibody Stain: 2X Stain Buffer 300 µl, H₂O 266.4 µl, BSA 24 ul, Goat
IgG 6 µl, Biotinylated Ab 3.6 µl

Example 2Identification of *Arabidopsis* Genes Induced by *Peronospora* Infection

10

To define the transcriptional profile for *Peronospora*-induced and/or *RPP7*- and *RPP8*- dependent genes, four *Arabidopsis* lines were infected with one of two different *P. parasitica* isolates (see Table 2). One *Arabidopsis* line was Col-0::*RPP8* which carries the cloned *RPP8* genomic clone (*RPP8* mediates resistance of the ecotype La-er against Emco5; McDowell et al. 1998) and is 15 Emco5 resistant. Wild-type Col-0 plants are Emco5 susceptible. *RPP7* mediates resistance of *Arabidopsis* against the *Peronospora* isolate Hiks1, and occurs naturally in Col-0. Another *Arabidopsis* line had a loss of function *rpp7* mutant allele (Col-0 (*rpp7*)) (McDowell et al., 2000). Finally, three mutants in the 20 signaling pathway for *RPP7*, i.e., they lack a *RPP7*-mediated response, were identified, i.e., *edm1*, *edm2* and *edm3*, and a line with one of the mutant alleles, i.e., *edm1*, was used.

RNA samples were collected from two week old seedlings at three time points, 0, 12 and 24 hours post infection with 100,000 spores/ml. Twelve hours 25 post-inoculation was determined to be an appropriate time point for analysis of both incompatible interactions, based on trypan blue staining of HR sites and *PR-1* and *sen1* induction. Forty-eight hours post-inoculation was determined to be a time point where both compatible interactions exhibit dense hyphal growth and both *PR-1* and *sen1* expression. Three independent sets of RNA were 30 pooled.

Table 2

<u>Plant</u>	<u><i>Peronospora</i> isolate</u>	<u>Time of RNA collection</u>
Col-0 (<i>RPP7</i> , <i>incomp.</i>)	Hiks1	0, 12, 48 hours
35 Col-0 (<i>rpp7</i> , <i>comp.</i>)	Hiks1	0, 12, 48 hours

Col-0 (<i>edm1</i> , <i>comp.</i>)	Hiks1	0, 12, 48 hours
Col-0 (<i>tgRPP8</i> , <i>incomp.</i>)	Emco5	0, 12, 48 hours
Col-0 (<i>rpp8</i> , <i>comp.</i>)	Emco5	0, 12, 48 hours

5 RNAs were labeled as described in Example 1 and hybridized to an Affymetrix Gene Chip having sequences corresponding to about 8,200 *Arabidopsis* genes. The data collected from these chips was employed to determine:

- 1) the difference, if any, between *RPP7* and *RPP8* triggered signaling (and how these profiles compare to other profiles, for example, to the profiles of *RPM1* and *RPS2*);
- 2) which portion of the transcriptional response is *R* dependent;
- 3) which genes are either commonly or uniquely induced during two different compatible interactions;
- 4) which genes are specifically activated during the incompatible interactions (gleaned by comparison with isogenic compatible controls) and, hence, may be important for the plant's defense against *Peronospora*;
- 5) which genes whose expression is a prerequisite for induced defense reactions against *Peronospora*; and
- 6) which genes are specifically repressed during the incompatible interactions, which may be required for successful Oomycete infections.

Results

Genes Expressed Early and Transiently After Infection

The normalized "average difference" (AD) from the chip experiments were processed as follows. All values together with the respective gene identifiers were loaded in EXCEL. Genes having, for a given treatment, AD values of 25 or less were considered as being not expressed. To reduce spurious background fluctuation, this cut off level was elevated to 75 for most of the analyses and normalized all AD values of 75 or less. For all five infection time courses, the AD values were divided by the corresponding 0 hour time point AD value. To visualize differences in gene expression ground states between the four experimental *Arabidopsis* lines, the following ratios were calculated for the 0 hour AD values: Col-0 (from Emco5 series)/Col-0-*RPP8* and *rpp7*/Col-0 (from Hiks1 series) and *edm1*/Col-0 (from Hiks1 series). These ratios indicate whether

a given gene is up- or down-regulated by the *RPP7* or *RPP8* pathway, respectively. The resulting set of 18 expression ratio series was then loaded into CLUSTER (Eisen et al., 1998). The AD values were log transformed (base 2) and filtered to include only genes in the final data set that showed at least a 3-
 5 fold expression change (which equals a 1.6-fold change of the log transformed values). These criteria were fulfilled by 464 genes that define the final data set. With this data set Average linkage clustering was performed (uncentered correlation). The resulting clustergram was displayed using TREEVIEW (Eisen et al., 1998). A second clustergram was generated in the same way applying a cut
 10 off value of 50 on the normalized AD values. This clustergram includes 619 genes (probe sets).

Based on these clustergrams, gene clusters showing distinct expression behaviors were defined. Cluster cR7/R8 (see Table 3) contained genes that are early and transiently upregulated early and transiently after *P. parasitica*
 15 infection of *Arabidopsis* in an *RPP7/8* dependent manner. Upregulation by the *RPP8* pathway was generally stronger. Strong induced expression of cR7/R8 genes was detectable 12 hours after Emco5 infection in Col-0(*tgRPP8*) plants (incompatible interaction), whereas no elevated expression can be observed 48
 20 hours post infection in the same plants (as compared to untreated control plants). Only weakly elevated or no elevated expression was detected at all tested time points in Col-0 plants (compatible interaction). After Hiks1 infection, elevated
 25 expression of these genes was only observed in Col-0 plants (incompatible interaction) after 12 hours. At no other time point following Hiks1 infection was substantially elevated expression of these genes observed. The expression ground state of these genes is similar in all four *Arabidopsis* lines.

Table 3

20245 s at	cut off = 75
18716 At	
18022 at	
14609 at	
17014 s at	
17051 s at	
19640 at	
14248 at	
13176_at	

15978 at cut off +50
 17014 s at
 14609 at
 13764 at
 16649 s at Subcluster A
 13215 s at
 17653 at
 17008 at
 15042 at
 12778_r_at

 14614 at
 17051 s at
 14248 at Subcluster B
 20245 s at
 19640 at
 18716 at
 18022_at

 17500 s at
 13217 s at
 18928 at

The cR7/R8 cluster was originally defined using the clustergram based on a cut off value of 75 and comprised only 9 genes. Applying a cut off value of 50, the cluster became larger, comprising 21 genes, which could be divided into two subclusters (Table 4). Subcluster cR7/R8 A includes genes strongly and transiently upregulated by the *RPP8* pathway, but either not, or only faintly, upregulated by the *RPP7* pathway. Members of subcluster B showed pronounced upregulation by both *RPP* pathways after 12 hours and also elevated expression during compatible Emco5 infections in Col-0.

10

Table 4

Subcluster AGene-identifier (probe set)

15978_at
 17014_s_at*
 14609_at
 16649_s_at+

13215_s_at*
 17653_at
 17008_at

Related to

X68592.6_at
 atu05206_s_at
 AC002340.147_at
 athorf_s_at
 CafferoylCoAmethyltrans_s_a
 t
 AL035679.144_at
 AC006585.212_at

15042_at	AL021961.3_at
12778_r_at	AC006577.16_r_at

Subcluster B

<u>Gene-identifier (probe set)</u>	<u>Related to</u>
14614_at	AC004165.66_at
17051_s_at	af098947_s_at
14248_at	PAD3_at
20245_s_at	AC005309.97_s_at
19640_at	AC004561.78_at
18716_at	X91916_at
18022_at	AJ010971_at
17500_s_at [†]	athcallga_s_at
13217_s_at [†]	calmodulinlike_s_at
18928_at	AC002333.181_at

*Genes printed in **bold** were identified using a cut off value of 75; all others were identified using a cut off value of 50.

[†]The probe sets 16649 and 13215 as well as 17500 and 13217 correspond to the same genes.

Thus, the predominant feature of genes of the cR7/R8 cluster is more pronounced expression along with *RPP7* and *RPP8* mediated *Peronospora* resistance in comparison to the corresponding compatible interactions. Expression of these genes peaks in around 12 hours post infection and returns to ground state by 48 hours post infection. Hence, increased transcript levels of these genes coincide with the time window of decision between disease or resistance. Within 48 hours after infection with each tested *Peronospora* isolate, the plant either responds with HR and hinders development of oomycete hyphae or allows successful infection.

Identification of Conserved Sequence Motifs Within cR7/R8 Upstream Regions

To identify potential *cis*-elements involved in the specific regulation of cR7/R8 genes, stretches comprising 1.1 to 1.2 kb localized directly upstream of the translation start sites of coding regions from this cluster were collected from genomic *Arabidopsis* sequences (see Figure 2). Two motif search algorithms were used to recognize conserved motifs: AlignAce (Roth et al., 1998) and MEME (Bailey and Elkan, 1994). A search with AlignAce (default settings) revealed two conserved motifs within a set of 8 promoters comprising 7 from the originally defined cR7R8 using a cut off value of 75 and the promoter of a gene encoding a putative Myb-like transcription factor (Martin & Paz-Ares, 1997)

(probe set 13176, SEQ ID NO:36), which shows a similar expression behavior as cR7/R8. The AlignAce output is shown below in Table 5:

Table 5

Motif 1 *****	MAP Score: 6.87857	SEQ ID NO.	Corresponding Probe Set
CAACAATTAT	0 36 1	685	17014
CAACTATGTC	0 981 1	686	17014
CAACAATGAC	1 934 0	687	20245
CAACAATGAC	2 271 1	688	14609
AAACAATGAT	2 1184 1	689	14609
CAACATTGAC	3 163 0	690	17051
CAACATTGTT	3 298 0	691	17051
CAACAATGTT	4 613 1	692	19640
CAACTATGAT	4 791 0	693	19640
CAACAATGAT	4 1064 0	694	19640
CAAAAATGAT	7 397 0	695	17008
CAACATTGAT	7 415 1	696	17008
CATATCA/TA/TTGAC (Consensus)		697	N.A.

5

Motif 2 *****	MAP Score: 2.22382	SEQ ID NO.	Corresponding Probe Set
TTTGGGCAAAA	1 368 0	698	20245
GTTGGGTCAAA	1 739 0	699	20245
GATGGGCACAA	2 691 0	700	14609
GATGGGCCAAA	3 700 0	701	17051
GATGGGTATAA	4 344 0	702	19640
GATGGGACTAA	5 98 1	703	14248
TTTGGGCCTAA	5 971 1	704	14248
TATGGGCCCAA	5 1012 0	705	14248
CTTGGGACAAA	7 579 1	706	17008
GATGGGTCAAC	7 1009 0	707	17008
CATGGGAATAA	7 1072 1	708	17008
NATTGGGNC/ANAA (Consensus)		709	N.A.

For each motif, examples from cR7/R8 promoters are listed. Nucleotides evaluated by AlignAce as being conserved are indicated by a "*" above the examples. Besides motifs 1 and 2, a variety of additional ones were found by AlignAce, which, however, consisted almost exclusively of Ts and As. These motifs probably do not constitute functional *cis*-elements. Promoter sequences

10

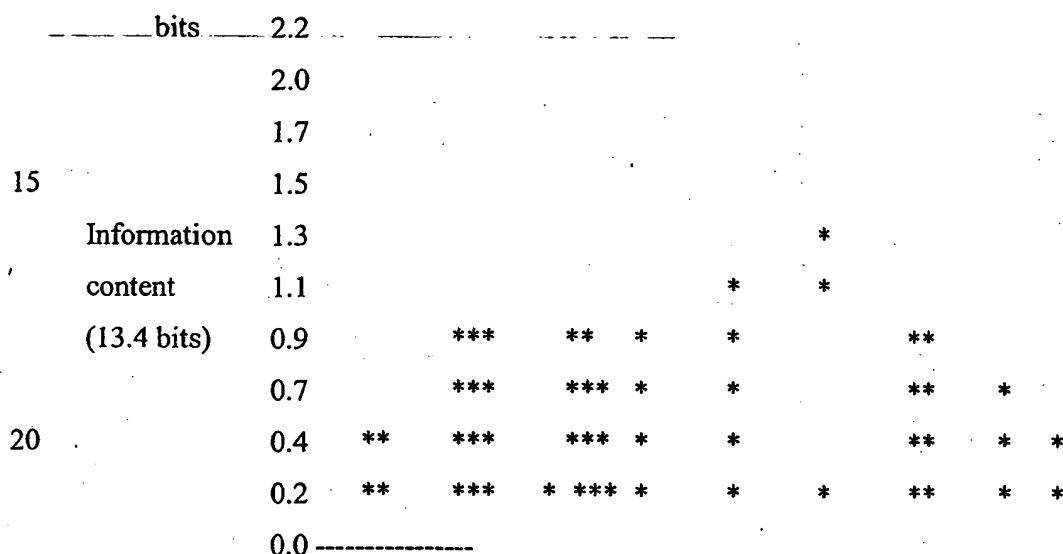
are generally enriched in As or Ts (A/T content in cR7/R8 promoters is 70%) and regulatory *cis*-elements usually contain also Cs or Gs.

Motif 1 (CAACA/TA/TTGA/TC/T, SEQ ID NO:710) resembles the type I Myb binding site consensus (MBS;T/CAACT/GG), which is bound by animal and some plant Myb transcription factors (Yang & Klessig, 1996). The 3' portion of the motif 1 consensus allows overlap with binding sites of WRKY (TTTGACC/T; Eulgem et al., 2000) or TGA-bZIP transcription factors (TGACG; Schindler et al. 1992). Interestingly, a gene encoding a putative Myb-like transcription factor (gene identification number 13176) is upregulated along with cR7/R8 genes in an *RPP7/RPP8*-dependent, early and transient manner. The factor encoded by this gene may be a regulator of cR7/R8 genes. Motif 1 is particularly enriched in promoters of the originally defined cR7/R8 cluster (cut off = 75). This motif, which consists of six strictly defined positions and four positions allowing two base pairs each, should occur by random roughly once per 20,000 bp in each of both possible orientations (assuming a T/A content of 70% and a G/C content of 30%). In the 8,441 bp of cR7/R8 promoter sequences, the motif occurs 9 times (roughly 20 times the statistically expected frequency). Consistent with the statistical expectation, motif 1 occurs only two times within 15,873 bp from a set of control promoters of genes showing no defense related expression (data not shown).

In the extended set of cR7/R8 genes (cut off = 50), the enrichment of motif 1 is less striking. It occurs only 9 times within 16,519 bp in total and, more importantly, none of the promoters added to the set by lowering the cut off value contains this motif. Thus, if motif 1 is involved in the specific regulation of cR7/R8 genes it cannot alone be responsible for the particular expression features of these genes, and may rather be responsible for the more pronounced R7/R8-triggered expression of members of the originally defined cluster (cut off = 75).

Motif 2 (A/TTGGGNC/ANAA; SEQ ID NO:711) does not resemble any other known plant *cis*-element. The consensus sequence consists of six strictly defined positions, two positions with two alternatives and two positions with four alternatives; and, hence, should occur by random once per 10,000 bp. Motif 2 can be found 10 times within 8,441 bp of the promoters from the originally defined cR7/R8 (cut off = 75) and 14 times within 16,519 bp of the extended

cR7/R8 promoter set. Thus, its occurrence in cR7/R8 promoters is roughly 10 times the statistical expectation. Motif 2 is absent in the 15,873 bp of promoters of genes showing no defense related expression (data not shown). It is, however, also enriched in the promoters of previously defined clusters of defense related genes, such as the PR1 regulon (SAR genes) and SOMc3 (genes up regulated in Ws-0 after infection with avirulent Noco2; data not shown). The latter two clusters may also include genes sharing expression features with cR7/R8 genes. In addition to AlignAce, a motif 2-like sequence was also recognized by MEME. Within the extended set of cR7/R8 promoters, MEME found the following sequence stretch to be conserved:



Multilevel Consensus sequence T/C TTT G/C A/T/G C/T
 25 CCAAG/A/CAA/GAC/A (SEQ ID NO:712)

The reverse complement of this consensus sequence is (positions with three alternatives were given as "N") given below with motif 2 for comparison:

30 MEME motif: G/T T C/T T N T T G G G N G/C A A A A/C (SEQ ID NO:713)
 Motif 2: T G G G N A N/C A A (SEQ ID NO:714)

MEME was run using the default settings of "advanced MEME" choosing the options "one motif per sequence", "narrow motifs" and "additional strand: reverse complement".

To confirm these results, Northern blots using probes of representatives of each cluster are performed. In addition, T-DNA lines are screened for knock out in Myb-like gene (AL031394.56_at) and selected members of cR7/R8, such as RNS1 (atu05206_s_at) or the gene encoding a calmodulin-like protein (identification number 13217_s_at). Also, yeast one hybrid screens are performed to clone transcription factors binding to motifs 1 and 2, or other identified motifs. Transgenic *Arabidopsis* plants carrying fusions of GUS with a representative promoter from cR7/R8 can be used to further evaluate the functional significance of motifs 1 and 2, and to perform a genetic screening for mutants impaired in regulation of cR7/R8 genes.

15 Genes Induced by *Peronospora* Infection in a Manner that Requires *RPP7* or *RPP8*

The data sets described above were employed to identify genes that were induced by *Peronospora* infection and were RPP7/8-dependent. All expression values less than 5 were set to 5. Using ratios calculated in Excel, and database sorting using Access, a subset of genes was identified whose expression depends on RPP7 or RPP8 using the following criteria:

Col Hiks1 12 hour/Col untreated > 2.5 AND Col Hiks1 12 hour > 30
AND Col Hiks1 12 hour/Col rpp7 Hiks1 12 hour > 2
OR
25 Col Hiks1 48 hour/Col untreated > 2.5 AND Col Hiks1 48 hour > 30
AND Col Hiks1 48 hour/Col rpp7 Hiks1 48 hour > 2
OR
Col RPP8 Emco5 12 hour/Col RPP8 no treatment > 2.5 AND Col RPP8
Emco5 12 hour > 30 AND Col RPP8 Emco5 12 hour/Col (rpp8) Emco5
30 12 hour > 2
OR
Col RPP8 Emco5 48 hour/Col RPP8 no treatment AND Col RPP8
Emco5 48 hour > 30 AND Col RPP8 Emco5 48 hour/Col (rpp8) Emco5
48 hour > 2

This yielded 217 probe sets ("RPP7 or 8") which correspond to sequences, the expression of which were increased by at least 2.5 fold and were *RPP7*- or *RPP8*-dependent (Table 6).

5

Table 6

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
12360_at (AL022347.131_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
12556_at (AL079344.155_AT)	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
12630_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]

12777_i_at (AC006577.16_I_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12778_r_at (AC006577.16_R_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12779_f_at (AC006577.16_F_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1 (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]
12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]

13154_s_at (AC002333.210_S_AT)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13198_i_at (ATTS0190_I_AT)	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
13631_at (AC002387.185_AT)	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13697_at (NI16_AT)	No hits found.

13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
13880_s_at (AL049480.183_S_AT)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
14096_at (AC002291.12_AT)	No hits found. emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14110_i_at (AL035528.279_I_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14111_s_at (AL035528.279_S_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
14116_at (AF077407.30_AT)	
14141_at (NOVARTIS31_AT)	No hits found less than or equal to 1e-15. dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
14145_at (NOVARTIS35_AT)	
14146_at (NOVARTIS36_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
14201_at (NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15.
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]

14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from <i>Arabidopsis thaliana</i> and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [<i>Arabidopsis thaliana</i>]
14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [<i>Arabidopsis thaliana</i>]
14254_s_at (PAL1-MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [<i>Arabidopsis</i>
14256_f_at (PAL1-INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [<i>Arabidopsis thaliana</i>]
14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [<i>Arabidopsis thaliana</i>]
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [<i>Arabidopsis thaliana</i>]
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [<i>Arabidopsis thaliana</i>]
14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [<i>Arabidopsis thaliana</i>]
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [<i>Arabidopsis thaliana</i>]
14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [<i>Arabidopsis thaliana</i>]
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [<i>Arabidopsis thaliana</i>]
14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [<i>Arabidopsis thaliana</i>]
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [<i>Arabidopsis thaliana</i>]
14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [<i>Arabidopsis thaliana</i>]
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [<i>Arabidopsis thaliana</i>]
14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [<i>Arabidopsis thaliana</i>]
14682_i_at (WT1012A_RC_I_AT)	No hits found.
14691_at (WT1096_AT)	No hits found.

14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
14709_at (WT788_AT)	No hits found less than or equal to 1e-15.
14763_at (X86958.1_AT)	emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
15532_r_at (AL078637.191_R_AT)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]
15616_s_at (ATHPRO25A_S_AT)	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
15629_s_at (AB003280_S_AT)	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]

15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]
15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16061_s_at (AB004796_S_AT)	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
16150_s_at (ATHPEAR_S_AT)	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]
16257_at (AC004138.105_AT)	gb AAC32915.1 (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16360_at (AL031187.126_AT)	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]
16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	gb AAC48925.1 (U05206) ribonuclease [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]
17068_s_at (ATHRLPKA_S_AT)	gb AAA32857.1 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana]
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475, gb ATTS4362 come from this gene. [Arabidopsis thaliana]
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]

17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
17499_s_at (AF107726_S_AT)	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
17653_at (AL035679.144_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
17775_at (AC004392.2_AT)	gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
17840_s_at (AC002333.223_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
17843_s_at (AC002391.150_S_AT)	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]
18022_at (AJ010971_AT)	emb CAB52675.1 (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]
18551_at (AC002391.163_AT)	gb AAB87112.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
18567_at (AC004411.25_AT)	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana] gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]
18625_at (AC005278.22_AT)	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
18716_at (X91916_AT)	gb AAC33239.1 (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
18844_at (AC005315.131_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC16927.1 (AC002338) putative laccase [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
18946_at (Y11788.1_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18969_g_at (AF163823.4_G_AT)	emb CAB41722.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
19158_at (X95738.2_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
19171_at (AC002335.160_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
19177_at (X99923.1_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
19182_at (AL031804.245_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	

19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
20232_s_at (AL022347.12_S_AT)	emb CAA18460.1 (AL022347) protein kinase-like protein [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate

	synthase alpha subunit [Arabidopsis thaliana]
20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]
20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
20429_s_at (Z97336.167_S_AT)	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	gb AAC98070.1 (AC005896) putative C2H2- type zinc finger protein [Arabidopsis thaliana]
20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]

The functions of RPP7 and RPP8 are independent of *PAD4*, *NDR1*, *NahG*, *COI1*, and *EDS1*. Consequently, it is unlikely that genes whose expression is reduced in *pad4* or *NahG* backgrounds are important for RPP7- or RPP8- mediated resistance. Although data from *Peronospora* infection of *pad4* or *nahG* plants was not available, data from *Pseudomonas syringae* (ES4326) infection of *pad4* and *NahG* plants was available and employed to determine which genes depended on *PAD4* or were interfered with by *NahG*. Resistance to *P. syringae* mediated by *RPS2* requires *NDR1* function. Genes whose expression requires *RPS2* are less likely to be important for RPP7 or RPP8 mediated resistance than genes whose expression is independent of *RPS2*. Gene expression data was available for wild-type plants infected with *Pseudomonas syringae* pv. tomato DC3000 *avrRpt2*, and *rps2* mutant plants infected with *Pseudomonas syringae* pv. tomato DC3000 *avrRpt2*, 6 hours after infection. *EDM1* is required for resistance mediated by RPP7. Thus, genes whose expression requires *EDM1* are likely to be important for RPP7-mediated resistance. Gene expression data was available for an *edm1* mutant (see above).

The data from the 7 additional data sets (Col Psm ES4326 30 hour; Col Mock 30 hour; Col *NahG* Psm ES4226 30 hour; Col *pad4* Psm ES4326 30 hour; Col water control; Col DC3000 *avrRpt2* and *rps2* DC3000 *avrRpt2* was added to the 217 probe sets in "RPP7 or 8". The following sets were identified: *edm1*:

Col edm1 Hiks1 12 hour/Col Hiks1 12 hour < 0.5 OR Col edm1 Hiks1
48 hour/Col Hiks1 48 hour < 0.5.

rps2:

- 5 Col DC3000 *avrRpt2* 6 hour/Col water control > 2 AND *rps2* DC3000
avrRpt2 6 hour/Col DC3000 *avrRpt2* 6 hour < 0.5.

pad4 or NahG:

- 10 Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col pad4 Psm
ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.

OR

Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col NahG Psm
ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.

- 15 There are 8 possible combinations of these three sets. Access was used to divide
the 217 probe sets into 8 sets, numbered 2-9 (considering the whole set of 217
probe sets as set 1) as shown in Tables 7 and 8:

Table 7

20	<u>Set</u>	<u>Content</u>	<u>Number of probe</u>
		<u>sets</u>	
	2	RPP7 or 8 not edm1 not rps2 not pad4 or NahG	62 probe sets
	3	edm1 not rps2 not pad4 or NahG	50 probe sets
	4	rps2 not edm1 not pad4 or NahG	14 probe sets
25	5	pad4 or NahG not edm1 not rps2	21 probe sets
	6	edm1 and rps2 not pad4 or NahG	23 probe sets
	7	edm1 and pad4 or NahG not rps2	25 probe sets
	8	rps2 and pad4 or NahG not edm1	8 probe sets
	9	edm1 and rps2 and pad4 or NahG	<u>14 probe sets</u>
30	Total		217 probe sets

Table 8

2 RPP7 or 8 not edm1 not rps2
not pad4 or NahG

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
12556_at (AL079344.155_AT)	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657-
12777_i_at (AC006577.16_I_AT)	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657
12779_f_at (AC006577.16_F_AT)	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana]
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13880_s_at (AL049480.183_S_AT)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]
14111_s_at (AL035528.279_S_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]

14145_at (NOVARTIS35_AT)	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana]
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana]
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]
16257_at (AC004138.105_AT)	gb AAC32915.1 (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]
16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]

17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]
17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]
18625_at (AC005278.22_AT)	gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]
18844_at (AC005315.131_AT)	gb AAC33239.1 (AC005315) putative ligand- gated ion channel protein [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	gb AAC16927.1 (AC002338) putative laccase [Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAB41722.1 (AL049730) pEARLI 1- like protein [Arabidopsis thaliana]
19158_at (X95738.2_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]

Duplicates

12777 and 12779 (lipase)
 12889 and 20291 (ASA1)
 12908 and 16536 (ERF5)
 17464 and 19982 (RLK5)
 18216 and 18217 (T22C5.18)
 18908 and 18909 (subtilisin-like protease)
 20238 and 20239 (beta-fructofuranosidase)

3 edm1 without rps2 without pad4orNahG

ProbeSet

	Description
12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]

	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
12500_s_at (AF081067.3_S_AT)	[Arabidopsis thaliana]
	gb AAC14413.1 (AF049236) unknown
12521_at (AF049236.28_AT)	[Arabidopsis thaliana]
	emb CAA57944.1 (X82624) SRG2At
12574_at (X82624.2_AT)	[Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577)
	Belongs to the PF00657
	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AJ099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12778_r_at (AC006577.16_R_AT)	
	gb AAC63850.1 (U73786) ACC synthase
12891_at (ATACS6_AT)	[Arabidopsis thaliana]
	gb AAC63850.1 (U73786) ACC synthase
12892_g_at (ATACS6_G_AT)	[Arabidopsis thaliana]
	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2
12905_s_at (ATERF2_S_AT)	[Arabidopsis thaliana]
	gb AAC13947.1 (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]
12916_s_at (ATHCOR1_S_AT)	
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
13198_i_at (ATTS0190_I_AT)	
	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
13435_at (AF003102.3_AT)	
	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
13631_at (AC002387.185_AT)	
14096_at (AC002291.12_AT)	No hits found.
	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
14223_at (NOVARTIS9_AT)	
	gb AAF16756.1 AC010155_9 (AC010155)
14232_at (NOVARTIS95_AT)	F3M18.20 [Arabidopsis thaliana]
14254_s_at (PAL1-MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
14614_at (AC004165.66_AT)	
14691_at (WT1096_AT)	No hits found.
	gb AAA32835.1 (M96073)
	phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14838_s_at (M96073.6_S_AT)	
	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
15161_s_at (ATU90522_S_AT)	

15532_r_at (AL078637.191_R_AT)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana] dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
15629_s_at (AB003280_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]
16232_s_at (AL080252.77_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
16609_s_at (AB008104_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
16817_s_at (AL096882.91_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
17008_at (AC006585.212_AT)	gb AAC48925.1 (U05206) ribonuclease [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
17500_s_at (ATHCALLGA_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]
17653_at (AL035679.144_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
17843_s_at (AC002391.150_S_AT)	emb CAB52675.1 (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
18022_at (AJ010971_AT)	gb AAB87112.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
18551_at (AC002391.163_AT)	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
18716_at (X91916_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
18946_at (Y11788.1_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
19171_at (AC002335.160_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
19177_at (X99923.1_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
19182_at (AL031804.245_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	

19672_at (AC005687.19_AT) gb|AAC36019.1| (AC005687) RAP2.6
[Arabidopsis thaliana]
emb|CAB36812.1| (AL035527) peptide
19762_at (AL035527.204_AT) transporter-like protein [Arabidopsis thaliana]
gb|AAC79626.1| (AC005770) putative
19892_at (AC005770.30_AT) protease inhibitor [Arabidopsis thaliana]
20232_s_at emb|CAA18460.1| (AL022347) protein
(AL022347.12_S_AT) kinase-like protein [Arabidopsis thaliana]
emb|CAB10219.1| (Z97336) hypothetical
20429_s_at (Z97336.167_S_AT) protei [Arabidopsis thaliana]
emb|CAA63012.1| (X91919) LEA76
homologue type1 [Arabidopsis thaliana]
Arabidopsis thaliana. ESTs gb|N97082,
gb|Z27056 and gb|Z29902 come from this
gene.

Duplicates

12905 and 16609 (ERF2)

13188 and 16981 (thioredoxin h)

12891 and 12892 (ACC
synthase)

14838 (phosphoribosyl
anthranilate transferase) has a
duplicate in set 2 (14620).
Counted in set 2

14254 (PAL1) has a duplicate in
set 2 (14256) Counted in set 2.

12778 (lipase) has duplicates in
set 2 (12777 and 12779) Counted
in set 2.

4 rps2 without edm1 without pad4orNahG

ProbeSet

Description

emb|CAA09731.1| (AJ011674) receptor-like
12278_at (AJ011674.2_AT) protein kinase, RLK3 [Arabidopsis thaliana]
emb|CAA18468.1| (AL022347)
serine/threonine kinase-like protein
12360_at (AL022347.131_AT) [Arabidopsis thaliana]
13154_s_at gb|AAB64047.1| (AC002333) putative
(AC002333.210_S_AT) endochitinase [Arabidopsis thaliana]
gb|AAC31756.1| (U68017) heat shock
13273_s_at (HSF4_S_AT) transcription factor 4 [Arabidopsis thaliana]
gb|AAD25552.1|AC005850_9 (AC005850)
Highly Simlilar to Mlo proteins [Arabidopsis
13685_s_at (MLOLIKE2_S_AT) thaliana]
14141_at (NOVARTIS31_AT) No hits found less than or equal to 1e-15.

15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]

Duplicates

12360 and 20223 (serine threonine kinase)
13685 and 20365 (similar to Mlo)

5 pad4orNahG without rps2 without edm1

ProbeSet	Description
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]

14146_at (NOVARTIS36_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]
16360_at (AL031187.126_AT)	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1, 3- glucanase class I precursor [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]

Duplicates:

15778 and 15779 (zinc finger
protein)

**6 edm1 and rps2 without
pad4orNahG**

ProbeSet	Description
12630_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T43869 come from from this gene. [Arabidopsis thaliana]
13187_i_at (ATTHIREDA_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13189_s_at (ATTHIREDA_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]

13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
14116_at (AF077407.30_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14682_i_at (WT1012A_RC_I_AT)	No hits found.
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16061_s_at (AB004796_S_AT)	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S- linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5- trisphosphate 5-Phosphatase [Arabidopsis thaliana]

19640_at (AC004561.78_AT) gb|AAC95192.1| (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Duplicates

13187 and 13189 (thioredoxin h)
There are two duplicates of this
in set 3 (13188 and 16981) Count
it in set 3.

13215 and 16649 (putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase)

13285 and 16091 (heat shock protein 83)

13217 (calmodulin-like) has a duplicate in set 3 (17500). Count in set 3

16105 (hsf4) has a duplicate in set 4 (13273) Count in set 4

7 pad4orNahG and edm1 without rps2

ProbeSet

14110_i_at
(AL035528.279_I_AT)

14148_at (NOVARTIS38_AT)

14249_i_at (PAD4_I_AT)

14250_r_at (PAD4_R_AT)

14672_s_at (TSA1_S_AT)

14673_s_at (TSB2_S_AT)

14704_s_at (WT768_RC_S_AT)

14709_at (WT788_AT)

14882_at (AL022605.63_AT)

15616_s_at
(ATHPRO25A_S_AT)

Description

emb|CAB36854.1| (AL035528) putative disease resistance protein [Arabidopsis thaliana]

gb|AAF34713.1|AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]

emb|CAB43438.1| (AL050300) putative protein [Arabidopsis thaliana]

emb|CAB43438.1| (AL050300) putative protein [Arabidopsis thaliana]

gb|AAC49117.1| (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]

gb|AAA32879.1| (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]

gb|AAD15461.1| (AC006067) unknown protein [Arabidopsis thaliana]

No hits found less than or equal to 1e-15.

emb|CAA18753.1| (AL022605) putative protein [Arabidopsis thaliana]

emb|CAA08794.1| (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
16150_s_at (ATHPEAR_S_AT)	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]
17068_s_at (ATHRLPKA_S_AT)	gb AAA32857.1 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana]
17499_s_at (AF107726_S_AT)	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
17775_at (AC004392.2_AT)	gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18969_g_at (AF163823.4_G_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]

Duplicates

14249 and 14250 (PAD4)

14704 and 15846 and 15847
(unknown protein)

18968 and 18969
(endoxyloglucan transferase)

20287 and 20288 (class IV chitinase)
 14110 (putative disease-resistance gene) is an incomplete probe set with very low signal. It has a duplicate (14111) in set 2.
 Count in set 2.
 14672 (trp synthase alpha) has a duplicate in set 2 (17487)
 Counted in set 2.

8 rps2 and pad4orNahG without edm1

ProbeSet	Description
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]

Duplicates:

14635 and 17128 (PR-1)

9 edm1 and rps2 and pad4orNahG

ProbeSet	Description
12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]

12989_s_at (AC004077.149_S_AT) 13697_at (NI16_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana] No hits found.
14201_at (NOVARTIS73_AT) 14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15. No hits found less than or equal to 1e-15.
14609_at (AC002340.147_AT) 14638_s_at (PRXCB_S_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana] emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana] emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
14763_at (X86958.1_AT) 15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana] gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
17544_s_at (ATU40856_S_AT) 17840_s_at (AC002333.223_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana] gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana] gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
18567_at (AC004411.25_AT) 20269_at (AC002387.237_AT)	
Duplicates 12879 and 17544 (AIG1) 14201 and 14202 (Novartis 73) 14638 (peroxidase) has a duplicate in set 7 (15970). Counted in set 7.	

- The first set (set 2 above) do not require *EDM1* and are not affected by *rps2*, *pad4* or *NahG*. These genes are less likely to be important for resistance mediated by *RPP7* and *RPP8* than the genes in the second set (set 3 above). The
- 5 genes in the second set require *EDM1* but are not affected by *rps2*, *pad4* or *NahG*. These genes are more likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the third set (set 4 above) are affected by *rps2*, do not require *EDM1*, and are not affected by *pad4* or *NahG*. The genes in the
- 10 fourth (set 5 above), seventh (set 8 above) and eight (set 9 above) sets include genes that are affected by *pad4* or *NahG*, and so are less likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the sixth set (set 7 above) require *RPP7* or *RPP8* for increased expression after infection by

Peronospora and are affected by *rps2*. These genes are also less likely to be important for resistance mediated by *RPP7* and *RPP8*.

Duplicates were identified by sorting "RPP7 or 8" by description, which put duplicated genes adjacent to one another. Most duplicates were in the same set, but there were nine cases of duplicates that had one probe set in one set, and another in another set. Examination of the data revealed that in these cases, the expression values were close to the cut-offs used to define the various sets. If one copy met the criteria, e.g., for *rps2*-dependent, but the other copy did not, the gene was classified as not *rps2*-dependent. Duplicates are noted. One hundred eighty four unique genes remained (SEQ ID NOs:1-211 and 792, Table 9 and Table 10).

Table 9

SEQ ID NO	ProbeSet	Description
1	12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
2	12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
3	12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
4	12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
5	12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
6	12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
7	12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
8	12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
9	12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
10	12360_at (AL022347.131_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
11	20223_at (AL022347.145_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]

		gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
12	12500_s_at (AF081067.3_S_AT)	[Arabidopsis thaliana]
13	12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]
14	12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
15	12556_at (AL079344.155_AT)	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
16	12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
17	12630_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
18	12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana] gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene.
19	12777_i_at (AC006577.16_I_AT)	[Arabidopsis thaliana] gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene.
20	12778_r_at (AC006577.16_R_AT)	[Arabidopsis thaliana] gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene.
21	12779_f_at (AC006577.16_F_AT)	[Arabidopsis thaliana]
22	12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
23	17744_s_at (AC004684.168_S_A T)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
24	12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
25	20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]

26	12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
27	12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
28	12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
29	16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
30	12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
31	16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
32	12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1 (AF021244) coronatine- induced protein 1 [Arabidopsis thaliana]
33	12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis- related protein 1 [Arabidopsis thaliana]
34	12989_s_at (AC004077.149_S_A T)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
35	13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
36	13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
37	13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T43869 come from from this gene. [Arabidopsis thaliana]
38	13154_s_at (AC002333.210_S_A T)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
39	13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
40	13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
41	13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
42	13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
43	16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
44	13198_i_at (ATTS0190_I_AT)	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

45	13215_s_at (CAFFEROYLCOAM ETHYLTRANS_S_A T)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
46	16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
47	13217_s_at (CALMODULINLIK E_S_AT)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
48	17500_s_at (ATHCALLGA_S_A T)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
49	13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
50	16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
51	13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
52	13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
53	16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
54	13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
55	13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
56	13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
57	13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
58	13631_at (AC002387.185_AT)	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
59	13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
	13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]

		gb AAD25552.1 AC005850_9 (AC005850)
	20365_s_at	Highly Similar to Mlo proteins [Arabidopsis
60	(AC005850.19_S_AT)	thaliana]
61	13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
no cds	13697_at (NI16_AT)	No hits found.
	13751_at	gb AAF16751.1 AC010155_4 (AC010155)
62	(NOVARTIS127_AT)	F3M18.8 [Arabidopsis thaliana]
	13764_at	gb AAD39641.1 AC007591_6 (AC007591)
63	(NOVARTIS22_AT)	F9L1.6 [Arabidopsis thaliana]
	13818_s_at	gb AAD15433.1 (AC006218) putative
	(AC006218.175_S_A	aspartate aminotransferase [Arabidopsis
64	T)	thaliana]
	13880_s_at	emb CAB39611.1 (AL049480) possible
	(AL049480.183_S_A	apospory-associated like protein
65	T)	[Arabidopsis thaliana]
	13966_at	emb CAA17775.1 (AL022023) putative
66	(AL022023.172_AT)	protein [Arabidopsis thaliana]
		gb AAC78535.1 (AC005662) putative
	14083_at	embryo-abundant protein [Arabidopsis
67	(AC005662.56_AT)	thaliana]
	14096_at	
68	(AC002291.12_AT)	No hits found.
	14110_i_at	emb CAB36854.1 (AL035528) putative
	(AL035528.279_I_AT	disease resistance protein [Arabidopsis
69)	thaliana]
	14111_s_at	emb CAB36854.1 (AL035528) putative
	(AL035528.279_S_A	disease resistance protein [Arabidopsis
70	T)	thaliana]
		gb AAC26243.1 (AF077407) contains
		similarity to sugar transporters (Pfam:
		sugar_tr.hmm, score: 395.39) [Arabidopsis
71	14116_at	thaliana]
	(AF077407.30_AT)	
	14141_at	
72	(NOVARTIS31_AT)	No hits found less than or equal to 1e-15.
		dbj BAA22813.1 (D26015) CND41,
	14145_at	chloroplast nucleoid DNA binding protein
73	(NOVARTIS35_AT)	[Nicotiana tabacum]
	14146_at	gb AAD25550.1 AC005850_7 (AC005850)
74	(NOVARTIS36_AT)	Hypothetical protein [Arabidopsis thaliana]
	14148_at	gb AAF34713.1 AF224762_1 (AF224762)
75	(NOVARTIS38_AT)	SigA binding protein [Arabidopsis thaliana]
	14201_at	
76	(NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
	14202_at	
	(NOVARTIS73_RC_	
77	AT)	No hits found less than or equal to 1e-15.
	14223_at	emb CAA19683.1 (AL024486) putative
78	(NOVARTIS9_AT)	protein [Arabidopsis thaliana]

79	14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]
		gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
80	14248_at (PAD3_AT)	emb CAB43438.1 (AL050300) putative
81	14249_i_at (PAD4_I_AT)	protein [Arabidopsis thaliana]
82	14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
83	14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
84	14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
85	14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana]
86	14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
87	14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
88	14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
89	14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
90	14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
91	14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
92	14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
93	14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana]
94	14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
95	17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
96	14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]

97	15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
98	14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
99	17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
100	14673_s_at (TSB2_S_AT)	thaliana]
101	14682_i_at (WT1012A_RC_I_AT)	No hits found.
102	14691_at (WT1096_AT)	No hits found.
103	14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
104	15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
105	15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
106	14709_at (WT788_AT)	No hits found less than or equal to 1e-15. emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
107	14763_at (X86958.1_AT)	thaliana]
108	14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
109	15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
110	15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana] gb AAB53975.1 (U90522) lysine- ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
111	15161_s_at (ATU90522_S_AT)	dehydrogenase [Arabidopsis thaliana]
112	15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
113	15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
114	15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
115	15523_s_at (AL078637.213_S_A T)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
116	15532_r_at (AL078637.191 R A	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]

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- 117 15616_s_at
(ATHPRO25A_S_AT) emb|CAA08794.1| (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
) dbj|BAA24440.1| (AB010407)
- 118 15629_s_at
(AB003280_S_AT) phosphoglycerate dehydrogenase
[Arabidopsis thaliana]
gb|AAD10829.1| (AF117063) putative
- 119 15641_s_at
(AF117063_S_AT) inositol polyphosphate 5-phosphatase At5P2
[Arabidopsis thaliana]
gb|AAB80922.1| (AF022658) putative c2h2
- 120; 682 15665_s_at
(AF022658_S_AT) zinc finger transcription factor [Arabidopsis thaliana]
- 121 15778_at
(X98676.2_AT) emb|CAA67234.1| (X98676) zinc finger
protein [Arabidopsis thaliana]
- 122 15779_g_at
(X98676.2_G_AT) emb|CAA67234.1| (X98676) zinc finger
protein [Arabidopsis thaliana]
- 123 15859_at
(AC006587.164_AT) gb|AAD15461.1| (AC006067) unknown
protein [Arabidopsis thaliana]
- 124 15978_at
(X68592.6_AT) gb|AAD15461.1| (AC006067) unknown
protein [Arabidopsis thaliana]
- 125 16053_i_at
(Y14251.4_I_AT) emb|CAA74639.1| (Y14251) glutathione S-
transferase [Arabidopsis thaliana]
- 126 16061_s_at
(AB004796_S_AT) gb|AAB97145.1| (AF000977) MEK1
[Arabidopsis thaliana] thaliana
gb|AAD34615.1|AF153283_1 (AF153283)
- 127 16083_s_at
(AF153283_S_AT) putative progesterone-binding protein
homolog [Arabidopsis thaliana]
- 128 16150_s_at
(ATHPEAR_S_AT) emb|CAB41718.1| (AL049730) pEARLI 1
[Arabidopsis thaliana]
- 129 16232_s_at
(AL080252.77_S_AT) emb|CAB45796.1| (AL080252) putative
protein [Arabidopsis thaliana]
gb|AAC32915.1| (AC004138) putative
- 130 16257_at
(AC004138.105_AT) nucleoside triphosphatase [Arabidopsis
thaliana]
- 131 16298_at
(AL021890.71_AT) emb|CAA17152.1| (AL021890) putative
protein [Arabidopsis thaliana]
- 132 16299_at
(AL024486.185_AT) emb|CAA19705.1| (AL024486) putative
protein [Arabidopsis thaliana]

gb|AAD40144.1|AF149413_25 (AF149413)
contains similarity to protein kinase domains.
(Pfam F00069, Score=162.6, E=6.8e-45,
N=1) and leucien rich repeats (Pfam
PF00560, Score=210.7, E=2.2e-59, N=10)
- 133 16357_at
(AF149413.38_AT) [Arabidopsis thaliana]
emb|CAA20203.1| (AL031187) receptor-like
- 134 16360_at
(AL031187.126_AT) serine/threonine protein kinase ARK3
[Arabidopsis thaliana]

- 135 16365_at (AC003974.136_AT) gb|AAC04495.1| (AC003974) putative disease resistance protein [Arabidopsis thaliana]
- 136 16578_s_at (ATHRPRP1B_S_AT) emb|CAB68132.1| (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
- 137 16817_s_at (AL096882.91_S_AT) emb|CAB51412.1| (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
- 138 16914_s_at (AL049500.57_S_AT) emb|CAB39936.1| (AL049500) osmotin precursor [Arabidopsis thaliana]
- 139 16995_at (AC002391.188_AT) gb|AAB87114.1| (AC002391) unknown protein [Arabidopsis thaliana]
- 140 17008_at (AC006585.212_AT) gb|AAD23027.1|AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
- 141 17014_s_at (ATU05206_S_AT) gb|AAC48925.1| (U05206) ribonuclease [Arabidopsis thaliana]
- 142 17051_s_at (AF098947_S_AT) gb|AAD09952.1| (AF098947) CTF2B [Arabidopsis thaliana]
- 143 17068_s_at (ATHRLPKA_S_AT) gb|AAA32857.1| (M84658) receptor-like protein kinase [Arabidopsis thaliana]
- 144 17083_s_at (ATU18770_S_AT) gb|AAD25838.1|AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
- 145 17097_s_at (ATU66345_S_AT) gb|AAC49697.1| (U66345) calreticulin [Arabidopsis thaliana]
- 146 17278_at (AC000107.5_AT) gb|AAD36959.1|AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
- 147 17413_s_at (AJ006961.4_S_AT) emb|CAA67551.1| (X99097) peroxidase [Arabidopsis thaliana]
- 148 17464_at (AC000132.72_AT) gb|AAB60752.1| (AC000132) Similar to A. thaliana receptor-like protein kinase (gb|RLK5_ARATH). ESTs gb|ATTS0475, gb|ATTS4362 come from this gene. [Arabidopsis thaliana]
- 149 17485_s_at (Z97340.345_S_AT) emb|CAB10405.1| (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]
- 150 17499_s_at (AF107726_S_AT) gb|AAD19610.1| (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
- 151 17511_s_at (AF067605_S_AT) gb|AAB71482.1| (AC002294) similar to S-linalool synthase gp|U58314|1491939 [Arabidopsis thaliana]
- 152 17522_s_at (D78606_S_AT) dbj|BAA28538.1| (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
- 153 17544_s_at (ATU40856_S_AT) gb|AAC49282.1| (U40856) AIG1 [Arabidopsis thaliana]

- 154 17653_at (AL035679.144_AT) emb|CAB38823.1| (AL035679) putative protein [Arabidopsis thaliana]
gb|AAC28500.1| (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb|AF020814 from Pisum sativum. [Arabidopsis thaliana]
- 155 17775_at (AC004392.2_AT) 17840_s_at (AC002333.223_S_A T) gb|AAB64049.1| (AC002333) putative endochitinase [Arabidopsis thaliana]
- 156 17843_s_at (AC002391.150_S_A T) gb|AAB87109.1| (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
- 157 17899_at (Z97339.197_AT) emb|CAB10339.1| (Z97339) hypothetical protein [Arabidopsis thaliana]
- 158 17930_s_at (AJ006960.4_S_AT) emb|CAA07352.1| (AJ006960) peroxidase [Arabidopsis thaliana]
- 159 18012_s_at (AJ002295_S_AT) emb|CAB59428.1| (AJ002295) inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]
- 160 18022_at (AJ010971_AT) emb|CAB52675.1| (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
- 161 18054_at (AJ238846_AT) emb|CAB54517.1| (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
- 162 18216_at (X95573.2_AT) gb|AAF24959.1|AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
- 163 18217_g_at (X95573.2_G_AT) gb|AAF24959.1|AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
- 164 18551_at (AC002391.163_AT) gb|AAB87112.1| (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
- 165 18567_at (AC004411.25_AT) gb|AAC34217.1| (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
- 166 18590_at (AJ222713.4_AT) emb|CAA10955.1| (AJ222713) unnamed protein product [Arabidopsis thaliana]
- 167 18591_at (X74756.2_AT) emb|CAA52772.1| (X74756) ATAF2 [Arabidopsis thaliana]
- 168; 665 18625_at (AC005278.22_AT) gb|AAC72125.1| (AC005278) ESTs gb|H36966, gb|R65511, gb|T42324 and gb|T20569 come from this gene. [Arabidopsis thaliana]
- 169 18716_at (X91916_AT) gb|AAF26754.1|AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
- 170 18844_at (AC005315.131_AT) gb|AAC33239.1| (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
- 171 18908_i_at (AF055848.2_I_AT) gb|AAC62611.1| (AF055848) subtilisin-like protease [Arabidopsis thaliana]
- 172

173	18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
174	18946_at (Y11788.1_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
175	18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
176	18969_g_at (AF163823.4_G_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
177	18983_s_at (AL049730.104_S_A T)	emb CAB41722.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
178	19158_at (X95738.2_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
179	19171_at (AC002335.160_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
180	19177_at (X99923.1_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
181	19182_at (AL031804.245_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
182	19229_at (AC003027.39_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
183	19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
184	19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
185	19415_at (AL080253.32_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
186	19594_i_at (X98321.2_I_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
187	19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
188	19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
189	19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]
190	19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
191	19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
192	19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

193	19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
194	19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
195	19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
196	20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
197	20232_s_at (AL022347.12_S_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
198	20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
199	20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
200	20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
201	20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
202	20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
203	20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
204	20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
205	20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
206	20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
207	20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
208	20429_s_at (Z97336.167_S_AT)	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
209	20620_g_at (AC005896.161_G_A T)	gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
210	20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]
211	20641_at (X91919.1_AT)	emb CAA63012.1 (X91919) LEA76 homologue type1 [Arabidopsis thaliana]
789	18224_s_at (AL021890.57_S_AT)	Arabidopsis thaliana. ESTs gb N97082, gb Z27056 and gb Z29902 come from this gene.
790	16522_at (X77500.2_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
		emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]

		gb AAC17040.1 (AC002986) Similarity to
		A. thaliana gene product F21M12.20,
		gb AC000132. EST gb Z25651 comes from
		this gene. [Arabidopsis thaliana]
791	19982_at (AC002986.28_AT)	gb AAC16927.1 (AC002338) putative
367	18920_at (AC002338.11_AT)	laccase [Arabidopsis thaliana]
212	12324_i_at	AC007212
793	12345_at	L36246
213	12500_s_at	AF081067
214; 662	12505_s_at	AC005309
215	12608_i_at	S70188
216	12642_at	AC006920
217	12746_i_at	AL096882
218	12748_f_at	AL096882
219	12761_s_at	AC006577
220	12773_at	AC005727
221	12778_r_at	AC006577
222	12798_at	AC003028
223	12802_at	AL022373
	12842_s_at	No hits found less than or equal to 1e-15
224	12843_s_at	AC007195
	12845_s_at	AJ004810
225	12879_s_at	U40856
226	12891_at	U73786
227	12892_g_at	U73786
228; 658	12904_s_at	AB008103
229	12905_s_at	AB008104
230	12908_s_at	AB008107
231	12909_s_at	Z97343
232	12911_s_at	X84229
233	12916_s_at	AF021244
234	13138_at	AL096882
235	13177_at	AL049640
236	13178_at	U93215
237	13187_i_at	U35829
238	13189_s_at	U35829
239	13198_i_at	AL021749
240	13212_s_at	AL137080
241	13217_s_at	AL049862
242	13258_s_at	AC005309
243	13273_s_at	U68017
244	13284_s_at	AJ002551
245	13604_at	AC000104
246	13615_at	AC002332
247	13617_at	AC006592
248	13718_at	Z72152
249	13771_at	AC006593
250	13785_at	AC007087
251	14052_at	AC004122

252	14096_at	AC002291
253	14097_at	AC005309
254	14116_at	AF077407
255	14141_at	AC011437
256; 683	14148_at	AF224762
257	14196_at	AC012563
258	14201_at	AL163972
259	14219_at	AC068667
260	14223_at	AL024486
261	14248_at	AC007357
262	14250_r_at	AL050300
263	14595_at	AL022580
264	14608_at	AC007357
265	14614_at	AC004165
266	14621_at	AC004747
267	14627_i_at	X76609
268	14628_r_at	X76609
269	14635_s_at	AC005398
270	14636_s_at	AC013258
271	14643_s_at	AC006836
272	14672_s_at	U18993
273	14675_s_at	D85191
274	14691_at	AP002046
275	14704_s_at	AC006067
276	14706_r_at	AL137189
277	14709_at	AP002046
278	14711_s_at	AF085279
279	14731_s_at	AF014960
280	14784_at	AC005310
281	14951_at	AL049481
282	15057_at	AL035440
283	15085_s_at	AL031018
284	15105_s_at	Z14987
285	15116_f_at	AF121356
286	15125_f_at	D85190
287	15141_s_at	D85191
288	15145_s_at	D64155
289	15154_s_at	AL096860
290	15161_s_at	U90522
291	15178_s_at	U43489
292	15216_s_at	U75198
293	15431_at	AL030978
294	15496_at	AC006282
295	15523_s_at	AL078637
296	15593_s_at	U54561
297	15611_s_at	L22567
298	15616_s_at	AJ009696
299	15622_s_at	U43945

300	15629_s_at	AB010407
301	15665_s_at	AF022658
302	15680_s_at	D42061
303	15846_at	AC006067
304	15847_g_at	AC006067
305	15866_s_at	AC005770
306	15950_at	AC006429
307	15954_at	U72155
308	15978_at	X68592
309	16038_s_at	L04173
310	16063_s_at	AB008103
311	16105_s_at	U68017
312	16150_s_at	AL049730
313	16153_s_at	AC013258
314	16393_s_at	AC006436
315	16412_s_at	AL022603
316	16442_s_at	AJ002551
317	16504_s_at	Z97335
318	16510_at	AL034567
319	16536_s_at	AB008107
320	16539_s_at	Z97343
321	16569_s_at	L23968
322	16578_s_at	AL137080
323	16609_s_at	AB008104
324	16620_s_at	AF051338
325	16637_s_at	Z97336
326	16817_s_at	AL096882
327	16864_i_at	AL133248
328	16951_i_at	AC005662
329	16952_s_at	AC005662
330	16981_s_at	U35829
331	17014_s_at	U05206
332	17033_s_at	U83179
333	17054_s_at	AF134128
334	17073_s_at	AC006836
335	17119_s_at	AF132212
336	17123_s_at	AF106087
337	17128_s_at	AC005398
338	17187_at	AF128396
339; 669	17303_s_at	AC005499
340; 663	17379_at	AC018721
341	17386_at	AC006264
342	17413_s_at	X99097
343	17499_s_at	AF107726
344	17500_s_at	AL049862
345	17544_s_at	U40856
346	17567_at	AL162751
347	17886_at	AC004484

348	17899_at	Z97339
349	17917_s_at	AC004261
350	17961_at	AC007323
351	17963_at	AL049730
352	18003_at	AF188334
	18064_r_at	No hits found
	18069_at	No hits found
	18070_r_at	No hits found
353	18216_at	AC012375
354	18217_g_at	AC012375
355	18235_at	AC000348
356	18252_at	AL096882
357	18255_at	AC005770
358	18272_at	AF002109
359	18533_at	AL021684
360	18556_at	AC006264
361	18590_at	AJ222713
362	18591_at	X74756
363	18607_s_at	U78721
364	18635_at	AC004005
365	18716_at	AC007396
366	18876_at	AF002109
367	18920_at	AC002338
368	18928_at	AC002338
369	19034_at	AL021768
370	19171_at	AC002335
371	19178_at	AB035137
372	19182_at	AL031804
373	19251_at	AL035538
374	19640_at	AC004561
375	19977_at	AL049659
376	20017_at	AC004521
377	20034_i_at	A71607
378	20201_at	AL078470
379	20227_s_at	AB027252
380	20269_at	AC002387
381	20297_at	AC007153
382	20314_s_at	AL096882
383	20335_s_at	Y14208
384	20429_s_at	Z97336
385	20585_s_at	AC005309
386	20641_at	X91919
387	12333_at	AJ286345
388	14028_at	
389	14295_s_at	Z54356
390	14965_at	AC002329
391	15969_s_a	AJ133036
392	15982_s_a	X98190

393	16461_I_at	AC004683
394	16462_s_a	AC004683
395	16514_at	AL035538
396	17549_s_a	L37126
397	18706_s_a	X75782
398	19594_i_at	X98321
399	20555_s_a	AL080318
400	16212_at	gb AAD17366.1 (AF128396) similar to human phosphotyrosyl phosphatase activator PTPA (GB:X73478) [Arabidopsis thaliana]
794	14985_s_at	gb AAC32233.2 (AC005168) unknown protein [Arabidopsis thaliana]
401	16411_s_at	emb CAB71046.1 (AL137898) shaggy-like kinase beta [Arabidopsis thaliana]
402	15920_i_at	gb AAD39561.1 AC007067_1 (AC007067) T10O24.1 [Arabidopsis thaliana]
403	16299_at	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
404	18445_at	gb AAC98458.1 (AC005851) putative glucosyltransferase [Arabidopsis thaliana]
405	19215_at	gb AAC23400.1 (AC004005) putative methyl chloride transferase [Arabidopsis thaliana]
406	16439_at	emb CAA50905.1 (X72022) ORF1 [Arabidopsis thaliana]
407	16047_at	gb AAD20710.1 (AC006300) unknown protein [Arabidopsis thaliana]
408	18003_at	gb AAF01328.1 AF188334_1 (AF188334) Toll/interleukin-1 receptor-like protein [Arabidopsis thaliana]
409	20429_s_at	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
410	17917_s_at	gb AAD12002.1 (AC004261) calcium binding protein (CaBP-22) [Arabidopsis thaliana]
411	17963_at	emb CAB41717.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
412	16150_s_at	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
413	20239_g_at	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
414	20238_at	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
415	15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
416	18591_at	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]

417	14116_at	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
418	12759_at	gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb 84105 and gb A1100071 come from this gene. [Arabidopsis thaliana]
419	19060_at	gb AAC18809.1 (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomycetes occidentalis. [Arabidopsis thaliana]
420	12998_at	emb CAB41863.1 (AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]
421	13172_s_at	gb AAD30608.1 AC007369_18 (AC007369) Sugar transporter [Arabidopsis thaliana]
422	14709_at	No hits found less than or equal to 1e-15.
423	15931_at	gb AAD41420.1 AC007727_9 (AC007727) F8K7.9 [Arabidopsis thaliana]
424	20369_s_at	emb CAB41109.1 (AL049656) ammonium transport protein (AMT1) [Arabidopsis thaliana]
425	14201_at	No hits found less than or equal to 1e-15.
426	14691_at	No hits found.
75	14148_at	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
426	16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2 [Arabidopsis thaliana]
427	13625_s_at	emb CAB42924.1 (AL049862) putative disease resistance protein [Arabidopsis thaliana]
428	13702_s_at	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
429	17886_at	gb AAC14530.1 (AC004484) unknown protein [Arabidopsis thaliana]
430	12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase [Arabidopsis thaliana]
431	12353_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase [Arabidopsis thaliana]
432	17899_at	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]

433	18894_at	emb CAB43665.1 (AL050352) Ca ²⁺ -transporting ATPase-like protein [Arabidopsis thaliana]
434	14978_at	gb AAB64024.1 (AC002333) putative glucosyltransferase [Arabidopsis thaliana]
435	14223_at	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
436	16109_s_at	gb AAC05342.1 (AC002521) putative protein kinase [Arabidopsis thaliana]
437	18820_at	gb AAD28055.1 AC007166_3 (AC007166) putative protein kinase [Arabidopsis thaliana]
438	20345_at	gb AAC72865.1 (AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]
439	14170_at	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]
440	15143_s_at	gb AAD38519.1 AF138281_1 (AF138281) phospholipase D-gamma-2 [Arabidopsis thaliana]
441	17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
442	20590_at	emb CAB37511.1 (AL035540) Phospholipase like protein [Arabidopsis thaliana]
443	14608_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana]
444	13550_at	emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
445	13355_at	emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana]
446	13564_at	gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis thaliana]
447	19845_g_at	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
448	12764_f_at	gb AAC32912.1 (AC004138) putative glutathione S-transferase [Arabidopsis thaliana]
449	17922_at	gb AAB16855.1 (U71122) pyruvate decarboxylase [Arabidopsis thaliana]

450	15982_s_at	emb CAA66863.1 (X98190) peroxidase ATP2a [Arabidopsis thaliana]
451	12227_at	gb AAD39285.1 AC007576_8 (AC007576) Unknown protein [Arabidopsis thaliana]
452	20555_s_at	emb CAB45975.1 (AL080318) copper amine oxidase like protein (fragment2) [Arabidopsis thaliana]
453	19844_at	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
454	13985_s_at	gb AAC31242.1 (AC004747) unknown protein [Arabidopsis thaliana]
455	13548_at	gb AAD41421.1 AC007727_10 (AC007727) ESTs gb N96028, gb F14286, gb T20680, gb F14443, gb AA657300 and gb N65244 come from this gene. [Arabidopsis thaliana]
456	15611_s_at	gb AAA32775.1 (L22567) cor78 [Arabidopsis thaliana]
457	19840_s_at	gb AAD25759.1 AC007060_17 (AC007060) Strong similarity to F19I3.2 gi 3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb AC004238. EST gb R90518 comes from this gene.
458	15985_at	emb CAA67340.1 (X98808) peroxidase ATP3a [Arabidopsis thaliana]
459	14584_at	gb AAD32844.1 AC007658_3 (AC007658) unknown protein [Arabidopsis thaliana]
460	15422_at	gb AAD36948.1 AF069441_8 (AF069441) hypothetical protein [Arabidopsis thaliana]
461	20150_at	gb AAB61076.1 (AF007271) A_TM021B04.14 gene product [Arabidopsis thaliana]
462	18844_at	gb AAC33239.1 (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
463	16360_at	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
464	20292_at	gb AAB87113.1 (AC002391) putative protein kinase [Arabidopsis thaliana]
465	14554_at	gb AAC18798.1 (AC003671) F17O7.4 [Arabidopsis thaliana]
466	18604_at	gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]

467	16061_s_at	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
468	14145_at	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
469	16144_s_at	dbj BAA04870.1 (D21843) MAP kinase [Arabidopsis thaliana]
470	17097_s_at	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
471	19718_at	gb AAB71447.1 (AC000098) Similar to Arabidopsis Fe(II) transport protein (gb U27590). [Arabidopsis thaliana]
472	14298_g_at	gb AAC25507.1 (AC003979) T22J18.6 [Arabidopsis thaliana]
473	12307_at	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
474	20232_s_at	emb CAA18460.1 (AL022347) protein kinase-like protein [Arabidopsis thaliana]
475	19322_at	gb AAF19738.1 AC012463_12 (AC012463) T2E6.14 [Arabidopsis thaliana]
476	14224_at	gb AAF07386.1 AC010675_9 (AC010675) putative peptide transporter [Arabidopsis thaliana]
477	14270_at	gb AAD39269.1 AC007203_1 (AC007203) Putative UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]
478	15479_at	emb CAB39671.1 (AL049483) putative protein [Arabidopsis thaliana]
479	14090_i_at	gb AAD41981.1 AC006438_13 (AC006438) unknown protein [Arabidopsis thaliana]
480	16162_s_at	gb AAB05099.1 (U39944) BELL1 [Arabidopsis thaliana]
481	20149_at	gb AAB70415.1 (AC000106) Similar to Beta integral membrane protein (gb U43629). [Arabidopsis thaliana]
482	12765_at	gb AAD15574.1 (AC006340) unknown protein [Arabidopsis thaliana]
214	12505_s_at	gb AAC63643.1 (AC005309) putative CONSTANS-like B-box zinc finger protein [Arabidopsis thaliana]
483	13140_at	gb AAC79588.1 (AC005727) putative RING zinc finger ankyrin protein [Arabidopsis thaliana]
484	15022_at	gb AAC72124.1 (AC005278) ESTs gb H37641 and gb AA651422 come from this gene. [Arabidopsis thaliana]

485	16306_at	emb CAB41935.1 (AL049751) putative protein [Arabidopsis thaliana] gb AAC26246.1 (AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
486	18611_at	emb CAB43428.1 (AL050300) putative protein [Arabidopsis thaliana]
487	20199_at	emb CAA18626.1 (AL022580) putative protein [Arabidopsis thaliana]
488	14595_at	gb AAD31337.1 AC007354_10 (AC007354) Strong similarity to gb Y09533 involved in starch metabolism from Solanum tuberosum and contains a PF01326 Pyruvate phosphate dikinase, PEP/pyruvate binding domain. EST gb N96757 comes from this gene. [Arabidopsis thaliana]
489	12532_at	emb CAB41162.1 (AL049659) putative protein [Arabidopsis thaliana]
490	19977_at	gb AAC79594.1 (AC005727) putative membrane channel protein [Arabidopsis thaliana]
491	12773_at	gb AAD32870.1 AC005489_8 (AC005489) F14N23.8 [Arabidopsis thaliana]
492	19632_at	emb CAA16957.1 (AL021811) putative protein [Arabidopsis thaliana]
493	19359_s_at	emb CAA78712.1 (Z14988) glycine rich protein [Arabidopsis thaliana]
494	14716_f_at	gb AAC19269.1 (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
495	13648_at	gb AAD41977.1 AC006438_9 (AC006438) unknown protein [Arabidopsis thaliana]
496	12768_at	gb AAC69134.1 (U78721) putative auxin-regulated protein [Arabidopsis thaliana]
497	16422_at	gb AAC26203.1 (AF053747) dormancy-associated protein [Arabidopsis thaliana]
498	15131_s_at	emb CAB38829.1 (AL035679) drought-inducible cysteine proteinase RD19A precursor
499	14659_s_at	emb CAB38829.1 (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]
500	14658_s_at	emb CAB36513.1 (AL035440) putative protein [Arabidopsis thaliana]
501	15057_at	emb CAB56039.1 (AJ133786) gigantea protein [Arabidopsis thaliana]
502	17581_g_at	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
503	18567_at	

504	17047_s_at	gb AAC68674.1 (AF078825) RING-H2 finger protein RHA3b [Arabidopsis thaliana]
505	15105_s_at	emb CAA78711.1 (Z14987) glycine rich protein [Arabidopsis thaliana]
506	14196_at	gb AAF16557.1 AC012563_10 (AC012563) unknown protein [Arabidopsis thaliana]
507	17599_s_at	gb AAD50976.1 AF170494_1 (AF170494) ionotropic glutamate receptor ortholog GLR6 [Arabidopsis thaliana]
508	18556_at	gb AAD29803.1 AC006264_11 (AC006264) cyclophilin (CYP2) [Arabidopsis thaliana]
509	16486_at	gb AAB04606.1 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana]
510	18272_at	gb AAB95293.1 (AF002109) unknown protein [Arabidopsis thaliana]
795	12219_at	gb AAD31373.1 AC006053_15 (AC006053) unknown protein [Arabidopsis thaliana]
511	20446_s_at	gb AAC80600.1 (AC005106) T25N20.21 [Arabidopsis thaliana]
512	12561_at	emb CAA16701.1 (AL021687) putative protein [Arabidopsis thaliana]
513	12060_at	gb AAD46000.1 AC005916_12 (AC005916) Contains similarity to gb AF113001 silencing mediator of retinoic acid and thyroid hormone receptor alpha and gb AF109179 cyclin T1 from Mus musculus. ESTs gb N95317, gb Z29139 and gb Z30853 come from this gene. [Arabidopsis thaliana]
514	18235_at	gb AAB61480.1 (AC000348) T7N9.4 [Arabidopsis thaliana]
515	14021_r_at	emb CAA04134.1 (AJ000497) Starch branching enzyme II [Arabidopsis thaliana]
516	14020_i_at	emb CAA04134.1 (AJ000497) Starch branching enzyme II [Arabidopsis thaliana] emb CAA44630.1 (X62818) Metallothionein-like protein [Arabidopsis thaliana]
517	16011_s_at	gb AAD09232.1 (U83179) unknown [Arabidopsis thaliana]
518	17033_s_at	
519	16050_at	gb AAD24630.1 AC006919_10 (AC006919) putative fructose biphosphate aldolase [Arabidopsis thaliana]

520	19692_at	gb AAC14039.1 (AC003981) F22O13.13 [Arabidopsis thaliana]
521	19181_s_at	gb AAC39464.1 (AF053065) late embryogenesis abundant protein homolog [Arabidopsis thaliana]
792	13435_at	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
522	17128_s_at	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
523	14635_s_at	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
524	15846_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
525	15847_g_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
526	14704_s_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
527	17456_at	gb AAB80678.1 (AC002332) putative steroid dehydrogenase [Arabidopsis thaliana]
528	14895_s_at	emb CAB10562.1 (Z97344) acetylornithine deacetylase [Arabidopsis thaliana]
529	19979_at	gb AAB95235.1 (AC002130) F1N21.7 [Arabidopsis thaliana]
530	20325_s_at	emb CAA78152.1 (Z12162) protein phosphatase 1A [Arabidopsis thaliana]
531	18234_at	gb AAB61479.1 (AC000348) T7N9.3 [Arabidopsis thaliana]
532	16474_s_at	emb CAA35838.1 (X51474) kin1 [Arabidopsis thaliana]
533	18701_s_at	emb CAA38894.1 (X55053) cold regulated [Arabidopsis thaliana]
534	13785_at	gb AAD23000.1 AC007087_19 (AC007087) cold-regulated protein cor15b precursor [Arabidopsis thaliana]
535	20387_at	gb AAC23422.1 (AC004005) putative methionine aminopeptidase [Arabidopsis thaliana]
536	13178_at	gb AAB63086.1 (U93215) unknown protein [Arabidopsis thaliana]
537	12103_at	gb AAD30603.1 AC007369_13 (AC007369) Unknown protein [Arabidopsis thaliana]
538	13225_s_at	emb CAA42483.1 (X59814) Cold and ABA regulated gene [Arabidopsis thaliana]

539	17003_at	gb AAB95275.1 (AF002109) putative LIM-domain protein [Arabidopsis thaliana]
540	15878_at	emb CAA19880.1 (AL031032) putative protein [Arabidopsis thaliana]
541	13004_at	gb AAD03574.1 (AC003952) putative senescence-related protein [Arabidopsis thaliana]
542	14052_at	gb AAC34333.1 (AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]
543	15798_at	gb AAC05351.1 (AC002521) putative receptor-like protein kinase [Arabidopsis thaliana]
793	12345_at	gb AAB67985.1 (L36246) anoxia-induced protein [Arabidopsis thaliana]
544	16818_s_at	emb CAA20206.1 (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]
545	13916_at	gb AAC62136.1 (AC005169) unknown protein [Arabidopsis thaliana]
666	20342_at	emb CAB41311.1 (AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
546	20421_at	emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
547	14250_r_at	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
548	14249_i_at	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
549	17544_s_at	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
550	12879_s_at	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
551	20017_at	gb AAC16079.1 (AC004521) unknown protein [Arabidopsis thaliana]
552	13177_at	emb CAB40989.1 (AL049640) growth factor like protein [Arabidopsis thaliana]
553	19946_at	gb AAF18611.1 (AC005170_1) (AC005170) similar to senescence-associated protein [Arabidopsis thaliana]
554	17894_at	gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]
555	15855_at	gb AAD15572.1 (AC006340) unknown protein [Arabidopsis thaliana]
556	15558_r_at	emb CAB45807.1 (AL080253) putative protein [Arabidopsis thaliana]
557	15208_s_at	No hits found less than or equal to 1e-15.

558	16153_s_at	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]
559	14636_s_at	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]
560	19178_at	dbj BAA86999.1 (AB035137) blue copper binding protein [Arabidopsis thaliana]
561	17580_at	emb CAB56039.1 (AJ133786) gigantea protein [Arabidopsis thaliana]
562	14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
563	18946_at	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
564	13009_i_at	emb CAA17138.1 (AL021889) putative protein [Arabidopsis thaliana]
565	18508_s_at	gb AAA33709.1 (L16797) glutamate decarboxylase [Petunia x hybrida]
566	12556_at	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
567	13115_at	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]
568	15046_s_at	gb AAB87120.1 (AC003000) unknown protein [Arabidopsis thaliana]
339	17303_s_at	gb AAC67339.2 (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]
569	18597_at	emb CAB45881.1 (AL080282) berberine bridge enzyme-like protein [Arabidopsis thaliana]
570	13908_s_at	emb CAB42588.1 (A71590) unnamed protein product [Arabidopsis thaliana]
571	14553_at	emb CAB41103.1 (AL049655) putative protein [Arabidopsis thaliana]
572	18928_at	gb AAB64044.1 (AC002333) putative endochitinase [Arabidopsis thaliana]

		gb AAC72119.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from <i>Daucus carota</i> . ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470, gb R65072, gb N76373, gb F15470, gb Z35182, gb H76373, gb Z34678 and gb Z35387>
573	12772_at	emb CAA18124.1 (AL022141) putative receptor protein kinase [<i>Arabidopsis thaliana</i>]
574	16326_at	
575	20479_i_at	emb CAB38908.1 (AL035708) cytochrome P450-like protein [<i>Arabidopsis thaliana</i>]
		gb AAD28318.1 AC006436_9 (AC006436) putative receptor-like protein kinase [<i>Arabidopsis thaliana</i>]
576	16393_s_at	emb CAA67551.1 (X99097) peroxidase [<i>Arabidopsis thaliana</i>]
577	17413_s_at	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [<i>Arabidopsis thaliana</i>]
578	14620_s_at	
579	20480_s_at	emb CAB38908.1 (AL035708) cytochrome P450-like protein [<i>Arabidopsis thaliana</i>]
580	15866_s_at	gb AAC79625.1 (AC005770) unknown protein [<i>Arabidopsis thaliana</i>]
581	19182_at	emb CAA21214.1 (AL031804) putative protein [<i>Arabidopsis thaliana</i>]
582	18255_at	gb AAC79625.1 (AC005770) unknown protein [<i>Arabidopsis thaliana</i>]
583	16054_s_at	emb CAA74639.1 (Y14251) glutathione S-transferase [<i>Arabidopsis thaliana</i>]
584	14672_s_at	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [<i>Arabidopsis thaliana</i>]
585	20291_s_at	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [<i>Arabidopsis thaliana</i>]
586	16053_i_at	emb CAA74639.1 (Y14251) glutathione S-transferase [<i>Arabidopsis thaliana</i>]
		gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [<i>Arabidopsis thaliana</i>]
587	17083_s_at	
588	12889_s_at	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [<i>Arabidopsis thaliana</i>]
589	12642_at	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [<i>Arabidopsis thaliana</i>]

590	17487_s_at	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
591	14838_s_at	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
592	17104_s_at	dbj BAA13640.1 (D88541) phosphoserine aminotransferase [Arabidopsis thaliana]
593	19892_at	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
594	16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
664	13273_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
595	12892_g_at	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
596	15141_s_at	dbj BAA22096.1 (D85191) vegetative storage protein [Arabidopsis thaliana]
597	18231_at	emb CAA55322.1 (X78585) Di21 [Arabidopsis thaliana]
598	15629_s_at	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
599	15978_at	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
600	20269_at	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
601	14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
602	17930_s_at	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
603	16952_s_at	gb AAC78532.1 (AC005662) calmodulin-like protein [Arabidopsis thaliana]
604	12930_s_at 12842_s_at	gb AAC49679.1 (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana] No hits found less than or equal to 1e-15.
605	16063_s_at	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
228	12904_s_at	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
606	12908_s_at	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

607	15937_at	emb CAA17127.1 (AL021889) hypothetical protein [Arabidopsis thaliana]
608	17843_s_at	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
609	18966_at	gb AAC95196.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
610	20519_at	gb AAC80599.1 (AC005106) T25N20.20 [Arabidopsis thaliana]
611	19641_at	gb AAC95189.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
612	17408_at	gb AAD32297.1 AC006533_21 (AC006533) putative glucosyltransferase [Arabidopsis thaliana]
613	15646_s_at	gb AAC37474.1 (L42212) serine acetyltransferase [Arabidopsis thaliana]
614	14731_s_at	gb AAC49988.1 (AF014960) multidrug resistance-associated protein 2; AtMRP2 [Arabidopsis thaliana]
615	20685_at	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]
616	16968_at	emb CAA17559.1 (AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]
617	18253_s_at	gb AAC78440.1 (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis thaliana] thaliana]
618	15496_at	gb AAD20156.1 (AC006282) putative glucosyl transferase [Arabidopsis thaliana]
619	19137_at	emb CAA52771.1 (X74755) ATAF1 [Arabidopsis thaliana]
620	19132_s_at	emb CAA18722.1 (AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]
621	13656_at	gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]
622	17024_s_at	gb AAB67854.1 (U61231) cytochrome P450 [Arabidopsis thaliana]
623	14705_i_at	emb CAB69849.1 (AL137189) anthranilate N-benzoyltransferase-like protein [Arabidopsis thaliana]
624	17500_s_at	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]

625	13217_s_at	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
626	15196_s_at	gb AAC49573.1 (U43412) 3'-phosphoadenosine 5'-phosphosulfate reductase [Arabidopsis thaliana]
627	18590_at	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
628	14700_at	No hits found less than or equal to 1e-15.
629	14665_r_at	emb CAA69879.1 (Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
630	12630_at	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
631	18953_at	gb AAC69851.1 (AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
632	13514_s_at	emb CAA16793.1 (AL021713) putative protein [Arabidopsis thaliana]
633	12490_at	gb AAF02787.1 AF195115_7 (AF195115) weak similarity to receptor protein kinase [Arabidopsis thaliana]
634	12246_s_at	emb CAB10404.1 (Z97340) phytochrome D [Arabidopsis thaliana]
635	20536_s_at	emb CAB37488.1 (AL035539) putative protein [Arabidopsis thaliana]
636	18409_at	gb AAC72122.1 (AC005278) F15K9.14 [Arabidopsis thaliana]
637	19387_at	gb AAD21475.1 (AC007017) unknown protein [Arabidopsis thaliana]
638	16117_s_at	gb AAB70244.1 (AF016848) WD-40 repeat protein [Arabidopsis thaliana]
639	18347_s_at	emb CAA21480.1 (AL031986) putative protein [Arabidopsis thaliana]
640	15880_at	emb CAB38906.1 (AL035708) putative protein [Arabidopsis thaliana]
667	20471_at	gb AAC49767.1 (AF003094) AP2 domain containing protein RAP2.1 [Arabidopsis thaliana]
641	16603_s_at	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]
642	12049_at	gb AAC13598.1 (AF058914) F21E10.13 gene product [Arabidopsis thaliana]
643	12048_at	gb AAC78704.1 (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

		gb AAB61117.1 (AC002062) ESTs
644	14064_at	gb N38288,gb T43486,gb AA395242 come from this gene. [Arabidopsis thaliana]
645	12149_at	gb AAC04492.1 (AC003974) unknown protein [Arabidopsis thaliana]
646	14295_s_at	emb CAA91183.1 (Z54356) HD-ZIP [Arabidopsis thaliana]
647	19034_at	emb CAA16930.1 (AL021768) TMV resistance protein N-like [Arabidopsis thaliana]
648	18624_at	gb AAC27848.1 (AC004218) unknown protein [Arabidopsis thaliana]
649	13181_at	gb AAC97218.1 (AC005936) unknown protein [Arabidopsis thaliana]
650	18866_at	gb AAD10163.1 (AC005917) putative Tall-like non-LTR retroelement protein [Arabidopsis thaliana]
651	19502_at	emb CAB44686.1 (AL078620) cytochrome P450-like protein [Arabidopsis thaliana]
652	16301_s_at	emb CAA19807.1 (AL031018) hypothetical protein [Arabidopsis thaliana]
653	19411_at	gb AAD32774.1 AC007661_11 (AC007661) unknown protein [Arabidopsis thaliana]
654	20300_g_at	emb CAA71588.1 (Y10556) CONSTANS [Arabidopsis thaliana]
655	20299_at	emb CAA71588.1 (Y10556) CONSTANS [Arabidopsis thaliana]
656	18696_s_at	gb AAB57688.1 (U96045) APS reductase [Arabidopsis thaliana]
657	15186_s_at	gb AAC26980.1 (AF016283) 5'-adenylylsulfate reductase [Arabidopsis thaliana]
659	16609_s_at	AtERF2 (, BAA32419.1; AB008104)
660	12909_s_at	EREBP4-like, AtERF6 (, CAB10530.1; Z97343)
661	16536_s_at	AtERF5 (, BAA32422.1; AB008107)
301	15665_s_at	put. C2H2 zinc finger transcription factor (, AAB80922.1; AF022658)
668	13176_at	Myb-like (, emb CAA20567.1 (AL031394)
670	15778_at	putative protein
671	20619_at	X98676.2_at
672	12966_s_at	AC005896.161_at
673	20335_s_at	AL023094.197_s_at
674	18949_at	Y14208.2_s_at
675	13015_s_at	Z54136.1_at
		X98673.2 s at emb CAB41311.1

		(AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
676	19646_s_at	AC005819.55_s_at
677	19855_at	AC007260.16_at
		AC007047.101_at gb AAC49767.1
		(AF003094) AP2 domain containing protein RAP2.1 [Arabidopsis thaliana]
678	18475_at	unspecified t-factor gb AAC49775.1
		(AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
679	13001_at	AC004665.101_at emb CAA67234.1
		(X98676) zinc finger protein [Arabidopsis thaliana]
680	15219_at	ATTHIRE4_s_at gb AAC98070.1
		(AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
681	13189_s_at	hsp70_s_at emb CAA18838.1 (AL023094)
		bZIP transcription factor ATB2 [Arabidopsis thaliana]
684	13284_s_at	

Table 10

<u>Set</u>	<u>Content</u>	<u>Number of unique genes</u>
2	7 or 8 not edm1 not	55 genes
5	rps2 not pad4 or NahG	
3	edm1 not rps2 not pad4 or NahG	44 genes
4	rps2 not edm1 not pad4 or NahG	12 genes
5	pad4 or NahG not edm1 not rps2	20 genes
6	edm1 and rps2 not pad4 or NahG	17 genes
10	7	edm1 and pad4 or NahG not rps2
	8	rps2 and pad4 or NahG not edm1
	9	edm1 and rps2 and pad4 or NahG
	Total	184 genes

- 15 For engineering resistance to pathogens whose growth is restricted by RPP7 or RPP8 dependent responses, such as oomycete pathogens, all 184 genes are potentially useful. The 128 genes in sets 2, 3, 4, and 6 are more likely to be useful, as *pad4* and *NahG* do not interfere with resistance mediated by *RPP7* or *RPP8*, so genes under their control should not be important for this type of
- 20 resistance. The 99 genes in sets 2 and 3 are even more likely to be useful, because they not affected by *rps2*, and *RPP7* and *RPP8* trigger a different kind of resistance response than the one triggered by *RPS2*. The 44 genes in set 3 are

most likely to be useful, as they require *EDM1*, and *EDM1* is required for resistance.

Example 3

5 Transcriptional Responses Triggered by the RPP7 Defense Signaling Pathway

The *RPP7* defense-signaling pathway (Figure 1) mediates resistance of the *Arabidopsis* ecotype Col-0 against the *Peronospora* isolate Hiks1. In contrast to conventional *R*-gene dependent defense signaling pathways in *Arabidopsis*, such as the *RPP4* pathway, the *RPP7* pathway does not essentially
10 require salicylic acid accumulation or previously described defense regulators, such as *EDS1*, *NDRI*, *NPRI*, *PAD4* and others.

A comparative analysis of transcriptional responses triggered by the *RPP7* and *RPP8* pathways was performed by gene expression profiling using Affymetrix oligonucleotide chips with roughly 8,200 different *Arabidopsis*
15 genes, representing roughly a third of the genome. For the analysis, 2 week old seedlings were harvested 0, 12 or 48 hours post infection with a particular *Peronospora* isolate (Table 11). To examine *RPP8* triggered transcriptional responses, a transgenic line Col-0 line carrying the *RPP8* resistance gene from the *Arabidopsis* ecotype Landsberg erecta was infected with the *Peronospora*
20 isolate Emco5. This interaction is incompatible. The interaction between Emco5 and Col-0 wild type plants served as compatible control. Responses triggered by the *RPP7* pathway were analyzed using the incompatible interaction between the *Peronospora* isolate Hiks1 and Col-0 wild type plants, as well as compatible interactions between Hiks1 and the susceptible mutants *rpp7*, *edm1*,
25 *edm2* and *edm3*. To compare transcriptional responses triggered by the unconventional *RPP7* and *RPP8* pathways with those triggered by the more conventional *RPP4* pathway, Col-0 wild type plants were infected with the *Peronospora* isolate Emoy2, which is avirulent on this ecotype. The interactions between Emoy2 and NahG plants, as well as the mutants *pad4*, *ndr1* and *npr1*,
30 served as compatible controls. Whereas *pad4* and NahG plants are fully Emoy2 susceptible, *ndr1* and *npr1* plants are only partly compromised in Emoy2 resistance.

Table 11

Plant	<u>Peronospora isolate</u>	<u>Interaction type</u>
Col-0 (tgRPP8)	Emco5	incompatible
Col-0 (<i>rpp8</i>)	Emco5	compatible
5 Col-0 (<i>RPP7</i>)	Hiks1	incompatible (2x)
Col-0 (<i>rpp7</i> ; 3929)	Hiks1	compatible
Col-0 (<i>edm1</i>)	Hiks1	compatible
Col-0 (<i>edm2</i>)	Hiks1	compatible
Col-0 (<i>edm3</i>)	Hiks1	compatible
10 Col-0 (<i>RPP4</i>)	Emoy2	incompatible
Col-0 (<i>ndr-1-1</i>)	Emoy2	intermediate
Col-0 (<i>pad4-1</i>)	Emoy2	compatible
Col-0 (<i>NahG</i>)	Emoy2	compatible
Col-0 (<i>npr1-1</i>)	Emoy2	intermediate

15

ResultsIdentification of Genes Potentially Required for *RPP7* Mediated *Peronospora* Resistance

Genes that play a role in the establishment of resistance may show differences in their regulation or their expression levels between compatible and incompatible interactions (e.g., genes may show lower expression levels in “loss of Hiks-resistance mutants” as compared to Col-0 wild type plants). Thus, for each gene expression, ratios were calculated between Col-0 and each of the four Hiks response mutants (*rpp7*, *edm1*, *edm2* or *edm3*) at each time point (0, 12 and 48 hours). The resulting data set, consisting of 12 expression ratios for each of the 8,775 probe sets on the chip, was first analyzed with “CLUSTER” and “TREE VIEW”, two commonly used programs for chip and micro-array data analysis (Eisen et al., 1998). Genes that demonstrated only minor or less significant expression differences between Col-0 wild type and the mutants were excluded from analysis. Genes that showed at least one 3-fold expression difference over all 12 calculated expression ratios were first considered for further analysis.

Table 12 shows 194 probe sets corresponding to genes having SEQ ID NOs: 301-494, the expression of which is altered after infection of *Arabidopsis* with *P. parasitica* (wild-type relative to *rpp7*, *edm1*, *edm2*, or *edm3*). Table 13

depicts about 100 genes (genes comprising SEQ ID NOs: 373, 385, 242, 369,
 306, 232, 346, 367, 212, 221, 307, 322, 240, 313, 270, 252, 383, 245, 377, 212,
 327, 297, 375, 263, 250, 282, 358, 257, 332, 560, 284, 220, 259, 355, 248, 281,
 215, 236, 309, 386, 253, 333, 336, 296, 319, 414, 354, 353, 293, 278, 324, 339,
 5 345, 225, 249, 264, 310, 228, 214, 311, 343, 298, 384, 277, 314, 372, 331, 338,
 370, 352, 365, 261, 374, 238, 344, 241, 380, 371, 262, 258, 256, 304, 275, 303,
 274, 254, 223, 348, 318, 251, 291, 289, 361, 285, 368, 342, 290, 351, 312, 286,
 287, 273, 239, 326, 226, 227, 350, 280, 317, 359, 294, 279, 382, 356, 234, 218,
 217, 347, 379, 401, 378, 363, 341, 208, 268, 267, 364, 266, 337, 269, 269, 325,
 10 793 and 224) represented by 137 probe sets that show at least one 3-fold-
 expression difference in comparisons between wild type *Arabidopsis* Col-0 and
 mutants *rrp7* or *edm1*, *edm2*, or *edm3* infected with *P. parasitica* Hiks1 (i.e.,
 probe sets that show at least one 3-fold difference in expression levels over all 12
 expression ratios calculated between Col-0 wild type and each of the 4 Hiks
 15 response mutants at each of the time points). Genes were grouped together
 according to similarities of their expression characteristics. Expression ratios
 were color encoded. Positive expression ratios were red and negative ratios were
 green. Black indicated no expression difference. Genes were represented in
 rows and infection treatments in columns. Red generally indicated that a gene at
 20 a given time point is more strongly expressed in Col-0 wild type plants as
 compared to the respective mutant. One cluster represented genes that are
 upregulated in response to Hiks1 infection by the *RPP7* pathway (Table 14;
 genes comprising SEQ ID NOs: 365, 261, 374, 238, 344, 241, 380, 371, 262,
 258, 256, 304, 275, 303, 274, 254, 310, 228, 214, 347 and 225, which are
 25 induced by Hiks1-infection and which are *RPP7*, *EDM1*, *EDM2*, *EDM3*-
 dependent genes and so may encode regulators acting downstream of those
 genes; see probe sets 12505, 13217 and 12904 which correspond to genes that
 encode potential regulators of Hiks response pathway). Genes in this cluster
 represent genes that are more strongly expressed in Col-0 wild type than in all
 30 four mutants predominantly at the 12 hour time-point in each comparison. The
 expression difference is less pronounced in the case of *edm2* and *edm3*, but it is
 consistent over all four comparisons.

Table 12

Affy ID (Probe Set)	Reference No.
12324_i_at	AC007212
12333_at	AJ286345
12345_at	L36246
12500_s_at	AF081067
12505_s_at	AC005309
12608_i_at	S70188
12642_at	AC006920
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843_s_at	AC007195
12845_s_at	AJ004810
12879_s_at	U40856
12891_at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12911_s_at	X84229
12916_s_at	AF021244
13138_at	AL096882
13177_at	AL049640
13178_at	U93215
13187_i_at	U35829
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13273_s_at	U68017
13284_s_at	AJ002551
13604_at	AC000104
13615_at	AC002332
13617_at	AC006592
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14028_at	AF075597
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309

14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14295_s_at	Z54356
14595_at	AL022580
14608_at	AC007357
14614_at	AC004165
14621_at	AC004747
14627_i_at	X76609
14628_r_at	X76609
14635_s_at	AC005398
14636_s_at	AC013258
14643_s_at	AC006836
14672_s_at	U18993
14675_s_at	D85191
14691_at	AP002046
14704_s_at	AC006067
14706_r_at	AL137189
14709_at	AP002046
14711_s_at	AF085279
14731_s_at	AF014960
14784_at	AC005310
14951_at	AL049481
14965_at	AC002329
15057_at	AL035440
15085_s_at	AL031018
15105_s_at	Z14987
15116_f_at	AF121356
15125_f_at	D85190
15141_s_at	D85191
15145_s_at	D64155
15154_s_at	AL096860
15161_s_at	U90522
15178_s_at	U43489
15216_s_at	U75198
15431_at	AL030978
15496_at	AC006282
15523_s_at	AL078637
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15622_s_at	U43945

15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15950_at	AC006429
15954_at	U72155
15969_s_a	AJ133036
15978_at	X68592
15982_s_a	X98190
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16412_s_at	AL022603
16442_s_at	AJ002551
16461_I_at	AC004683
16462_s_a	AC004683
16504_s_at	Z97335
16510_at	AL034567
16514_at	AL035538
16536_s_at	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16578_s_at	AL137080
16609_s_at	AB008104
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
16951_i_at	AC005662
16952_s_at	AC005662
16981_s_at	U35829
17014_s_at	U05206
17033_s_at	U83179
17054_s_at	AF134128
17073_s_at	AC006836
17119_s_at	AF132212
17123_s_at	AF106087
17128_s_at	AC005398
17187_at	AF128396
17303_s_at	AC005499
17379_at	AC018721
17386_at	AC006264
17413_s_at	X99097

17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17549_s_a	L37126
17567_at	AL162751
17886_at	AC004484
17899_at	Z97339
17917_s_at	AC004261
17961_at	AC007323
17963_at	AL049730
18003_at	AF188334
18064_r_at	
18069_at	
18070_r_at	
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18255_at	AC005770
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590_at	AJ222713
18591_at	X74756
18607_s_at	U78721
18635_at	AC004005
18706_s_a	X75782
18716_at	AC007396
18876_at	AF002109
18920_at	AC002338
18928_at	AC002338
19034_at	AL021768
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19594_i_at	X98321
19640_at	AC004561
19977_at	AL049659
20017_at	AC004521
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20297_at	AC007153
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336

20555_s_a	AL080318
20585_s_at	AC005309
20641_at	X91919

Table 13

Probe Set	Description
12324_i_at	AC007212
12345_at	L36246
12505_s_at	AC005309
12608_i_at	S70188
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843_s_at	AC007195
12845_s_at	AJ004810
12879_s_at	U40856
12891_at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12908_s_at	AB008107
12911_s_at	X84229
13138_at	AL096882
13178_at	U93215
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13604_at	AC000104
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309
14116_at	AF077407
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14248_at	AC007357
14250_r_at	AL050300
14595_at	AL022580

14608_at	AC007357
14621_at	AC004747
14627_i_at	X76609
14628_r_at	X76609
14635_s_at	AC005398
14636_s_at	AC013258
14675_s_at	D85191
14691_at	AP002046
14704_s_at	AC006067
14709_at	AP002046
14711_s_at	AF085279
14731_s_at	AF014960
14784_at	AC005310
14951_at	AL049481
15057_at	AL035440
15105_s_at	Z14987
15116_f_at	AF121356
15125_f_at	D85190
15141_s_at	D85191
15145_s_at	D64155
15154_s_at	AL096860
15161_s_at	U90522
15178_s_at	U43489
15431_at	AL030978
15496_at	AC006282
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15846_at	AC006067
15847_g_at	AC006067
15950_at	AC006429
15954_at	U72155
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16504_s_at	Z97335
16510_at	AL034567
16536_s_at	AB008107
16578_s_at	AL137080
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
17014_s_at	U05206
17033_s_at	U83179

17054_s_at	AF134128
17123_s_at	AF106087
17128_s_at	AC005398
17187_at	AF128396
17303_s_at	AC005499
17386_at	AC006264
17413_s_at	X99097
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17567_at	AL162751
17886_at	AC004484
17899_at	Z97339
17961_at	AC007323
17963_at	AL049730
18003_at	AF188334
18064_r_at	
18069_at	
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590_at	AJ222713
18607_s_at	U78721
18635_at	AC004005
18716_at	AC007396
18920_at	AC002338
18928_at	AC002338
19034_at	AL021768
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19640_at	AC004561
19977_at	AL049659
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336
20585_s_at	AC005309
20641_at	X91919

Table 14

Probe Set	Description
12505_s_at	AC005309
12879_s_at	U40856
12904_s_at	AB008103
13189_s_at	U35829
13217_s_at	AL049862
14116_at	AF077407
14148_at	AF224762
14201_at	AL163972
14248_at	AC007357
14250_r_at	AL050300
14691_at	AP002046
14704_s_at	AC006067
15846_at	AC006067
15847_g_at	AC006067
16063_s_at	AB008103
17500_s_at	AL049862
17544_s_at	U40856
18716_at	AC007396
19178_at	AB035137
19640_at	AC004561
20269_at	AC002387

Thus, Hiks1 induced upregulation is compromised in all four tested “loss of Hiks1 resistance mutants” and there is a correlation between breakdown of resistance and deregulation of these genes. This may indicate that these genes play important roles in mediating Hiks1 resistance. Furthermore, these genes appear to act downstream of all four genetically defined *RPP7* pathway components, *RPP7*, *EDM1*, *EDM2* and *EDM3*. Some genes of this set may encode important regulators; whereas others may indicate metabolic processes required for Hiks1 resistance.

Seventy-eight genes (Table 15; genes comprising SEQ ID NOs:330, 292, 311, 243, 237, 302, 315, 283, 300, 372, 308, 335, 272, 305, 357, 213, 362, 331, 254, 384, 277, 343, 298, 349, 314, 265, 262, 258, 256, 303, 321, 304, 275, 274, 323, 238, 374, 241, 344, 244, 365, 261, 380, 371, 295, 255, 316, 233, 345, 225, 260, 229, 324, 301, 235, 340, 278, 320, 231, 319, 230, 354, 353, 293, 376, 247, 246, 366, 216, 214, 276, 299, 310, 334, 271, 381 and 228) that show the same, but less pronounced, expression characteristics were selected using relaxed selection criterion (at least one 2-fold expression difference over all 12 calculated expression ratios). With a lower cutoff criterion of at least one 2-fold-expression difference across all twelve expression ratios, this cluster is larger

than that shown in Table 14. Genes that are part of this less stringently defined cluster were included in further analyses so as to not exclude potentially important genes. Potential regulators in this cluster are listed in Table 16 (genes comprising SEQ ID NOs: 220, 323, 231, 319, 214, 301, 340, 243, 227, 321, 235, 5 315, 298, 314, 328, 344 and 349). Four different ERF transcription factors genes are upregulated by the *RPP7*-pathway. Genes encoding ERFs are known to be upregulated in response to several stress-related stimuli, such as wounding, pathogens or ethylene. Moreover, ERF transcription factors bind to GCC boxes, which are ethylene, wounding and pathogen-responsive *cis*-elements. This 10 cluster also contains a gene encoding an ACC synthase, a component of the ethylene biosynthetic pathway. Therefore, ethylene may play a role in the Hiks response pathway.

Table 15

Probe Set	Description
12500_s_at	AF081067
12505_s_at	AC005309
12642_at	AC006920
12879_s_at	U40856
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12916_s_at	AF021244
13177_at	AL049640
13187_i_at	U35829
13189_s_at	U35829
13217_s_at	AL049862
13273_s_at	U68017
13284_s_at	AJ002551
13615_at	AC002332
13617_at	AC006592
14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14201_at	AL163972
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14614_at	AC004165
14643_s_at	AC006836
14672_s_at	U18993

14691_at	AP002046
14704_s_at	AC006067
14706_r_at	AL137189
14709_at	AP002046
14711_s_at	AF085279
15085_s_at	AL031018
15216_s_at	U75198
15431_at	AL030978
15523_s_at	AL078637
15616_s_at	AL078637
15622_s_at	U43945
15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15978_at	X68592
16063_s_at	AB008103
16105_s_at	U68017
16393_s_at	AB008103
16412_s_at	U68017
16442_s_at	AJ002551
16536_s_at	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16609_s_at	AB008104
16620_s_at	AF051338
16952_s_at	AC005662
16981_s_at	U35829
17073_s_at	AC006836
17119_s_at	AF132212
17379_at	AC018721
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17917_s_at	AC004261
18070_r_at	
18216_at	AC012375
18217_g_at	AC012375
18255_at	AC005770
18591_at	X74756
18716_at	AC007396
18876_at	AF002109
19178_at	AB035137
19182_at	AL031804
19640_at	AC004561
20017_at	AC004521

20269_at	AC002387
20297_at	AC007153
20429_s_at	Z97336

Additionally, a gene encoding a lipoxygenase, a component of the jasmonic acid biosynthetic pathway, is upregulated. Other regulators potentially acting downstream of RPP7, EDM1, EDM2 and EDM3 include some putative
 5 zinc finger transcription factors and protein kinases as well as two calmodulin-like proteins and a calcium binding protein, which may point to a role of calcium in the *RPP7*-pathway.

Table 16

10 I. Transcriptional regulators:

- 1.) AtERF1 (12904_s_at, BAA32418.1; AB008103)
- 2.) AtERF2 (16609_s_at, BAA32419.1; AB008104)
- 3.) EREBP4-like (12909_s_at, CAB10530.1; Z97343)
- 4.) AtERF5 (16536_s_at, BAA32422.1; AB008107)
- 15 5.) putative CONSTANS-like zinc finger (12505_s_at, AAC63643.1; AC005309)
- 6.) putative C2H2 zinc finger transcription factor (15665_s_at, AAB80922.1; AF022658)
- 7.) putative C3H zinc finger protein (17379_at, AAF18728.1; AC018721)
- 20 8.) heat shock transcription factor 4 (13273_s_at, AAC31756.1; U68017)
- 9.) SigA binding protein (14148_s_at, AAF34713.1; AF224762)

II. Other signaling proteins

- 10.) AtACS-6 (12892_g_at, CAB51412.1, AL096882, 35400..37154)
- 11.) lipoxygenase (16569_s_at, AAA32749.1; L23968)
- 25 12.) growth factor like protein (13177_at, CAB40989.1; AL049640)
- 13.) serine/threonine protein kinase (16412_s_at, CAA18704.1; AL022603)
- 14.) wall associated kinase 1 (15616_s_at, CAB08794.1; AJ009696)
- 15.) putative receptor-like protein kinase (16393_s_at, AAD28318.1; AC006436)
- 30 16.) calmodulin-like (16951_i_at, AAC78532.1; AC005662)
- 17.) calmodulin-like (17500_s_at; CAB42906.1; AL049862)
- 18.) calcium binding protein (17917_s_at, AAD12002.1; AC004261)

Twenty-six genes (genes comprising SEQ ID NOs: 300, 308, 272, 213, 362, 265, 374, 241, 261, 380, 310, 228, 233, 330, 311, 243, 237, 254, 230, 244, 365, 216, 316, 345, 225, 301, 278, 354, 353, 293, 335, 271 and 321, also shown in Table 15), represented by 33 probe sets, were found to be commonly
 5 upregulated in response to both *Peronospora* isolates, Hiks1 and Emco5, in an RPP7- or RPP8-dependent (and EDM1, EDM2 and EDM3-dependent) manner (Table 17). Elevated expression of these genes may be required for resistance against both *Peronospora* isolates or against *Peronospora parasitica* in general. Among these 26 genes are those encoding ERF1, putative zinc finger
 10 transcription factors, two proteins potentially involved in calcium signaling, a lipoxxygenase, and a cysteine rich antifungal protein.

Table 17

15	26 <i>Peronospora</i> (Hiks1 and Emco5) induced RPP8, RPP7, EDM1,2,3-dependent genes	
	Transcription factors	
	AtERF1	
	Putative salt-tolerance zinc finger transcription factor (18217_g_at)	
20	(ZFPI) hypothetical Cys-3-His zinc finger protein	
	Putative C2H2 zinc finger transcription factor	
	Heat shock transcription factor 4	
	Other potential proteins	
25	Calmodulin-like protein	
	Similarity to centrin, <i>Marsilea vestita</i> contains EF-hand calcium-binding domain (15431_at)	
	Lipoxxygenase	
30	Others	
	heat shock protein 70	
	putative steroid sulfotransferase	tryptophan synthase alpha chain
	putative glucosyltransferase	similar to xyloglucan fucosyltransferase (12642_at)
35	phosphoglycerate dehydrogenase	Pad3 (Cytochrome P450)
	ATAF2	putative pectinesterase
	OPDA-reductase homolog	AIG1
	coronatine-induced protein 1	putative glutathione S-transferase
	thioredoxin h	adenosine nucleotide translocator
40	IAA-amino acid hydrolase	contains similarity to sugar transporters
		CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 PRECURSOR (AFP1) (18716_at)

Thirteen of these 26 genes (genes comprising SEQ ID NOs: 308, 300, 272, 362, 265, 242, 261, 380, 228, 243, 254, 216 and 225, *Peronospora* (Hiks1, Emco5 and Emoy2) induced and *RPP4*, *RPP8* and *RPP7* dependent) were also found to be more strongly expressed during the incompatible interaction between the *Peronospora* isolate Emoy2 and Col-0 plants as compared to Emoy2 infections of the compatible or intermediate type (see Table 18). These 13 genes may play an important role in defense against *Peronospora parasitica* in general. Among these genes is PAD3, which was previously demonstrated to be required for pathogen-induced phytoalexin production. Strikingly, Hiks1 resistance is partially compromised in the *pad1-1/pad3-1* double mutant, whereas Emoy2 resistance is reduced in the *pad3-1* single mutant (Glazebrook et al. 1997).

Table 18

13 *Peronospora* (Hiks1, Emco5 and Emoy2) induced
RRP4-pathway, RPP7-pathway, and RPP8-dependent genes

- adenosine nucleotide translocator (15978_at)
- phosphoglycerate dehydrogenase (15629_s_at)
- tryptophan synthase alpha chain (14672_s_at)
- ATAF2 (18591_at)
- putative glucosyltransferase (14614_at)
- calmodulin-like protein (13217_s_at)
- pad3 (cytochrome P450)(14248_at)
- putative pectinesterase (20269_at)
- ethylene responsive element binding factor 1 (12904_s_at)
- heat shock transcription factor 4 (13273_s_at)
- sugar transporter-like (14116_at)
- similar to xyloglucan fucosyltransferase (12642_at)
- AIG1 (12879_s_at)

Identification of promoter motifs common to *RPP7* and *RPP8* controlled genes

Sequence motifs conserved in the promoters of genes co-regulated by the *RPP7* or *RPP8* pathways may lead to information about the types of transcription factors controlling expression of these genes and may serve as starting points for isolating and/or cloning of such factors. Sub-categorization of *RPP7*-

- 5 upregulated genes by K-means clustering, based on the absolute expression levels of the genes, revealed the existence of only a few basic expression profiles. K-means clustering into five gene sets gave the most consistent and tight clusters. For each of the five gene sets (Table 19), the expression changes in two repetitions of the Col-0 wild type/Hiks1 interaction are shown as well as
10 in the *rpp7* mutant and *edm1*, *edm2* and *edm3*.

- The first set comprises genes (genes comprising SEQ ID NOs: 292, 302, 315, 300, 308, 213, 265, 374, 241, 344, 261, 299, 365 and 276) that show early and transient upregulation. The genes peak at 12 hours and return to their ground-states at approximately the 48 hours post infection. Genes of the second
15 set (genes comprising SEQ ID NOs: 267, 305, 357, 362, 380, 310, 228, 295, 233, 329, 312, 243, 237, 283, 372, 254, 314, 323, 216, 260, 229 and 235) are also rapidly upregulated, but show a less pronounced or no decline after the peak. In both sets, the response is weaker in the mutants. Only a few genes in the first set respond almost as strongly in *edm2* and *edm3* plants as in wild type plants.
20 Genes of the third (genes comprising SEQ ID NOs: 258, 256, 303, 304, 275, 244, 316, 354 and 225) and fifth (genes comprising SEQ ID NOs: 330, 384, 277, 343, 298, 349, 262, 274, 238 and 301) set show an almost linear increase of transcript level in wild type. In the mutants, this increase is delayed and in some cases less steep. In the fourth set (genes comprising SEQ ID NOs: 432, 347,
25 370, 412, 323, 411, 322, 449, 448, 385, 471, and 339) the expression levels rise in the first repetition of the Col-0 wild type/Hiks interaction, but respond very little in the second one. In *edm3*, the transcript levels drop from a high ground state. The probe sets and genes corresponding to each of these K-means cluster sets are shown in Table 19.

30

Table 19

K-means set 1	Description	K-means set2	Description
12500_s_at	AF081067	12642_at	AC006920
13217_s_at	AL049862	12904_s_at	AB008103
14248_at	AC007357	12905_s_at	AB008104

14614_at	AC004165	12916_s_at	AF021244
14706_r_at	AL137189	13177_at	AL049640
15216_s_at	U75198	13187_i_at	U35829
15622_s_at	U43945	13273_s_at	U68017
15629_s_at	AB010407	14116_at	AF077407
15680_s_at	D42061	14223_at	AL024486
15978_at	X68592	14672_s_at	X76609
16412_s_at	U68017	15085_s_at	AL031018
17500_s_at	AL049862	15523_s_at	AL078637
18070_r_at		15866_s_at	AC005770
18716_at	AC007396	16063_s_at	AB008103
19640_at	AC004561	16105_s_at	AL049730
		16393_s_at	AC006436
		16609_s_at	AB008104
		16952_s_at	AC005662
		18255_at	AC005770
		18591_at	X74756
		19182_at	AL031804
		20269_at	AC002387
K-means set 3 Description			
12879_s_at	U40856		
13284_s_at	AJ002551		
14148_at	AF224762		
14201_at	AC068667		
14704_s_at	AC006067		
15846_at	AC006067		
15847_g_at	AC006067		
16442_s_at	AJ002551		
17544_s_at	U40856		
K-means set 4 Description			
12908_s_at	AB008107		
12909_s_at	Z97343		
13617_at	AC006592		
14141_at	AC011437		
14711_s_at	AF085279		
15431_at	AL030978		
16536_s_at	AB008107		
16539_s_at	Z97343		
17379_at	AC018721		
18216_at	AC012375		
18217_g_at	AC012375		
20017_at	AC004521		
		K-means set 5 Description	
		13189_s_at	U35829
		14250_r_at	AL050300
		14691_at	AP002046
		14709_at	AP002046
		15616_s_at	AJ009696
		15665_s_at	AF022658
		16981_s_at	U35829
		17499_s_at	AF107726
		17917_s_at	AC004261
		20429_s_at	Z97336

Recently, the plant specific family of WRKY transcription factors has been implicated in the regulation of defense-associated genes. Promoters of genes upregulated during systemic acquired resistance were found to be strongly enriched in potential WRKY binding sites. WRKY factors comprise a large family of 72 different members in *Arabidopsis*. Generally these factors appear to bind to sequence motifs containing the core T G A C (W box). It has not yet

been determined whether individual WRKY family members differ in their preferences for distinct W box variations. However, it is probable that a given WRKY protein has a binding preference for a certain variation of the W box motif.

5 Using the program AlignACE, three variations of potential WRKY binding sites were found to be conserved in sub-sets of *RPP7* controlled genes. Two of these motifs are highly enriched in promoters of genes from K-means cluster 3, representing genes that show a linear increase in transcript level after *Peronospora* infection (Table 20; genes comprising SEQ ID NOs: 384, 298, 349, 10 262 and 238 for W box I and genes comprising SEQ ID NOs: 384, 349, 262, 238 and 301 for W box II). These motifs are also present in promoters of K-means cluster 5, which represents a similar expression profile. Focusing on sustained up-regulated genes, that show a particularly pronounced expression difference between Col-0 wild type plants and the Hiks1 response mutants, a third variation 15 of potential WRKY binding sites was found to be significantly enriched (Table 21; genes comprising SEQ ID NOs: 397, 371, 238, 262, 256, 275, 254, 214 and 225). In all three cases, sequence conservation clearly exceeds the core motif of WRKY binding sites that appears to be recognized by all members of this family. These additionally conserved positions may confer specificity for 20 certain WRKY family members. They may provide a highly defined binding site preferentially recognized by a distinct WRKY factor or may serve as binding sites for another transcription factor binding closely adjacent to and specifically interacting with a distinct WRKY factor. In any case, the high conservation of extended potential WRKY binding motifs strongly suggests that specific 25 members of this family participate in the regulation of certain sub-sets of *RPP7*-controlled genes.

Table 20

<u>W box I</u> MAP Score: 8.98114	
30	GTCATCTTTTAATCTCTGG 0 638 1
	GTCATCTTTTAATCGCCGG 0 932 1
	GCCTTTGCTTATTTATAGG 0 1036 1
	GTCATTTGTTACAAAGAGG 1 318 1
	GTCATTGATCATAAACTGT 1 389 0
35	GCCACTGCTGAATTGTCGG 1 494 1
	GTCCATTGTCAATAAATGG 2 689 1
	GTCCATTGTAAATAAATGT 2 949 1

5 GTCATCTTTTAATCTCTGT 3 475 0
 GTCACGTATGAATGGAAGG 4 73 1
 GTCAACGTTTATGTTTCATGT 4 226 0
 GTCAAGTTTTTAAATTGTGG 4 352 1
 GTCAACGTTTATGTTTCATGT 4 401 0
 *** * * * * **

GTCANNTNTNANTNNNNGG

G A T

Expected frequency by chance: 0.02/1kb
 10 Observed frequency: 1.2/1kb
 Enrichment: ~60 fold
 W box II- MAP Score: 15.2966

15 ATTAAAAGATGAC 0 638 0
 ATTAAAAGATGAC 0 932 0
 ATTAAATGCTGTC 2 752 0
 ATTAAATGCTGTC 2 1011 0
 AGCAAAAGCTGAC 2 1092 1
 ATTAAAAGATGAC 3 481 1
 ATCAAAAGTTGTC 3 829 1
 20 ACTAAACGTTGAC 4 232 1
 ACTAAACGTTGAC 4 407 1
 ACTAAAAAGTGAC 5 755 1
 * * * * *

25 W II ANTAAANGNTGAC
 C A T

W I: CCNNNNANTNANCNNTGAC
 A T A

30 Expected frequency by chance: 0.04/1kb
 Observed frequency: 1.35/1kb
 Enrichment: ~30 fold
 Table 21

35 ATAGGTGGTCAAGT 1 106 0
 AATTGTGGTCATTT 1 823 0
 ACTTGTGGTCAATT 2 804 0
 AAAAGGGGTCATTT 2 970 1
 ATATGTCGTCTCTT 2 994 0
 AGTTGTGGTCTACC 3 502 0
 40 AAAAGTTGTCAATT 3 732 1
 AGACGTCGTAATTT 4 400 0
 ACGTGGCGTCATAT 5 179 0
 ATGTGGCGTCTCCT 6 249 1
 AGTTGGTGTACGCT 6 925 1
 45 ATTCGTGGTCAACT 7 582 1
 ATATGTCGTCACTT 7 875 1
 * * * * *

ANNNGTNGTCANNT

G

50

expected: 0.05/1kb;
 in random set: 0/1kb;
 this set: 1/1kb;
 enrichment: 10-20 fold;

5

Novel, conserved promoter motifs were also found. Genes of K-means set 1, which are early and transient *RPP7*-pathway specific genes, share two similar highly conserved promoter motifs, G G T/C C C A (SEQ ID NO:714; genes comprising SEQ ID NOs: 302, 315, 308, 265, 374, 241, 261, 299 and 365) and G N C C A A A (SEQ ID NO:715; genes comprising SEQ ID NOs: 292, 302, 308, 265, 374, 241, 261, 299, 365 and 276) (Table 22). Both motifs are almost perfectly conserved and are represented in nearly all promoters of this gene set. They are compact six- or seven-mers, which is typical for transcription factor binding sites. For the second motif, the permutations G A C C A A A and G T C C A A A are strongly represented. These permutations may constitute the preferred binding site of a so far unknown transcription factor.

15

Table 22

20

Two related novel motifs are highly enriched in all
 11 promoters of K-means set1

25

30

35

40

GGTCCA 1 232 0
 GGCCCA 1 289 1
 GGTCCA 1 597 1
 GGTCCA 2 517 0
 GGTCCA 3 211 1
 GGCCCA 3 360 1
 GGTCCA 4 597 1
 GGCCCA 4 681 1
 GGTCCA 5 352 0
 GGTCCA 5 1060 1
 GGTCCA 6 358 0
 GGCCCA 7 776 0
 GGCCCA 7 816 0
 GGTCCA 8 285 0
 GGTCCA 9 888 1

GGTCCA C

Expected frequency by chance: 0.22/1kb

Observed frequency: 1.2/1kb

Enrichment: 5.4 fold

GCCCAA 0 601 1

GTCCAAA 10 1186 1

GTCCAAA 9 562 1

```

GACCAAA 8 640 0
GCCCAAA 7 774 0
GTCCAAA 7 717 1
GTCCAAA 6 712 1
5 GACCAAA 5 970 1
  GTCCAAA 5 350 0
  GACCAAA 4 1164 1
  GACCAAA 4 1072 1
  GTCCAAA 4 784 0
10 GACCAAA 4 714 0
   GGCCAAA 4 698 0
   GCCCAAA 3 361 1
   GACCAAA 1 920 0
   GTCCAAA 1 230 0
15 *****
   GNCCAAA
Expected frequency by chance: 0.32/1kb
Observed frequency:          1.3/1kb
Enrichment: 4 fold

```

20

Following a similar approach as for the Hiks1-induced *RPP7* pathway controlled genes, a cluster of early and transiently Emco5-induced *RPP8*-dependent genes were defined (Table 23). In Col-0-*RPP8* plants these genes (genes comprising SEQ ID NOs: 364, 341, 288, 378, 363, 379 and 219) show a

25 very pronounced upregulation 12 hours post Emco5 infection, after which they return to expression ground states. Using AlignACE, two different motifs (see Example 2) were found to be strongly enriched in the promoters of this cluster. The first motif strongly resembles the type I consensus binding site of Myb transcription factors. This motif is also almost identical to a recently identified

30 *cis*-element conferring rapid elicitor responsive gene expression in parley cell culture (Kirsch et al., 2001). Interestingly, a gene encoding a Myb-like transcription factor (highlighted in yellow) is co-regulated with other genes of this cluster. The Myb-like transcription factor gene is the only gene of this cluster that does not contain this conserved motif in its promoter. This MYB-

35 like factor could be a regulator of this cluster. The second motif does not resemble any known stress responsive plant *cis* element or transcription factor binding site. However, the second motif was found to be strongly represented in promoters from other defense related genes, such as SAR genes. As is typical of many transcription factor binding sites, certain permutations of its consensus

sequence may constitute palindromes. This motif was also found to be conserved by the program MEME.

Table 23

5	Glutathione-conjugate transporter AtMRP4 putative GST putative cytochrome P450 (AC002340) PAD3 (similar to cytochrome P450) CTF2B (similarity to proteins involved in Hydroxylation and oxidation of aromatic rings)	
10	Ribonuclease RNS1 Putative Myb-like protein AlignACE Motif 1:	CAACTTTGAC AA TT CAACTG T G
15	type I Myb binding site:	
	Frequency by chance: 0.05/1kb Observed frequency in control cluster: 0.13/1kb Observed frequency in this cluster: 1.10/1kb	
20	AlignACE Motif2:	TTGGGNCNAA A A GTCTNTTGGGNCNAAA T T A G C
	MEME motif:	
25	Frequency by chance: 0.13/1kb Observed frequency in control cluster: 0/1kb Observed frequency in this cluster: 1.2/1kb	

Different types of transcription factors may participate in the control of distinct *RPP7*-pathway dependent expression profiles. Promoters of genes showing a linear sustained increase of transcript are enriched in different variations of WRKY binding sites. However, no *WRKY*-pathway gene was found to be upregulated by the *RPP7* pathway. Therefore, WRKY factors involved in *RPP7* mediated up-regulation of K-means cluster 3 and 5 genes may already be pre-formed when the pathogen signal is perceived. However, only 21 *WRKY* genes out of 72 members of this family in *Arabidopsis* are represented on the oligonucleotide chip. Upregulated WRKY factors participating in *RPP7* mediated gene regulation may not be present on the chip. A novel type of transcription factor may be involved in regulation of early and transient *RPP7*-controlled genes (K-means cluster 1). Promoter stretches containing this motif may be used in yeast one hybrid screenings for novel factors. In addition, transgenic plants carrying appropriate promoter-reporter constructs could be used

as a basis for mutant screenings with the aim of identifying regulators acting on this motif.

A Myb-like transcription factor appears to be involved in the regulation of early and transient *RPP8*-controlled genes. A gene showing a similar pattern of regulation may encode a candidate factor controlling this cluster. The potential role of this factor in regulating *RPP8*-controlled genes may be examined using T-DNA insertion mutants.

Potential constitutive effects of the *RPP7*-pathway

In order to focus on genes showing multiple expression differences between Col-0 wild type plants and Hiks response mutants, all genes that showed at least four 1.8-fold expression differences across all comparisons were selected. The resulting clustergram contains the majority of *RPP7* pathway-dependent Hiks1-induced genes. Two more clusters of genes behaving consistently in all four tested Hiks1-response mutants were found. The first cluster comprises genes that show at all tested time points (including the 0 hpi time point) elevated transcript levels in Col-0 wild type plants as compared to all four mutants (Table 24; genes comprising SEQ ID NOs: 364, 288, 378, 363, 379, 219, 399, 389 and 390). In most cases, expression levels are not affected by Hiks1 infection. These elevated expression levels may be directed by constitutive (non Hiks1-triggered) signal flow via the *RPP7* pathway. This signal flow is disrupted in the *rpp7*, *edm1*, *edm2* and *edm3* mutants. Constitutive expression of these genes may be required for effective disease resistance and may be a prerequisite for induction of subsequent defense responses. A HD-ZIP transcription factor, which is included in this cluster, may act as a pre-formed regulator controlling genes responding to Hiks1-recognition. Its potential role in regulating *RPP7* pathway-dependent genes may be examined using T-DNA insertion mutants.

Table 24

The *RPP7* pathway constitutively activates a cluster of genes including a HD-ZIP transcription factor

PROBE SET	DESCRIPTION
14965 at	AC002329
18635 at	AC004005
14295 s at	Z54356
17386 at	AC006264

15145_s_at	D64155
20201_at	AL078470
18607_s_at	U78721
20227_s_at	AC007153
12761_s_at	AC006577
20555_s_a	AL080318

Genes of the second cluster show the opposite behavior (Table 25). Their transcript levels are elevated in all four Hiks1 response mutants as compared to Col-0 wild type plants. Hiks1-infection does also not affect their expression levels. Surprisingly, this cluster contains six genes encoding peroxidases. Since peroxidases are believed to play roles in conferring disease resistance, the biological significance of this phenomenon is obscure. Perhaps the mutant plants “realize” disruption of the *RPP7*-defense pathway and compensate for their reduced defense capacity by constitutively up-regulating some defense mechanisms. Alternatively, elevated expression of these peroxidases may be advantageous for invading *Peronospora* hyphae. Therefore, expression of these genes could be constitutively reduced by the *RPP7* pathway.

Table 25

Probe Set	Description
15982_s_at	X98190
15954_at	U72155
12333_at	AJ286345
19594_i_at	X98321
15969_s_at	AJ133036
16462_s_at	AC004683
16461_i_at	AC004683
12324_i_at	AC007212
12778_r_at	AC006577
16514_at	AL035538
17549_s_at	L37126
14028_at	AF075597
17054_s_at	AF134128

Predictions about *RPP7*-pathway hierarchy

Clustering of the Hiks1-infection data in the “treatment” dimension, instead of the “gene” dimension, revealed that at all three infection time points, gene expression profiles of the *rpp7* mutant resemble most those of the *edm1* mutant. Similarly, expression profiles of the *edm2* mutant resemble those of the

edm3 mutant. This may indicate that RPP7 and EDM1 closely act together at a certain level in the *RPP7* signalling cascade, whereas EDM2 and EDM3 may act closely together at a different level of the pathway. Close interaction of RPP7 and EDM1 is also suggested by a T-DNA tagged *rpp7* mutant that

5 phenotypically resembles the *edm1* mutant. In contrast to *rpp7*, *edm2* and *edm3*, which appear only to be compromised in resistance against the *Peronospora* isolate Hiks1, *edm1* is also compromised in resistance to other *Peronospora* isolates that are avirulent on Col-0 plants. Like *edm1*, the putatively T-DNA tagged *rpp7* mutant is also susceptible to a variety of normally Col-0

10 incompatible *Peronospora* isolates. This observation may indicate that the EDM1 protein requires a portion of the RPP7 protein for proper function, which is disrupted in the T- DNA tagged *rpp7* mutant. Assuming that RPP7, which appears to constitute an NBS-LRR receptor, acts at the top of the Hiks1 recognition pathway hierarchy, EDM1 could act at a high level as well and

15 EDM2 and EDM3 may act more downstream in the cascade.

Table 26

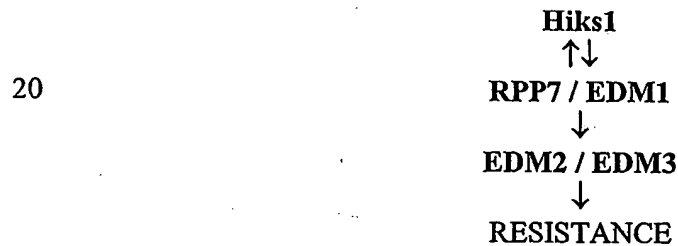


Table 27 shows the plant and fungal orthologs of the *Arabidopsis* sequences identified herein.

Table 27

Query= AIG1_s_at 12879_s_at/id_source genbank /description
gb|aac49282.1|(u40856) aig1 [arabidopsis thaliana] /blast_score
1.00e-150

5 (1381 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10 Searching.....done

	Score	E	
	Sequences producing significant alignments:	(bits)	Value
15	gb U64925 NTU64925 Nicotiana tabacum geranylgeranylated protein ...	260	1e-68
	emb AW625701 AW625701 EST319608 tomato radicle, 5 d post-imbibit...	228	6e-59
	emb AW720227 AW720227 LjNEST17c4r Lotus japonicus nodule library...	219	4e-56
	emb AW220184 AW220184 EST302667 tomato root during/after fruit s...	208	7e-53
	emb AI774580 AI774580 EST255680 tomato resistant, Cornell Lycopersicon...	173	2e-42
20	emb AW685484 AW685484 NF030E02NR1F1000 Nodulated root Medicago t...	171	2e-41
	emb AI443867 AI443867 sa44d09.y1 Gm-c1004 Glycine max cDNA clone...	170	3e-41
	emb AW397252 AW397252 sg76f06.y1 Gm-c1007 Glycine max cDNA clone...	168	1e-40
	emb AW033368 AW033368 EST276939 tomato callus, TAMU Lycopersicon...	162	5e-39
	emb AV417858 AV417858 AV417858 Lotus japonicus young plants (two...	153	4e-36
25	emb AI780050 AI780050 EST260929 tomato susceptible, Cornell Lyco...	138	9e-32
	emb AW039095 AW039095 EST281068 tomato mixed elicitor, BTI Lycopersicon...	111	2e-23
	emb AI780139 AI780139 EST261018 tomato susceptible, Cornell Lyco...	86	7e-16
	emb AW164180 AW164180 Ljirmp21-672-c8 Ljirmp Lambda HybriZap ...	84	2e-15
	emb AI781596 AI781596 EST262475 tomato susceptible, Cornell Lyco...	75	1e-12
30	emb AW774764 AW774764 EST333915 KV3 Medicago truncatula cDNA clo...	62	7e-09
	emb AW348781 AW348781 GM210003A22H11R Gm-r1021 Glycine max cDNA ...	54	2e-06
	emb AI491210 AI491210 EST241919 tomato shoot, Cornell Lycopersicon...	29	0.010
	emb AW651526 AW651526 EST329980 tomato germinating seedlings, TA...	29	0.011
	emb AW220594 AW220594 EST296979 tomato fruit mature green, TAMU ...	29	0.011
35	emb AW926585 AW926585 HVSMEg0007J19 Hordeum vulgare pre-anthesis...	29	0.025
	emb AW032321 AW032321 EST275775 tomato callus, TAMU Lycopersicon...	28	0.026
	emb AW736598 AW736598 EST333090 KV3 Medicago truncatula cDNA clo...	37	0.39
	emb AW736597 AW736597 EST333089 KV3 Medicago truncatula cDNA clo...	37	0.39
	emb AW713727 AW713727 h1f12ne.fl Neurospora crassa evening cDNA ...	35	1.0
40	emb AW711542 AW711542 f3g07ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AB009972 AB009972 Aspergillus oryzae gene for beta-1,4-xylos...	35	1.0
	emb AW713709 AW713709 h1e09ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AW712721 AW712721 g3a07ne.fl Neurospora crassa evening cDNA ...	35	1.0
	emb AW709185 AW709185 d3e02ne.fl Neurospora crassa evening cDNA ...	35	1.0
45	emb Y09354 SPABC1 S.pombe ABC1 gene.	35	1.4
	emb Z99262 SPAC9E9 S.pombe chromosome I cosmid c9E9.	35	1.4
	emb AJ225108 STA225108 Solanum tuberosum (cultivar Bintje) mitoc...	35	1.4
	emb AW933326 AW933326 EST359169 tomato fruit mature green, TAMU ...	26	1.5
	emb Z25870 CACDC10G C.albicans CDC10 gene for cell division cycl...	31	1.5
50	emb AC008368 AC008368 Trypanosoma brucei chromosome II clone RPC...	35	1.9
	emb AQ942780 AQ942780 Sheared DNA-42B15.TR Sheared DNA Trypanoso...	35	1.9
	emb AQ953508 AQ953508 Sheared DNA-33G8.TR Sheared DNA Trypanosom...	35	1.9
	emb AC009463 AC009463 Trypanosoma brucei chromosome II clone RPC...	35	1.9
	emb AQ950237 AQ950237 Sheared DNA-39C11.TF Sheared DNA Trypanoso...	35	1.9
55	emb AQ643883 AQ643883 RPC193-DpnII-26C13.TV RPC193-DpnII Trypano...	35	1.9
	emb AQ948491 AQ948491 Sheared DNA-49H2.TF Sheared DNA Trypanosom...	35	1.9
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60	emb Z28341 PSCLOEP P.sativum (miranda) mRNA for chloroplast oute...	28	2.1

- emb|AW776020|AW776020 EST335085 DSIL Medicago truncatula cDNA cl... 28 2.2
 emb|AW685649|AW685649 NF032G04NR1F1000 Nodulated root Medicago t... 28 2.2
 emb|AW690755|AW690755 NF037H10ST1F1000 Developing stem Medicago ... 28 2.2
 emb|AW256896|AW256896 EST305033 KV2 Medicago truncatula cDNA clo... 28 2.3
 5 emb|AV422565|AV422565 AV422565 Lotus japonicus young plants (two... 28 2.3
 emb|AW832303|AW832303 sm07c04.y1 Gm-c1027 Glycine max cDNA clone... 27 2.3
 emb|AL136538|SPAC30 S.pombe chromosome I cosmid c30. 34 2.6
 emb|AI724721|AI724721 RHIZ1_26_C05.y2_A001 Rhizome1 Sorghum hale... 34 2.6
 emb|AW256609|AW256609 EST304746 KV2 Medicago truncatula cDNA clo... 34 2.6
 10 emb|AI775696|AI775696 EST256796 tomato resistant, Cornell Lycopersicon... 28 3.1
 emb|Z71682|SCYNR067C S.cerevisiae chromosome XIV reading frame O... 34 3.6
 emb|AI776315|AI776315 EST257415 tomato resistant, Cornell Lycopersicon... 34 3.6
 emb|AF230371|AF230371 Lycopersicon esculentum allene oxide synth... 34 3.6
 emb|AA741645|AA741645 LmLv39p3/255A Leishmania major promastigot... 34 3.6
 15 gb|U08843|PPU08843 Porphyra purpurea putative polysaccharide bin... 34 3.6
 emb|AF124792|AF124792 Sporothrix schenckii protein kinase C (PCK... 29 4.7
 emb|AQ399149|AQ399149 mgxb0019C01f CUGI Rice Blast BAC Library P... 33 5.0
 emb|AW615911|AW615911 EST325409 tomato flower buds 0-3 mm, Corne... 33 5.0
 emb|AW035453|AW035453 EST281191 tomato callus, TAMU Lycopersicon... 33 5.0
 20 emb|AF051695|AF051695 Trypanosoma cruzi sialidase homolog (P85.1... 33 5.0
 emb|Z37538|LTGRR4 L.tarentolae mRNA encoding putative NADH subun... 28 5.5
 emb|X85021|SCXLTORFS S.cerevisiae DNA from left arm of chromosom... 33 6.8
 gb|L25088|YSCMEF2MIT Saccharomyces cerevisiae nuclear-encoded mi... 33 6.8
 emb|AQ443826|AQ443826 GSSTc01287 Trypanosoma cruzi random genomi... 33 6.8
 25 emb|AQ502942|AQ502942 V47H4 mTn-3xHA/lacZ Insertion Library Sacc... 33 6.8
 emb|Z85962|MSZ85962 Musa sp. DNA for sequence tagged microsatell... 33 6.8
 emb|Z49377|SCYJL102W S.cerevisiae chromosome X reading frame ORF... 33 6.8
 emb|AW224537|AW224537 EST302980 tomato root, plants pre-anthesis... 31 7.5
 emb|AW257183|AW257183 EST305320 KV2 Medicago truncatula cDNA clo... 32 9.4
 30 emb|AQ642922|AQ642922 RPCI93-DpnII-27E7.TV RPCI93-DpnII Trypanos... 32 9.4
 emb|AW738509|AW738509 EST339936 tomato flower buds, anthesis, Co... 32 9.4
 emb|AW217351|AW217351 EST296174 tomato flower buds 0-3 mm, Corne... 32 9.4
 emb|AW219255|AW219255 EST301737 tomato root during/after fruit s... 32 9.4
 emb|AC007865|AC007865 Trypanosoma brucei chromosome II clone RPC... 32 9.4
 35 emb|AW684118|AW684118 NF012F02NR1F1000 Nodulated root Medicago t... 32 9.4
 emb|AW622239|AW622239 EST313037 tomato root during/after fruit s... 32 9.4
 emb|AQ651543|AQ651543 Sheared DNA-7C22.TF Sheared DNA Trypanosom... 32 9.4
 emb|Y11565|NC11565 N.crassa acu-15 gene. 32 9.4
 emb|AW775944|AW775944 EST335009 DSIL Medicago truncatula cDNA cl... 32 9.4
 40 emb|AB014493|AB014493 Gibberella zeae gene for reductase, partia... 32 9.4

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- 45 gb|aaa32738.1|(m92353) anthranilate synthase alpha subunit
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 /gb_link /ncgi
 (1788 letters)

Database: plantfungal

- 50 661,018 sequences; 426,114,510 total letters

Searching.....done

- 55 Score E
 Sequences producing significant alignments: (bits) Value

- gb|L34344|RTAANTSYNB Ruta graveolens anthranilate synthase alpha... 772 0.0
 gb|L34343|RTAANTSYNB Ruta graveolens anthranilate synthase alpha... 467 0.0
 emb|AF079168|AF079168 Nicotiana tabacum feedback-insensitive ant... 365 0.0
 60 emb|AW931942|AW931942 EST357785 tomato fruit mature green, TAMU ... 356 3e-97
 emb|AW218352|AW218352 EST303535 tomato radicle, 5 d post-imbibit... 210 1e-73

- emb|AL031966|SPCC1442 *S.pombe* chromosome III cosmid c1442. 209 6e-69
- emb|AW651095|AW651095 EST329549 tomato germinating seedlings, TA... 222 2e-64
- dbj|D89256|D89256 *Schizosaccharomyces pombe* mRNA, partial cds, c... 205 5e-64
- emb|AW982499|AW982499 HVSMEg0003G22f *Hordeum vulgare* pre-anthesi... 215 2e-58
- 5 emb|AW460005|AW460005 si07d11.y1 *Gm-c1029* Glycine max cDNA clone... 116 1e-57
- gb|U18839|SCE9747 *Saccharomyces cerevisiae* chromosome V cosmids ... 123 4e-48
- emb|X68327|SCTRP2 *S.cerevisiae* TRP2 gene for anthranilate syntha... 123 4e-48
- emb|AW719463|AW719463 *LjNEST5b1r* *Lotus japonicus* nodule library,... 184 1e-45
- emb|AI736775|AI736775 sb33d01.y1 *Gm-c1012* Glycine max cDNA clone... 104 2e-40
- 10 gb|K01388|YSCTRP2 Yeast (*S.cerevisiae*) TRP2 gene coding for anth... 122 4e-38
- emb|AL032684|SPBP8B7 *S.pombe* chromosome II pl p8B7. 95 6e-25
- emb|AW509018|AW509018 si39b01.y1 *Gm-r1030* Glycine max cDNA clone... 113 5e-24
- gb|T14852|T14852 crs299 *lambdaZAPST* *Ricinus communis* cDNA clone ... 107 2e-22
- emb|AW223881|AW223881 EST300692 tomato fruit red ripe, TAMU Lyco... 103 4e-21
- 15 emb|AF119554|AF119554 *Plasmodium falciparum* para-aminobenzoic ac... 67 6e-10
- emb|AL111470|CNS019CM *Botrytis cinerea* strain T4 cDNA library un... 45 2e-05
- emb|AI329873|AI329873 b9g02ne.r1 *Neurospora crassa* evening cDNA ... 48 3e-04
- emb|AW224247|AW224247 EST300974 tomato fruit red ripe, TAMU Lyco... 46 7e-04
- emb|AF149719|AF149719 *Aspergillus fumigatus* para aminobenzoic ac... 42 0.012
- 20 emb|AQ448372|AQ448372 mgxb0020C12f CUGI Rice Blast BAC Library P... 39 0.15
- emb|AQ324360|AQ324360 mgxb0018K01r CUGI Rice Blast BAC Library P... 39 0.15
- emb|AQ160089|AQ160089 mgxb0003G09r CUGI Rice Blast BAC Library P... 39 0.15
- emb|AW599019|AW599019 gb01b03.y1 Moss EST library PPN Physcomitr... 37 0.38
- emb|AW599000|AW599000 ga99h03.y1 Moss EST library PPN Physcomitr... 37 0.38
- 25 emb|AW678847|AW678847 WS1_1_A04.g1_A002 Water-stressed 1 (WS1) S... 35 0.88
- emb|AW680390|AW680390 WS1_52_D12.g1_A002 Water-stressed 1 (WS1) ... 35 0.89
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- emb|AW678071|AW678071 WS1_13_E01.b1_A002 Water-stressed 1 (WS1) ... 35 0.90
- emb|AW747468|AW747468 WS1_68_B09.g1_A002 Water-stressed 1 (WS1) ... 35 0.90
- emb|AW672427|AW672427 LG1_359_A06.g1_A002 Light Grown 1 (LG1) So... 35 0.90
- 35 emb|AW744836|AW744836 LG1_384_E07.g1_A002 Light Grown 1 (LG1) So... 35 0.90
- emb|AW746170|AW746170 WS1_39_B05.g1_A002 Water-stressed 1 (WS1) ... 35 0.90
- emb|AW922317|AW922317 DG1_17_E06.g1_A002 Dark Grown 1 (DG1) Sorg... 35 0.91
- emb|AQ648582|AQ648582 RPCI93-EcoRI-1M22.TP RPCI93-EcoRI Trypanos... 36 0.99
- emb|AQ643551|AQ643551 RPCI93-EcoRI-3I24.TJ RPCI93-EcoRI Trypanos... 36 0.99
- 40 emb|AI443370|AI443370 sa31b05.x1 *Gm-c1004* Glycine max cDNA clone... 35 1.4
- emb|AW101313|AW101313 sd77d08.y1 *Gm-c1009* Glycine max cDNA clone... 35 1.4
- emb|AW678030|AW678030 WS1_12_B10.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
- emb|AW349006|AW349006 GM210004A12H10R *Gm-r1021* Glycine max cDNA ... 35 1.4
- emb|AW309961|AW309961 sf27b12.x1 *Gm-c1028* Glycine max cDNA clone... 35 1.4
- 45 emb|AW678582|AW678582 WS1_16_E09.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
- emb|AW317198|AW317198 sf38f03.x1 *Gm-c1028* Glycine max cDNA clone... 35 1.4
- emb|AW678305|AW678305 WS1_14_G05.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
- emb|AW680905|AW680905 WS1_8_A08.b1_A002 Water-stressed 1 (WS1) S... 35 1.4
- emb|AW679666|AW679666 WS1_30_B11.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
- 50 emb|AL031746|PFMALIP3 *Plasmodium falciparum* MALIP3, complete seq... 35 1.9
- emb|AI959816|AI959816 sc94f02.y1 *Gm-c1019* Glycine max cDNA clone... 35 1.9
- emb|AW924277|AW924277 WS1_52_D12.b1_A002 Water-stressed 1 (WS1) ... 35 1.9
- gb|J03998|PFAGAR *Plasmodium falciparum* glutamic acid-rich protei... 35 1.9
- emb|AW696796|AW696796 NF109A07ST1F1052 Developing stem *Medicago* ... 35 1.9
- 55 emb|AW396753|AW396753 sf37c11.x1 *Gm-c1028* Glycine max cDNA clone... 35 2.6
- gb|M98871|SOYCHS7A Glycine max chalcone synthase (chs7) gene, co... 35 2.6
- emb|AI460797|AI460797 sa69d02.y1 *Gm-c1004* Glycine max cDNA clone... 35 2.6
- emb|AW348617|AW348617 GM210002B22G1R *Gm-r1021* Glycine max cDNA 3... 35 2.6
- emb|AW310362|AW310362 sf35a09.x1 *Gm-c1028* Glycine max cDNA clone... 35 2.6
- 60 emb|AI437832|AI437832 sa40c07.y1 *Gm-c1004* Glycine max cDNA clone... 35 2.6
- gb|BE023927|BE023927 sm94c05.y1 *Gm-c1015* Glycine max cDNA clone ... 35 2.6

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	emb AW102370 AW102370 sd86h01.y1 Gm-c1009 Glycine max cDNA clone...	35	2.6
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5	emb AL355932 NCB5022 Neurospora crassa DNA linkage group II BAC ...	34	3.5
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	emb Z98056 SPAC5D6 S.pombe chromosome I cosmid c5D6.	34	3.5
	emb AW348286 AW348286 GM210001B23B6R Gm-r1021 Glycine max cDNA 3...	34	4.9
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10	emb AW734949 AW734949 sk93b10.y1 Gm-c1035 Glycine max cDNA clone...	34	4.9
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	emb Z28162 SCYKL162C S.cerevisiae chromosome XI reading frame OR...	33	6.7
	emb AW980990 AW980990 EST392143 GVN Medicago truncatula cDNA clo...	33	6.7
	gb BE037412 BE037412 MP20G03 MP Mesembryanthemum crystallinum cD...	33	6.7
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	emb AI726247 AI726247 BNLGHi5399 Six-day Cotton fiber Gossypium ...	33	6.7
	emb AE001401 AE001401 Plasmodium falciparum chromosome 2, sectio...	33	6.7
	emb AW573801 AW573801 EST316392 GVN Medicago truncatula cDNA clo...	33	6.7
	emb Z98547 PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque...	33	9.2
25	emb AQ659747 AQ659747 Sheared DNA-16J5.TR Sheared DNA Trypanosom...	33	9.2
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	emb AW222457 AW222457 EST299268 tomato fruit red ripe, TAMU Lyco...	33	9.2
	emb AB012116 AB012116 Vigna mungo UFGlyT mRNA for UDP-glycose:fl...	33	9.2
	emb AW725836 AW725836 GA_Ea0019N24 Gossypium arboreum 7-10 dpa ...	33	9.2
30	emb AQ324451 AQ324451 mgxb0018L23r CUGI Rice Blast BAC Library P...	33	9.2
	gb M73492 LEIHSP90 Leishmania donovani heat shock protein 90 mRN...	33	9.2
	emb AW132634 AW132634 se06h07.y1 Gm-c1013 Glycine max cDNA clone...	33	9.2
	emb AI166186 AI166186 a032p32u Hybrid aspen plasmid library Popu...	33	9.2
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<http://www.ncgr.org/cgi-bin/ff?atacs6>
(1567 letters)

45 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

50

Score E
Sequences producing significant alignments: (bits) Value

	emb X82273 BOACCS B.oleracea mRNA for ACC synthase.	944	0.0
55	emb X72676 BJMACC B. juncea mRNA for 1-Aminocyclopropane-1-carbo...	833	0.0
	emb AB034992 AB034992 Malus domestica MdACS-5A mRNA for 1-aminoc...	725	0.0
	emb AF057563 AF057563 Nicotiana glutinosa 1-aminocyclopropane-1-...	729	0.0
	emb AJ005002 NTAJ5002 Nicotiana tabacum mRNA for 1-aminocyclopro...	726	0.0
	emb AB034993 AB034993 Malus domestica MdACS-5B mRNA for 1-aminoc...	723	0.0
60	gb U72389 LEU72389 Lycopersicon esculentum 1-aminocyclopropane-1...	724	0.0
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- gb|U68216|CPU68216 *Carica papaya* ACC synthase mRNA, complete cds. 435 0.0
 emb|AB033503|AB033503 *Populus euramericana* peacs-2 mRNA for 1-am... 713 0.0
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 5 emb|AJ012551|CSI012551 *Citrus sinensis* mRNA for ACC synthase. 420 0.0
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 10 emb|X98492|NTACCS *Nicotiana tabacum* mRNA for ACC-synthase (clone... 425 0.0
 emb|X67100|GMCACCS1 *G. max* mRNA for ACC synthase. 429 0.0
 emb|AJ012696|CSI012696 *Citrus sinensis* mRNA for ACC synthase (AC... 422 0.0
 emb|Z18953|PHAMCRBSY *P. hybrida* mRNA for 1-aminocyclopropane 1-ca... 424 0.0
 emb|AJ011095|CSI011095 *Citrus sinensis* mRNA for ACC synthase (ac... 424 0.0
 15 emb|Z18952|DCAMCRBSY *D. caryophyllus* mRNA for 1-aminocyclopropane... 686 0.0
 emb|AB006804|AB006804 *Cucumis sativus* CS-ACS2 mRNA for ACC synth... 423 0.0
 emb|AF080258|AF080258 *Musa acuminata* 1-aminocyclopropane-1-carbo... 680 0.0
 emb|AF016459|AF016459 *Pisum sativum* 1-aminocyclopropane-1-carbox... 415 0.0
 dbj|D30805|CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy... 678 0.0
 20 emb|X65982|NTXACCSYN *N. tabacum* mRNA for 1-aminocyclopropane-1-ca... 417 0.0
 emb|AF109927|AF109927 *Musa acuminata* 1-aminocyclopropane-1-carbo... 676 0.0
 emb|AB006803|AB006803 *Cucumis sativus* CS-ACS1 mRNA for ACC synth... 676 0.0
 gb|U17231|PHU17231 *Pelargonium hortorum* clone pGAC-2 1-aminocycl... 423 0.0
 emb|AB021906|AB021906 *Musa acuminata* MA-ACS1 mRNA for ACC syntha... 671 0.0
 25 emb|AF129508|AF129508 *Musa acuminata* 1-aminocyclopropane-1-carbo... 671 0.0
 emb|AB015625|AB015625 *Pyrus pyrifolia* pPPACS3 mRNA for 1-aminocy... 393 0.0
 emb|AB031026|AB031026 *Prunus mume* PM-ACS1 mRNA for ACC synthase,... 405 0.0
 emb|Y11357|CP1A1CS *C. papaya* mRNA for 1-aminocyclopropane-1-carbo... 404 0.0
 dbj|D01032|CUCACCW *Cucurbita maxima* mRNA for 1-aminocyclopropane... 666 0.0
 30 dbj|E03724|E03724 cDNA encoding detriment induced type 1-aminocy... 666 0.0
 emb|X62536|LEACC *L. esculentum* mRNA for ACC synthase. 327 0.0
 gb|L20634|POTACCSYN *Solanum tuberosum* 1-aminocyclopropane-1-carb... 403 0.0
 emb|X59145|LEACC2MR *Lycopersicon esculentum* LE-ASCC2 mRNA (ptACC... 326 0.0
 gb|M58323|CUCACCSYN *Cucurbita pepo* 1-aminocyclopropane-1-carboxy... 663 0.0
 35 emb|AF057562|AF057562 *Nicotiana glutinosa* 1-aminocyclopropane-1-... 412 0.0
 emb|AF239987|AF239987 *Prunus persica* ACC synthase ACS1 mRNA, par... 662 0.0
 gb|M34289|TOMACS Tomato 1-aminocyclopropane-1-carboxylate syntha... 327 0.0
 gb|M63490|TOMACCS Tomato 1-aminocyclopropane-1-carboxylate synth... 657 0.0
 emb|X59146|LEACC4MR *Lycopersicon esculentum* LE-ACC4 mRNA (ptACC4... 656 0.0
 40 emb|Y15739|MAACSYNTH *Musa acuminata* mRNA for 1-aminocyclopropane... 655 0.0
 gb|U79999|MAU79999 *Musa acuminata* ACC synthase (acs3) mRNA, comp... 655 0.0
 emb|AF178076|AF178076 *Carica papaya* 1-aminocyclopropane-1-carbox... 395 0.0
 gb|U17229|PHU17229 *Pelargonium hortorum* clone pGAC-1 1-aminocycl... 407 0.0
 emb|X82265|CAACC1 *C. annuum* mRNA for 1-aminocyclopropane-1-carboxyl... 639 0.0
 45 gb|U70842|STU70842 *Solanum tuberosum* 1-aminocyclopropane-1-carbo... 637 0.0
 emb|AF144746|AF144746 *Solanum melongena* 1-aminocyclopropane-1-ca... 636 0.0
 emb|AJ276295|CSI276295 *Citrus sinensis* partial mRNA for ACC synt... 418 0.0
 emb|AJ012577|CPA012577 *Carica papaya* mRNA for 1-aminocyclopropan... 387 e-180
 emb|AF038945|AF038945 *Rumex palustris* 1-aminocyclopropane-1-carb... 372 e-179
 50 gb|U73815|MDU73815 *Malus domestica* ACC synthase (MdACS-2) mRNA, ... 623 e-178
 dbj|D37937|D37937 *Cucumis melo* mRNA for 1-aminocyclopropane-1-ca... 380 e-177
 emb|Z11562|VRACCSYN *V. radiata* mRNA for 1-aminocyclopropane-1-car... 375 e-176
 emb|AF177769|AF177769 *Carica papaya* 1-aminocyclopropane-1-carbox... 369 e-175
 emb|AF083814|AF083814 *Antirrhinum majus* ACC synthase 1 (ACS1) mR... 605 e-172
 55 emb|AF178077|AF178077 *Carica papaya* 1-aminocyclopropane-1-carbox... 316 e-171
 emb|AF239989|AF239989 *Prunus persica* ACC synthase ACS25 mRNA, pa... 597 e-170
 gb|U22523|MIU22523 *Mangifera indica* 1-aminocyclopropane-carboxyl... 359 e-169
 emb|X66605|DCACCS *D. caryophyllus* mRNA for 1-aminocyclopropane-1-... 396 e-168
 emb|AF049137|AF049137 *Dianthus caryophyllus* 1-aminocyclopropane-... 338 e-167
 60 emb|AF170705|AF170705 *Mangifera indica* 1-aminocyclopropane-1-car... 290 e-167
 emb|AJ277160|CPA277160 *Carica papaya* partial paccs1A gene for 1-... 266 e-165

- emb|AB015624|AB015624 *Pyrus pyrifolia* mRNA for 1-aminocyclopropane-1-carboxylate synthase... 359 e-163
 gb|U03294|MSU03294 *Malus sylvestris* 1-aminocyclopropane-1-carboxylate synthase... 359 e-163
 gb|L31347|MAUACCSYN *Malus domestica* 1-aminocyclopropane-1-carboxylate synthase... 357 e-162
 emb|AB015495|AB015495 *Passiflora edulis* PE-ACS2 mRNA for ACC synthase... 368 e-162
 5 emb|Z77854|PSPACS1 *Phalaenopsis species* mRNA for 1-aminocyclopropane-1-carboxylate synthase... 514 e-161
 dbj|D01033|CUCACCA *Cucurbita maxima* mRNA for 1-aminocyclopropane-1-carboxylate synthase... 349 e-159
 emb|X87112|PCPCACS1G *P. communis* mRNA for 1-aminocyclopropane-1-carboxylate synthase... 346 e-159
 emb|AB007449|AB007449 *Actinidia deliciosa* mRNA for 1-aminocyclopropane-1-carboxylate synthase... 336 e-159
 gb|U73816|MDU73816 *Malus domestica* ACC synthase (MdACS-3) mRNA, ... 504 e-158
 10 gb|U17972|LEU17972 *Lycopersicon esculentum* 1-aminocyclopropane-1-carboxylate synthase... 343 e-157
 emb|AB007639|AB007639 *Pyrus pyrifolia* mRNA for 1-aminocyclopropane-1-carboxylate synthase... 502 e-157
 gb|M66619|DINCARACC *D. caryophyllus* 1-aminocyclopropane-1-carboxylate synthase... 495 e-156
 emb|AB006805|AB006805 *Cucumis sativus* CS-ACS3 mRNA for ACC synthase... 342 e-156
 gb|U34987|VRU34987 *Vigna radiata* 1-aminocyclopropane-1-carboxylate synthase... 305 e-151
 15 emb|AB000679|AB000679 *Vigna radiata* mRNA for 1-aminocyclopropane-1-carboxylate synthase... 340 e-151
 gb|U34986|VRU34986 *Vigna radiata* 1-aminocyclopropane-1-carboxylate synthase... 340 e-149
 gb|U64031|DCU64031 *Dendrobium crumenatum* ACC synthase gene, complete cds... 259 e-149
 emb|AF016458|AF016458 *Pisum sativum* 1-aminocyclopropane-1-carboxylate synthase... 336 e-148
 emb|Z27233|STACCAS1 *S. tuberosum* (STAC1) gene for amino cyclopropane-1-carboxylate synthase... 238 e-147
 20 emb|Z27234|STACCAS2 *S. tuberosum* STACS2 gene for 1-Aminocyclopropane-1-carboxylate synthase... 234 e-146
 gb|U37774|CMU37774 *Cucurbita maxima* 1-aminocyclopropane-1-carboxylate synthase... 235 e-145
 emb|AF043122|AF043122 *Lycopersicon esculentum* ACC synthase (LE-A...)... 237 e-145
 emb|Z12135|VRACCSYN4 *V. radiata* gene for ACC synthase (pMAC-4)... 376 e-145
 gb|L34171|TOMACS3A *Lycopersicon esculentum* 1-aminocyclopropane-1-carboxylate synthase... 236 e-143
 25 gb|U18055|LEU18055 *Lycopersicon esculentum* 1-aminocyclopropane-1-carboxylate synthase... 236 e-143
 emb|AF074927|AF074927 *Sinapis arvensis* 1-aminocyclopropane-1-carboxylate synthase... 330 e-142
 emb|AF083815|AF083815 *Antirrhinum majus* ACC synthase 2 (ACS2) mRNA... 482 e-141
 emb|AF151961|AF151961 *Vigna radiata* 1-aminocyclopropane-1-carboxylate synthase... 234 e-141
 emb|AB021907|AB021907 *Musa acuminata* MA-ACS2 mRNA for ACC synthase... 310 e-140
 30 gb|L07883|DORAMICARB *Moth orchid* 1-aminocyclopropane-1-carboxylate synthase... 243 e-139
 emb|AB021908|AB021908 *Musa acuminata* MA-ACS3 mRNA for ACC synthase... 298 e-138

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40 Database: plantfungal
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Searching.....done

45 Score E
 Sequences producing significant alignments: (bits) Value

- emb|X82273|BOACCS *B. oleracea* mRNA for ACC synthase. 944 0.0
 emb|X72676|BJMACC *B. juncea* mRNA for 1-Aminocyclopropane-1-carboxylate synthase... 833 0.0
 50 emb|AB034992|AB034992 *Malus domestica* MdACS-5A mRNA for 1-aminocyclopropane-1-carboxylate synthase... 725 0.0
 emb|AF057563|AF057563 *Nicotiana glutinosa* 1-aminocyclopropane-1-carboxylate synthase... 729 0.0
 emb|AJ005002|NTAJ5002 *Nicotiana tabacum* mRNA for 1-aminocyclopropane-1-carboxylate synthase... 726 0.0
 emb|AB034993|AB034993 *Malus domestica* MdACS-5B mRNA for 1-aminocyclopropane-1-carboxylate synthase... 723 0.0
 gb|U72389|LEU72389 *Lycopersicon esculentum* 1-aminocyclopropane-1-carboxylate synthase... 724 0.0
 55 gb|U72390|LEU72390 *Lycopersicon esculentum* 1-aminocyclopropane-1-carboxylate synthase... 720 0.0
 gb|U68216|CPU68216 *Carica papaya* ACC synthase mRNA, complete cds. 435 0.0
 emb|AB033503|AB033503 *Populus euramericana* peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase... 713 0.0
 emb|AF061605|AF061605 *Nicotiana glutinosa* ACC synthase mRNA, complete cds... 712 0.0
 emb|AJ012551|CSI012551 *Citrus sinensis* mRNA for ACC synthase. 420 0.0
 60 emb|AB033502|AB033502 *Populus euphratica* peacs-1 mRNA for 1-aminocyclopropane-1-carboxylate synthase... 591 0.0
 emb|AB013100|AB013100 *Lycopersicon esculentum* LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase... 706 0.0

	emb AB013346 AB013346 <i>Lycopersicon esculentum</i> mRNA for 1-aminocy...	704	0.0
	gb U88971 PHU88971 <i>Pelargonium hortorum</i> 1-aminocyclopropane-1-ca...	423	0.0
	emb Z11613 VRACCSYNM <i>V. radiata</i> mRNA for ACC synthase.	428	0.0
	emb X98492 NTACCS <i>Nicotiana tabacum</i> mRNA for ACC-synthase (clone...	425	0.0
5	emb X67100 GMCACCS1 <i>G. max</i> mRNA for ACC synthase.	429	0.0
	emb AJ012696 CSI012696 <i>Citrus sinensis</i> mRNA for ACC synthase (AC...	422	0.0
	emb Z18953 PHAMCRBSY <i>P. hybrida</i> mRNA for 1-aminocyclopropane 1-ca...	424	0.0
	emb AJ011095 CSI011095 <i>Citrus sinensis</i> mRNA for ACC synthase (ac...	424	0.0
	emb Z18952 DCAMCRBSY <i>D. caryophyllus</i> mRNA for 1-aminocyclopropane...	686	0.0
10	emb AB006804 AB006804 <i>Cucumis sativus</i> CS-ACS2 mRNA for ACC synth...	423	0.0
	emb AF080258 AF080258 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	680	0.0
	emb AF016459 AF016459 <i>Pisum sativum</i> 1-aminocyclopropane-1-carbox...	415	0.0
	dbj D30805 CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy...	678	0.0
	emb X65982 NTXACCSYN <i>N. tabacum</i> mRNA for 1-aminocyclopropane-1-ca...	417	0.0
15	emb AF109927 AF109927 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	676	0.0
	emb AB006803 AB006803 <i>Cucumis sativus</i> CS-ACS1 mRNA for ACC synth...	676	0.0
	gb U17231 PHU17231 <i>Pelargonium hortorum</i> clone pGAC-2 1-aminocycl...	423	0.0
	emb AB021906 AB021906 <i>Musa acuminata</i> MA-ACS1 mRNA for ACC syntha...	671	0.0
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20	emb AB015625 AB015625 <i>Pyrus pyrifolia</i> pPPACS3 mRNA for 1-aminocy...	393	0.0
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	emb Y11357 CP1A1CS <i>C. papaya</i> mRNA for 1-aminocyclopropane-1-carbo...	404	0.0
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25	emb X62536 LEACC <i>L. esculentum</i> mRNA for ACC synthase.	327	0.0
	gb L20634 POTACCSYN <i>Solanum tuberosum</i> 1-aminocyclopropane-1-carb...	403	0.0
	emb X59145 LEACC2MR <i>Lycopersicon esculentum</i> LE-ASCC2 mRNA (ptACC...	326	0.0
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30	emb AF239987 AF239987 <i>Prunus persica</i> ACC synthase ACS1 mRNA, par...	662	0.0
	gb M34289 TOMACS Tomato 1-aminocyclopropane-1-carboxylate syntha...	327	0.0
	gb M63490 TOMACCS Tomato 1-aminocyclopropane-1-carboxylate synth...	657	0.0
	emb X59146 LEACC4MR <i>Lycopersicon esculentum</i> LE-ACC4 mRNA (ptACC4...	656	0.0
	emb Y15739 MAACSYNTH <i>Musa acuminata</i> mRNA for 1-aminocyclopropane...	655	0.0
35	gb U79999 MAU79999 <i>Musa acuminata</i> ACC synthase (acs3) mRNA, comp...	655	0.0
	emb AF178076 AF178076 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	395	0.0
	gb U17229 PHU17229 <i>Pelargonium hortorum</i> clone pGAC-1 1-aminocycl...	407	0.0
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	gb U70842 STU70842 <i>Solanum tuberosum</i> 1-aminocyclopropane-1-carbo...	637	0.0
40	emb AF144746 AF144746 <i>Solanum melongena</i> 1-aminocyclopropane-1-ca...	636	0.0
	emb AJ276295 CSI276295 <i>Citrus sinensis</i> partial mRNA for ACC synt...	418	0.0
	emb AJ012577 CPA012577 <i>Carica papaya</i> mRNA for 1-aminocyclopropan...	387	e-180
	emb AF038945 AF038945 <i>Rumex palustris</i> 1-aminocyclopropane-1-carb...	372	e-179
	gb U73815 MDU73815 <i>Malus domestica</i> ACC synthase (MdACS-2) mRNA, ...	623	e-178
45	dbj D37937 D37937 <i>Cucumis melo</i> mRNA for 1-aminocyclopropane-1-ca...	380	e-177
	emb Z11562 VRACCSYN <i>V. radiata</i> mRNA for 1-aminocyclopropane-1-car...	375	e-176
	emb AF177769 AF177769 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	369	e-175
	emb AF083814 AF083814 <i>Antirrhinum majus</i> ACC synthase 1 (ACS1) mR...	605	e-172
	emb AF178077 AF178077 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	316	e-171
50	emb AF239989 AF239989 <i>Prunus persica</i> ACC synthase ACS25 mRNA, pa...	597	e-170
	gb U22523 MIU22523 <i>Mangifera indica</i> 1-aminocyclopropane-carboxyl...	359	e-169
	emb X66605 DCACCS <i>D. caryophyllus</i> mRNA for 1-aminocyclopropane-1-...	396	e-168
	emb AF049137 AF049137 <i>Dianthus caryophyllus</i> 1-aminocyclopropane-...	338	e-167
	emb AF170705 AF170705 <i>Mangifera indica</i> 1-aminocyclopropane-1-car...	290	e-167
55	emb AJ277160 CPA277160 <i>Carica papaya</i> partial paccs1A gene for 1-...	266	e-165
	emb AB015624 AB015624 <i>Pyrus pyrifolia</i> mRNA for 1-aminocyclopropan...	359	e-163
	gb U03294 MSU03294 <i>Malus sylvestris</i> 1-aminocyclopropane-1-carbox...	359	e-163
	gb L31347 MAUACCSYN <i>Malus domestica</i> 1-aminocyclopropane-1-carbox...	357	e-162
	emb AB015495 AB015495 <i>Passiflora edulis</i> PE-ACS2 mRNA for ACC syn...	368	e-162
60	emb Z77854 PSPACS1 <i>Phalaenopsis</i> species mRNA for 1-aminocyclopro...	514	e-161
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- emb|X87112|PCPCACS1G *P. communis* mRNA for 1-aminocyclopropane-1-c... 346 e-159
 emb|AB007449|AB007449 *Actinidia deliciosa* mRNA for 1-aminocyclop... 336 e-159
 gb|U73816|MDU73816 *Malus domestica* ACC synthase (MdACS-3) mRNA, ... 504 e-158
 gb|U17972|LEU17972 *Lycopersicon esculentum* 1-aminocyclopropane-1... 343 e-157
 5 emb|AB007639|AB007639 *Pyrus pyrifolia* mRNA for 1-aminocyclopropa... 502 e-157
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 gb|U34987|VRU34987 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 305 e-151
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 10 gb|U34986|VRU34986 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 340 e-149
 gb|U64031|DCU64031 *Dendrobium crumenatum* ACC synthase gene, comp... 259 e-149
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 15 gb|U37774|CMU37774 *Cucurbita maxima* 1-aminocyclopropane-1-carbox... 235 e-145
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 emb|Z12135|VRACCSYN4 *V. radiata* gene for ACC synthase (pMAC-4). 376 e-145
 gb|L34171|TOMACS3A *Lycopersicon esculentum* 1-aminocyclopropane-1... 236 e-143
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 20 emb|AF074927|AF074927 *Sinapis arvensis* 1-aminocyclopropane-1-car... 330 e-142
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 (921 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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- 40 Score E
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- dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 144 7e-44
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 45 dbj|D38123|TOBBY4A *Nicotiana tabacum* mRNA for ERF1, complete cds. 134 6e-41
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- emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 111 6e-24
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dbj|D38125|TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 109 4e-23
10 emb|AW349638|AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3... 109 4e-23
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emb|AW618245|AW618245 EST314295 L. pennellii trichome, Cornell U... 108 8e-23
15 emb|AW776671|AW776671 EST335736 DSIL Medicago truncatula cDNA cl... 108 8e-23
emb|AW759181|AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone... 107 1e-22
emb|AW596384|AW596384 sj02f12.y1 Gm-c1032 Glycine max cDNA clone... 107 1e-22
emb|AI897797|AI897797 EST267240 tomato ovary, TAMU Lycopersicon ... 107 1e-22
emb|AI973653|AI973653 sd07h05.y1 Gm-c1020 Glycine max cDNA clone... 107 1e-22
20 emb|AW620490|AW620490 sj05h02.y1 Gm-c1032 Glycine max cDNA clone... 106 2e-22
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emb|AW574222|AW574222 EST316813 GVN Medicago truncatula cDNA clo... 105 4e-22
emb|AI778693|AI778693 EST259572 tomato susceptible, Cornell Lyco... 105 4e-22
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25 emb|AW774176|AW774176 EST333259 KV3 Medicago truncatula cDNA clo... 105 4e-22
emb|AI894873|AI894873 EST264316 tomato callus, TAMU Lycopersicon... 103 2e-21
gb|U89256|LEU89256 Lycopersicon esculentum DNA-binding protein P... 103 2e-21
emb|AW030009|AW030009 EST273264 tomato callus, TAMU Lycopersicon... 103 2e-21
emb|AW030386|AW030386 EST273641 tomato callus, TAMU Lycopersicon... 103 2e-21
30 emb|AI782381|AI782381 EST263260 tomato susceptible, Cornell Lyco... 100 1e-20
emb|AW980654|AW980654 EST391807 GVN Medicago truncatula cDNA clo... 100 2e-20
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emb|AI484961|AI484961 EST243224 tomato ovary, TAMU Lycopersicon ... 100 3e-20
emb|AW781602|AW781602 sl82d06.y1 Gm-c1037 Glycine max cDNA clone... 100 3e-20
35 emb|AW443265|AW443265 EST308195 tomato mixed elicitor, BTI Lycop... 100 3e-20
emb|AI440657|AI440657 sa63d09.y1 Gm-c1004 Glycine max cDNA clone... 99 4e-20
gb|U81157|NTU81157 Nicotiana tabacum S25-XP1 DNA binding protein... 98 8e-20
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emb|AW840611|AW840611 00057 leafy spurge Lambda HybriZAP 2.1 two... 97 1e-19
40 emb|AW559315|AW559315 EST306358 DSIR Medicago truncatula cDNA cl... 97 2e-19
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45 emb|AI055252|AI055252 coau0003H16 Cotton Boll Abscission Zone cD... 67 8e-19
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emb|AI896308|AI896308 EST265751 tomato callus, TAMU Lycopersicon... 94 1e-18
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50 emb|AW981323|AW981323 EST392476 DSIL Medicago truncatula cDNA cl... 92 5e-18
emb|AV417552|AV417552 AV417552 Lotus japonicus young plants (two... 92 5e-18
emb|AW618246|AW618246 EST314296 L. pennellii trichome, Cornell U... 92 5e-18
emb|AW685077|AW685077 NF024H04NR1F1000 Nodulated root Medicago t... 90 2e-17
emb|AW573782|AW573782 EST316373 GVN Medicago truncatula cDNA clo... 90 2e-17
55 emb|AW308784|AW308784 sf71h01.y1 Gm-c1013 Glycine max cDNA clone... 88 1e-16
emb|AW782252|AW782252 sm03d11.y1 Gm-c1027 Glycine max cDNA clone... 59 1e-16
emb|AW980481|AW980481 EST391634 GVN Medicago truncatula cDNA clo... 87 2e-16
gb|BE023264|BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone ... 87 2e-16
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60 emb|AW348322|AW348322 GM210001B23F6R Gm-r1021 Glycine max cDNA 3... 85 8e-16
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	emb AI897787 AI897787 EST267230 tomato ovary, TAMU Lycopersicon ...	52	1e-13
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40	emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone...	149	5e-35
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	emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl...	111	2e-32
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45	emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl...	125	2e-29
	emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon ...	128	3e-29
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(1188 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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	emb AF160869 AF160869	Citrus sinensis chlorophyllase mRNA, compl...	84	4e-54
40	emb AW039135 AW039135	EST281108 tomato mixed elicitor, BTI Lycopersicon...	127	2e-38
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45	emb AA887366 AA887366	L30-338T3 Ice plant Lambda Uni-Zap XR expr...	79	2e-26
	emb AA556157 AA556157	12 Loblolly pine N Pinus taeda cDNA clone ...	120	3e-26
	emb AW042994 AW042994	ST27H11 Pine TriplEx shoot tip library Pin...	106	7e-26
	emb AW265807 AW265807	L30-2522 T3 Ice plant Lambda Uni-Zap XR ex...	84	2e-21
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50	emb AW133452 AW133452	se19b10.y1 Gm-c1015 Glycine max cDNA clone...	62	1e-17
	emb AI777679 AI777679	EST258474 tomato susceptible, Cornell Lyco...	53	7e-17
	emb AW596770 AW596770	sj16e05.y1 Gm-c1032 Glycine max cDNA clone...	89	9e-17
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	emb AW626060 AW626060 EST319967 tomato radicle, 5 d post-imbibit...	35	1.6
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	emb AW649885 AW649885 EST328339 tomato germinating seedlings, TA...	34	2.2
	emb AW092862 AW092862 EST286042 tomato mixed elicitor, BTI Lycop...	34	2.2
	emb AW037417 AW037417 EST278919 tomato mixed elicitor, BTI Lycop...	34	2.2
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45	emb AW217951 AW217951 EST296665 tomato flower buds, anthesis, Co...	34	2.2
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15

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 (2616 letters)

- 25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

30

Score E

Sequences producing significant alignments: (bits) Value

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 (528 letters)

20 Database: plantfungal
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(528 letters)

Database: plantfungal
20 661,018 sequences; 426,114,510 total letters

Searching.....done

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25 Sequences producing significant alignments: (bits) Value

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 (528 letters)
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- Score E
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/chip nova /gb_link
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(433 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

15

Searching.....done

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	(bits)	Value	
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	emb X62120 BNCRU1 B.napus cru1 gene for cruciferin subunit.	169 4e-48	
	gb J05233 BNACRUCA B.napus cruciferin mRNA, 3' end.	169 9e-48	
	emb X59808 RSCRUG R.sativus pgCruRsE5 gene for cruciferin.	168 4e-43	
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25	emb X59804 RSCRUI R.sativus pAC2 mRNA for cruciferin.	123 1e-41	
	emb X57850 BNCRU4RN B.napus cru4 mRNA for cruciferin cru4 subunit.	138 2e-32	
	emb X57848 BNCRU4RNA B.napus cru4 mRNA for cruciferin cru4 subunit.	137 6e-32	
	gb M16860 BNACRUC Rapeseed cruciferin mRNA, complete cds.	132 1e-30	
	emb X59294 BNC1G B.napus BnC1 gene for cruciferin storage protein.	132 1e-30	
30	emb X14555 BNCRUA Brassica napus cruA gene for cruciferin.	132 1e-30	
	emb X57849 BNCRU23 B.napus cru2/3 mRNA for cruciferin cru2/3 sub...	132 1e-30	
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	emb X59806 RSCRUI R.sativus pBB6 mRNA for cruciferin.	131 3e-30	
	emb X59295 BNC2G B.napus BnC2 gene for cruciferin storage protein.	130 5e-30	
35	emb X82121 AHGLOBLN A.hypochondriacus mRNA for globulin.	118 3e-26	
	gb U38914 CSU38914 Citrus sinensis seed storage protein citrin m...	108 3e-23	
	emb X59803 RSCRUI R.sativus pAG4 mRNA for cruciferin.	81 3e-22	
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50	gb U64443 CAU64443 Coffea arabica 11S storage globulin mRNA, com...	94 5e-19	
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	gb M16936 COTSPB G.hirsutum (cotton) storage protein (beta-globu...	92 2e-18	
	emb AF054895 AF054895 Coffea arabica 11S storage globulin mRNA, ...	92 2e-18	
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	emb X82465 MSLEGB14 M.salicifolia mRNA for legumin precursor (B14).	89 2e-17	

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 gb|T24336|T24336 crs1452 lambdaZAPST Ricinus communis cDNA clone... 87 8e-17
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 10 emb|X68648|AS12S A.sativa pseudogene for 12S seed globulin. 86 1e-16
 gb|M69188|COTDGLA Cotton legumin A D-genome alloallele gene, co... 86 1e-16
 gb|M16905|COTSPD G.hirsutum (cotton) storage protein (beta-globu... 86 1e-16
 emb|X74741|ASGLAV3G A.sativa GLAV 3 gene for 11S globulin. 86 1e-16
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 30 emb|AW397311|AW397311 sg77c11.y1 Gm-c1007 Glycine max cDNA clone... 84 4e-16
 emb|AW318315|AW318315 sg63f06.y1 Gm-c1007 Glycine max cDNA clone... 84 4e-16
 emb|X95509|AELEG18GN A.europaeum mRNA for legumin. 84 6e-16
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 gb|T24371|T24371 crs1501 lambdaZAPST Ricinus communis cDNA clone... 82 3e-15
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 emb|X15123|GMYG3 Soybean Gy3 gene for glycinin subunit G3. 81 4e-15
 50 emb|AI748727|AI748727 sb61b06.y1 Gm-c1010 Glycine max cDNA clone... 81 4e-15
 emb|AF193433|AF193433 Elaeis guineensis glutelin (PKT9) mRNA, co... 81 4e-15
 emb|X76737|AS12SGL1 A.sativa (L) mRNA for 12S globulin (1556 bp). 81 5e-15
 gb|M21405|ASTSPGLBA Oat seed storage globulin mRNA, complete cds. 81 5e-15
 gb|T23264|T23264 crs1114 lambdaZAPST Ricinus communis cDNA clone... 81 5e-15
 55 gb|M16868|ASTGLOB Oat storage protein 12S globulin mRNA, partial... 81 5e-15
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 emb|AF180392|AF180392 Perilla frutescens legumin-like protein mR... 80 7e-15
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 /description gb|aaf16576.1|ac012563_29 (ac012563) putative
 s-adenosyl-L-methionine:trans-caffeoyl-coenzyme a
 3-o-methyltransferase [arabidopsis thaliana] /blast_score 1.00e-121
 5 /ec_number /family /chip nova /gb_link /ncgi
 (965 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	gb U20736 MSU20736 Medicago sativa S-adenosyl-L-methionine:trans...	142	2e-68
	emb AW624860 AW624860 EST313689 tomato radicle, 5 d post-imbibit...	139	2e-67
	emb AF022775 AF022775 Nicotiana tabacum cafferoyl-CoA 3-O-methyltr...	138	2e-67
20	emb Z54233 VVCCOAOMT V.vinifera mRNA for cafferoyl-CoA O-methyltr...	136	9e-67
	gb M69184 PUMCCOAMT Petroselinum crispum cafferoyl-CoA 3-O-methyl...	133	2e-66
	gb U27116 PTU27116 Populus tremuloides cafferoyl-CoA 3-O-methyltr...	135	3e-66
	emb AJ224894 PBT AJ4894 Populus balsamifera subsp. trichocarpa mR...	135	3e-66
	gb U13151 ZEU13151 Zinnia elegans S-adenosyl-L-methionine:trans-...	136	4e-66
25	emb AI489305 AI489305 EST247644 tomato ovary, TAMU Lycopersicon ...	139	4e-66
	emb AJ224895 PBT AJ4895 Populus balsamifera subsp. trichocarpa mR...	136	6e-66
	emb AJ224896 PBT AJ4896 Populus balsamifera subsp. trichocarpa mR...	136	6e-66
	emb AF168780 AF168780 Eucalyptus globulus cafferoyl-CoA O-methyltr...	133	8e-66
	emb AF053553 AF053553 Mesembryanthemum crystallinum cafferoyl-CoA...	132	1e-65
30	emb AF240466 AF240466 Populus tomentosa cafferoyl-CoA O-methyltra...	135	1e-65
	emb A22706 A22706 Cafferoyl-CoA-3-O-Methyltransferase gene.	129	3e-65
	gb U62734 NTU62734 Nicotiana tabacum cafferoyl-CoA O-methyltransf...	134	5e-65
	emb Z56282 NTCCOAOMT N.tabacum mRNA for cafferoyl-CoA O-methyltra...	132	5e-65
	gb U62736 NTU62736 Nicotiana tabacum cafferoyl-CoA O-methyltransf...	136	5e-65
35	gb U38612 NTU38612 Nicotiana tabacum cafferoyl-coenzymeA O-methyl...	136	5e-65
	emb Y12228 EG12228 E.gunnii mRNA for cafferoyl-CoA O-methyltransf...	133	7e-65
	gb L22203 SLASADEN Stellaria longipes S-adenosyl-L-methionine:tr...	124	8e-65
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	gb U62735 NTU62735 Nicotiana tabacum cafferoyl-CoA O-methyltransf...	134	3e-64
40	emb AF036095 AF036095 Pinus taeda cafferoyl-CoA O-methyltransfera...	130	6e-64
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	emb AJ130841 PBA130841 Populus balsamifera subsp. trichocarpa mR...	133	2e-57
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	emb AI166541 AI166541 xylem.est.363 Poplar xylem Lambda ZAPII li...	135	7e-55
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55	emb AW278810 AW278810 sf98g06.y1 Gm-c1019 Glycine max cDNA clone...	135	3e-54
	emb AI939180 AI939180 sc67h02.y1 Gm-c1016 Glycine max cDNA clone...	125	3e-54
	emb AW102461 AW102461 sd88d11.y1 Gm-c1009 Glycine max cDNA clone...	133	3e-54
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- emb|AW625527|AW625527 EST319434 tomato radicle, 5 d post-imbibit... 133 8e-53
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 5 emb|AW094365|AW094365 EST287545 tomato mixed elicitor, BTI Lycop... 133 1e-52
 gb|BE021597|BE021597 sm60a04.y1 Gm-cl028 Glycine max cDNA clone ... 135 1e-52
 emb|AW034347|AW034347 EST277918 tomato callus, TAMU Lycopersicon... 133 2e-52
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 10 emb|AI898952|AI898952 EST268395 tomato ovary, TAMU Lycopersicon ... 139 2e-51
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 emb|AW648499|AW648499 EST326953 tomato germinating seedlings, TA... 99 7e-50
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 emb|AW684885|AW684885 NF022F07NR1F1000 Nodulated root Medicago t... 142 2e-47
 20 emb|AA660318|AA660318 00189 MrHE Medicago truncatula cDNA 5' si... 144 2e-47
 emb|AW703717|AW703717 sk23e07.y1 Gm-cl028 Glycine max cDNA clone... 132 4e-47
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 35 emb|AI166314|AI166314 xylem.est.159 Poplar xylem Lambda ZAPII li... 136 4e-44
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 45 emb|AW683492|AW683492 NF012H09LF1F1079 Developing leaf Medicago ... 134 2e-41
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 50 emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40
 emb|AW625461|AW625461 EST319368 tomato radicle, 5 d post-imbibit... 99 1e-40
 emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40
 emb|AI960196|AI960196 sc80a08.y1 Gm-cl018 Glycine max cDNA clone... 132 5e-40
 emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39
 55 emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39

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 60 thaliana] /blast_score 6.00e-99 /ec_number /family /chip nova
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(827 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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emb|AI489346|AI489346 EST247685 tomato ovary, TAMU Lycopersicon ... 79 2e-28
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emb|AW102460|AW102460 sd88d10.y1 Gm-cl009 Glycine max cDNA clone... 70 2e-22
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emb|AI487362|AI487362 EST245684 tomato ovary, TAMU Lycopersicon ... 72 3e-20
20 gb|BE125690|BE125690 DG1_54_A02.g1_A002 Dark Grown 1 (DG1) Sorgh... 96 3e-19
emb|X80231|LTCAMA L.tarentolae CAM A gene for calmodulin. 73 1e-18
emb|AL115248|CNS01C9K Botrytis cinerea strain T4 cDNA library un... 65 4e-18
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emb|AF078679|AF078679 Olea europaea calcium-binding protein (PCA... 57 2e-17
emb|X56511|TBCALUBG T. brucei genes for calmodulin, EFH5 and ubi... 77 2e-17
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35 emb|Y08373|TGCM T.gondii mRNA for calmodulin. 74 2e-17
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emb|AI328739|AI328739 a6d02ne.fl Neurospora crassa evening cDNA ... 74 6e-17
emb|AF034964|AF034964 Glomerella cingulata calmodulin (cam) mRNA... 74 6e-17
45 gb|U12505|HCCMD Histoplasma capsulatum 186AS calmodulin mRNA, co... 74 8e-17
gb|M34540|PARCAM P.tetraurelia calmodulin gene, complete cds. 74 8e-17
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55 gb|K02944|TRBCMRSG Trypanosoma brucei gambiense calmodulin genes... 73 2e-16
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emb|X89890|BPCALMGEM B.pilosa mRNA for calmodulin. 73 2e-16
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 emb|Y13784|MSCALMODU Mougeotia scalaris mRNA for calmodulin. 70 3e-16
 emb|AI727960|AI727960 BNLGHi9833 Six-day Cotton fiber Gossypium ... 73 3e-16
 emb|AA660367|AA660367 00239 MtRHE Medicago truncatula cDNA 5' si... 71 3e-16
 10 emb|AW164628|AW164628 se74e01.y1 Gm-c1023 Glycine max cDNA clone... 60 3e-16
 emb|AF150059|AF150059 Brassica napus calmodulin (CaM1) mRNA, com... 72 3e-16
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 15 gb|BE033450|BE033450 ME02B08 ME Mesembryanthemum crystallinum cD... 73 4e-16
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 gb|L20691|VIRCALMOD Vigna radiata calmodulin mRNA, complete cds. 73 4e-16
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 20 gb|BE036340|BE036340 MO23E04 MO Mesembryanthemum crystallinum cD... 73 4e-16
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 25 gb|U49104|TAU49104 Triticum aestivum calmodulin TaCaM3-3 mRNA, c... 73 4e-16
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 30 gb|U48242|TAU48242 Triticum aestivum calmodulin TaCaM1-1 mRNA, c... 73 4e-16
 gb|M80836|PETCAM81 Petunia hybrida CAM81 mRNA, 73 4e-16
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 35 gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16
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 45 gb|BE051931|BE051931 GA_Ea0002G11f Gossypium arboreum 7-10 dpa ... 73 4e-16
 emb|AW666619|AW666619 GA_Ea0005C16 Gossypium arboreum 7-10 dpa ... 73 4e-16
 emb|AW108833|AW108833 gate0001L24f Gossypium arboreum 7-10 dpa f... 73 4e-16
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 gb|L18912|LILCALMODU Lilium longiflorum calmodulin mRNA, complet... 73 4e-16
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 (1408 letters)

55

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

60

Searching.....done

Score E

	Sequences producing significant alignments:	(bits) Value
	emb AB014483 AB014483 <i>Nicotiana tabacum</i> NtHSF1 mRNA for heat sho... 213 2e-62	
	emb X55347 LPHSF24 Tomato mRNA for heat stress transcription fac... 210 2e-53	
5	emb AI900223 AI900223 sc02f05.y1 <i>Gm-c1012</i> Glycine max cDNA clone... 205 3e-53	
	emb Z46953 GMHSF34 <i>G.max</i> mRNA for heat shock transcription facto... 203 6e-53	
	emb AV408054 AV408054 AV408054 <i>Lotus japonicus</i> young plants (two... 203 3e-51	
	emb AV415115 AV415115 AV415115 <i>Lotus japonicus</i> young plants (two... 197 2e-49	
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	emb AW689532 AW689532 NF021G10ST1F1000 Developing stem <i>Medicago</i> ... 194 1e-48	
	emb AI728175 AI728175 BNLGHi10028 Six-day Cotton fiber <i>Gossypium</i> ... 192 5e-48	
	emb AI055366 AI055366 coau0003M17 Cotton Boll Abscission Zone cD... 191 1e-47	
	emb AW703969 AW703969 sk14g08.y1 <i>Gm-c1023</i> Glycine max cDNA clone... 191 1e-47	
	emb AW428882 AW428882 Ljimp25-001-b9 Ljimp Lambda HybriZap ... 190 2e-47	
15	emb AW931781 AW931781 EST357624 tomato fruit mature green, TAMU ... 189 3e-47	
	emb AW686121 AW686121 NF033H01NR1F1000 Nodulated root <i>Medicago</i> t... 188 1e-46	
	emb Z46956 GMHSF5 <i>G.max</i> mRNA for heat shock transcription factor 5. 185 6e-46	
	emb AW109013 AW109013 gate0002O16f <i>Gossypium arboreum</i> 7-10 dpa f... 179 4e-44	
	gb BE054274 BE054274 GA_Ea0002O16f <i>Gossypium arboreum</i> 7-10 dpa ... 179 4e-44	
20	gb BE020791 BE020791 sm52h09.y1 <i>Gm-c1028</i> Glycine max cDNA clone ... 178 1e-43	
	emb AW696868 AW696868 NF111F05ST1F1046 Developing stem <i>Medicago</i> ... 166 3e-43	
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25	emb AW033421 AW033421 EST276992 tomato callus, TAMU <i>Lycopersicon</i> ... 165 1e-39	
	emb AW030725 AW030725 EST273980 tomato callus, TAMU <i>Lycopersicon</i> ... 165 1e-39	
	emb AW041695 AW041695 EST284559 tomato mixed elicitor, BTI <i>Lycop</i> ... 165 1e-39	
	emb AW217982 AW217982 EST296697 tomato flower buds, anthesis, Co... 165 1e-39	
	emb X67600 LPHSF8 <i>L.peruvianum</i> Lp-hsf8 mRNA for heat stress tran... 161 1e-38	
30	emb AW774397 AW774397 EST333548 KV3 <i>Medicago truncatula</i> cDNA clo... 160 2e-38	
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	emb AW776460 AW776460 EST335525 DSIL <i>Medicago truncatula</i> cDNA cl... 152 7e-36	
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	emb AW036683 AW036683 EST278726 tomato fruit mature green, TAMU ... 149 5e-35	
35	emb AI729182 AI729182 BNLGHi12855 Six-day Cotton fiber <i>Gossypium</i> ... 149 5e-35	
	emb AI489721 AI489721 EST248060 tomato ovary, TAMU <i>Lycopersicon</i> ... 149 5e-35	
	emb AW034402 AW034402 EST277973 tomato callus, TAMU <i>Lycopersicon</i> ... 148 7e-35	
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40	emb AW164509 AW164509 se74f12.y1 <i>Gm-c1023</i> Glycine max cDNA clone... 147 2e-34	
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45	emb AW559623 AW559623 EST314671 DSIR <i>Medicago truncatula</i> cDNA cl... 144 2e-33	
	emb AW222011 AW222011 EST298822 tomato fruit red ripe, TAMU <i>Lyc</i> ... 144 2e-33	
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	emb AB014484 AB014484 <i>Nicotiana tabacum</i> NtHSF2 mRNA for heat sho... 140 3e-32	
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50	emb AW738534 AW738534 EST339961 tomato flower buds, anthesis, Co... 139 5e-32	
	emb AI725043 AI725043 942 PtiFG2 <i>Pinus taeda</i> cDNA clone 8824r, m... 139 5e-32	
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	emb AW596493 AW596493 sj13a09.y1 <i>Gm-c1032</i> Glycine max cDNA clone... 138 1e-31	
	emb AV415736 AV415736 AV415736 <i>Lotus japonicus</i> young plants (two... 138 1e-31	
55	emb AW979619 AW979619 EST341218 tomato root deficiency, Cornell ... 137 2e-31	
	emb AW932142 AW932142 EST357985 tomato fruit mature green, TAMU ... 136 3e-31	
	emb Z46954 GMHSF33 <i>G.max</i> mRNA for heat shock transcription facto... 135 9e-31	
	emb AW569138 AW569138 si63g09.y1 <i>Gm-r1030</i> Glycine max cDNA clone... 134 1e-30	
	emb AW569256 AW569256 si64g09.y1 <i>Gm-r1030</i> Glycine max cDNA clone... 134 1e-30	
60	emb AW203851 AW203851 sf38h11.y1 <i>Gm-c1028</i> Glycine max cDNA clone... 133 3e-30	
	emb AW220758 AW220758 EST297227 tomato fruit mature green, TAMU ... 132 6e-30	

- emb|AI728806|AI728806 BNLGHi11701 Six-day Cotton fiber Gossypium... 108 2e-28
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 5 gb|Z46951|GMHSF29 G.max mRNA for heat shock transcription facto... 120 2e-26
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 10 emb|AW775388|AW775388 EST334453 DSIL Medicago truncatula cDNA cl... 66 1e-23
 emb|AW931892|AW931892 EST357735 tomato fruit mature green, TAMU ... 104 2e-21
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 15 emb|AV420766|AV420766 AV420766 Lotus japonicus young plants (two... 102 8e-21
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 20 emb|AW924303|AW924303 WS1_52_H11.b1_A002 Water-stressed I (WS1) ... 99 7e-20
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 gb|M94683|YSPHSF Schizosaccharomyces pombe heat shock transcript... 93 6e-18
 25 emb|X55149|KLHSFG K. lactis HSF gene for heat shock transcriptio... 76 2e-17
 emb|AW933448|AW933448 EST359387 tomato fruit mature green, TAMU ... 89 8e-17
 emb|AI896906|AI896906 EST266349 tomato callus, TAMU Lycopersicon... 89 1e-16
 emb|AZ045432|AZ045432 T234030b shotgun sub-library of BAC clone ... 84 2e-15
 emb|X83031|SCPOS9 S.cerevisiae POS9 gene. 83 5e-15
 30 gb|U00485|YSCSKN7 Saccharomyces cerevisiae putative transcriptio... 83 5e-15
 gb|U00029|YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm... 83 5e-15
 emb|Z69726|SPAC2E12 S.pombe chromosome I cosmid c2E12. 83 6e-15
 gb|M22040|YSCHSF1A S.cerevisiae heat shock transcription factor ... 81 2e-14
 emb|Z72596|SCYGL074C S.cerevisiae chromosome VII reading frame O... 81 2e-14
 35 gb|J03139|YSCHSF S.cerevisiae heat shock factor gene (HSF), comp... 81 2e-14
 emb|AI212342|AI212342 x3c12a1.r1 Aspergillus nidulans 24hr asexu... 73 8e-14
 emb|AW686674|AW686674 NF040F05NR1F1000 Nodulated root Medicago t... 79 8e-14
 emb|AZ048458|AZ048458 PSB119 Barley PstI genomic clones Hordeum ... 78 2e-13
 emb|AW034135|AW034135 EST277706 tomato callus, TAMU Lycopersicon... 57 9e-13
 40 emb|AW933529|AW933529 EST359288 tomato fruit mature green, TAMU ... 72 1e-11
 emb|AW307441|AW307441 sf57a06.y1 Gm-c1009 Glycine max cDNA clone... 70 5e-11
 emb|AW620962|AW620962 sj98b03.y1 Gm-c1023 Glycine max cDNA clone... 70 5e-11

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 thaliana] /blast_score 2.00e-75 /ec_number /family /chip nova
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 50 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|hsp176a/)
<http://www.ncgr.org/cgi-bin/ff?hsp176a>
 (613 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

- 55 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

- 60 gb|M33901|PEAHSP177A Pisum sativum 17.7 kDa heat shock protein (... 126 3e-44
 gb|M99429|PHNSHSPA Ipomoea nil small heat shock protein, complet... 171 4e-42

- emb|X98617|MSSH17KD M.sativa mRNA for 17kD heat shock protein. 171 6e-42
- emb|AF159562|AF159562 Prunus dulcis cytosolic class II low molec... 105 7e-42
- gb|L47740|PIAEMB29R Picea glauca class II cytoplasmic small mole... 169 2e-41
- emb|AW569703|AW569703 si79c12.y1 Gm-c1031 Glycine max cDNA clone... 107 6e-41
- 5 emb|X99346|PASHSP P.abies mRNA for small heat shock protein. 166 1e-40
- emb|AW667877|AW667877 GA_Ea0011C02 Gossypium arboreum 7-10 dpa ... 110 2e-40
- emb|AW725392|AW725392 GA_Ea0017J18 Gossypium arboreum 7-10 dpa ... 110 2e-40
- emb|AW569553|AW569553 si88e08.y1 Gm-c1031 Glycine max cDNA clone... 107 1e-39
- emb|AW620261|AW620261 si93g10.y1 Gm-c1031 Glycine max cDNA clone... 107 1e-39
- 10 gb|BE053976|BE053976 GA_Ea0002N06f Gossypium arboreum 7-10 dpa ... 110 3e-39
- emb|AW109163|AW109163 gate0002N06f Gossypium arboreum 7-10 dpa f... 110 3e-39
- emb|AW569987|AW569987 si85c01.y1 Gm-c1031 Glycine max cDNA clone... 107 2e-38
- emb|X07159|GMHSP179 Soybean gene for heat shock protein Gmhsp17... 103 2e-38
- emb|AW620254|AW620254 si93g03.y1 Gm-c1031 Glycine max cDNA clone... 103 2e-38
- 15 emb|AW569546|AW569546 si88e01.y1 Gm-c1031 Glycine max cDNA clone... 103 2e-38
- emb|AW569992|AW569992 si85c07.y1 Gm-c1031 Glycine max cDNA clone... 107 8e-38
- emb|AW570000|AW570000 si85d08.y1 Gm-c1031 Glycine max cDNA clone... 104 1e-37
- emb|AW730881|AW730881 GA_Ea0029C17 Gossypium arboreum 7-10 dpa ... 103 3e-37
- emb|AW870031|AW870031 NXNV_123_C02 F Nsf Xylem Normal wood Verti... 153 1e-36
- 20 emb|AI812703|AI812703 18B10 Pine Lambda Zap Xylem library Pinus ... 145 3e-34
- gb|U72396|LEU72396 Lycopersicon esculentum class II small heat s... 123 8e-31
- emb|X95716|PCSHSPGEN P.crispum mRNA for 17.9kDa heat shock prote... 105 3e-28
- emb|AI776971|AI776971 EST252063 tomato callus, TAMU Lycopersicon... 123 1e-27
- emb|AB027500|AB027500 Daucus carota Dchsp-1 mRNA, complete cds. 98 2e-26
- 25 emb|AJ225049|LPAJ5049 Lycopersicon peruvianum mRNA for Hsp20.2 p... 105 8e-26
- emb|AF090115|AF090115 Lycopersicon esculentum cytosolic class II... 106 3e-25
- emb|AI782242|AI782242 EST263121 tomato susceptible, Cornell Lyco... 106 4e-25
- emb|AF089846|AF089846 Funaria hygrometrica cytosolic II small he... 73 6e-25
- dbj|D21817|LILLIM11 Lily mRNA for small heat shock protein, part... 78 1e-24
- 30 emb|AW569456|AW569456 si87d04.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
- emb|AW569687|AW569687 si79b06.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
- emb|AW568954|AW568954 si73e12.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
- emb|AW569158|AW569158 si75b01.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
- emb|AW568867|AW568867 si73c04.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
- 35 emb|AW569632|AW569632 si89d12.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
- emb|AW569640|AW569640 si89e09.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
- emb|AW568707|AW568707 si72b01.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
- emb|AW569586|AW569586 si88h09.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
- emb|AW620228|AW620228 si93d08.y1 Gm-c1031 Glycine max cDNA clone... 111 7e-24
- 40 gb|L47717|PIAEMB27R Picea glauca heat shock protein 17.0 (EMB27)... 110 1e-23
- emb|AW570013|AW570013 si85f01.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23
- emb|AW185394|AW185394 se90h07.y1 Gm-c1027 Glycine max cDNA clone... 108 3e-23
- emb|AW620212|AW620212 si93c03.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23
- emb|AI900116|AI900116 sc01a11.y1 Gm-c1012 Glycine max cDNA clone... 108 3e-23
- 45 emb|AW569816|AW569816 si81h07.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23
- emb|AW569179|AW569179 si75e02.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23
- emb|AW289617|AW289617 NXNV003E01F Nsf Xylem Normal wood Vertical... 108 5e-23
- emb|Z29554|HA179HSP H.annuus (Sunweed) mRNA for 17.9 kDa heat-sh... 105 3e-22
- emb|X92983|PMLMWHSPA P.menziesii mRNA for low molecular weight h... 104 6e-22
- 50 emb|AW569996|AW569996 si85c11.y1 Gm-c1031 Glycine max cDNA clone... 104 6e-22
- emb|X92984|PMLMWHSPB P.menziesii mRNA for low molecular weight h... 104 6e-22
- dbj|D21816|LILLIM10 Lily mRNA for small heat shock protein, part... 68 1e-21
- emb|X58279|TAHSP173 T.aestivum mRNA for heat shock protein 17.3: 102 1e-21
- gb|M99430|PHNSHSPB Ipomoea nil small heat shock protein, complet... 102 3e-21
- 55 gb|M33899|PEAHSP181A Pisum sativum 18.1 kDa heat shock protein (... 65 5e-21
- emb|AF089843|AF089843 Funaria hygrometrica cytosolic I small hea... 64 9e-21
- gb|U63631|FXU63631 Fragaria x ananassa LMW heat shock protein mR... 63 2e-20
- gb|U46545|HAU46545 Helianthus annuus 17.7 kDa heat-shock protein... 63 2e-20
- emb|X13431|TAHSPLW Wheat mRNA for putative low molecular weight ... 65 2e-20
- 60 emb|AF123255|AF123255 Lycopersicon esculentum 17.7 kD class I sm... 61 3e-20
- emb|X58711|MSHSP182 M.sativa mRNA for heat shock protein (clone ... 61 3e-20

- emb|AW929084|AW929084 EST337788 tomato flower buds 8 mm to pre-a... 61 3e-20
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 5 emb|AW289567|AW289567 NXNV002G05F Nsf Xylem Normal wood Vertical... 98 5e-20
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 10 emb|AW597262|AW597262 si91d02.y1 Gm-c1031 Glycine max cDNA clone... 61 1e-19
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 15 emb|AF123256|AF123256 Lycopersicon esculentum 17.8 kD class I sm... 61 2e-19
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 35 emb|AF089845|AF089845 Funaria hygrometrica cytosolic II small he... 94 1e-18
 emb|X53852|DCHSP179 Carrot gene for a heat shock protein. 61 1e-18
 emb|AW223810|AW223810 EST300621 tomato fruit red ripe, TAMU Lyco... 57 1e-18

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- gb|M99431|PHNHSP83A Pharbitis nil heat shock protein 83 (Hsp83) ... 597 0.0
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 55 gb|U55859|TAU55859 Triticum aestivum heat shock protein 80 mRNA,... 575 0.0
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 emb|X63195|NTHSP82 N.tabacum mRNA for heat shock protein 82. 601 0.0
 emb|AF123259|AF123259 Lycopersicon esculentum heat shock protein... 483 0.0
 emb|AF165818|AF165818 Guillardia theta nucleomorph 5S ribosomal ... 505 0.0
 60 emb|AF042329|AF042329 Eimeria tenella heat shock protein 90 (hsp... 514 0.0
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- emb|Z29667|PFHESHP P. falciparum (7) mRNA for heat-shock protein. 507 0.0
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 5 gb|M15346|TRBHSC T. cruzi tandemly repeated gene encoding an 85 k... 457 0.0
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 10 gb|U92465|AFU92465 Aspergillus fumigatus heat shock protein (Hsp... 458 e-165
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 15 emb|Z67751|SC38KCXVI S. cerevisiae DNA (chromosome XVI; 38 kb). 448 e-159
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 20 emb|Z49808|SC8010 S. cerevisiae chromosome XIII cosmid 8010. 447 e-158
 emb|AF221856|AF221856 Euphorbia esula heat-shock protein 80 mRNA... 292 e-158
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 25 emb|AI489832|AI489832 EST248171 tomato ovary, TAMU Lycopersicon ... 471 e-132
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 35 emb|AW731352|AW731352 GA_Ea0030E22 Gossypium arboreum 7-10 dpa ... 449 e-125
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 40 emb|AW931002|AW931002 EST356845 tomato fruit mature green, TAMU ... 436 e-121
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 45 emb|AW217696|AW217696 EST296410 tomato flower buds 8 mm to pre-a... 422 e-117
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Database: plantfungal
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	emb AI729043 AI729043 BNLGHi12416 Six-day Cotton fiber Gossypium...	142	6e-42

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35 Database: plantfungal
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 55 emb|AW991095|AW991095 SsS0129 Suaeda salsa ZAP cDNA library Suae... 28 5.9
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Database: plantfungal
 15 661,018 sequences; 426,114,510 total letters

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	emb AW441936 AW441936 EST311332 tomato fruit red ripe, TAMU Lyco...	51	2e-06	
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40	emb AW775746 AW775746 EST334811 DSIL Medicago truncatula cDNA cl...	46	1e-04	
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55	emb X02873 DCEXTG Carrot gene for extensin.	37	0.062	
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 gb|BE034443|BE034443 MH05A01 MH *Mesembryanthemum crystallinum* cD... 34 0.42
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 emb|AW471567|AW471567 si12b01.y1 Gm-c1029 Glycine max cDNA clone... 33 1.1
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 45 emb|AW725658|AW725658 GA_Ea0019C15 *Gossypium arboreum* 7-10 dpa ... 27 1.5
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 55 emb|AF163952|AF163952 *Saccharomyces cerevisiae* isolate wt-1 telo... 27 1.5
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 gb|U66179|SCU66179 *Skeletonema costatum* fucoxanthin-chlorophyll ... 32 2.0
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Database: plantfungal
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	emb AW650581 AW650581 EST329035 tomato germinating seedlings, TA...	49	6e-06
	emb AW200887 AW200887 se94g08.y1 Gm-c1027 Glycine max cDNA clone...	50	3e-05
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	emb AW256640 AW256640 EST304777 KV2 Medicago truncatula cDNA clo...	42	0.006
30	emb AF133053 AF133053 Clarkia breweri S-adenosyl-L-methionine:sa...	42	0.006
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	emb AA495648 AA495648 c078 Zhou and Ragan 1993 Gracilaria gracil...	32 8.6
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Database: plantfungal
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60	gb U33335 U33335 Saccharomyces cerevisiae chromosome XVI, left a...	30 4.5	
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 5 gb|L16451|YSAAPRP Candida albicans acid proteinase-related prote... 29 8.5
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments:

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 emb|AW736637|AW736637 EST333129 KV3 Medicago truncatula cDNA clo... 142 6e-48
 emb|AI166286|AI166286 xylem.est.133 Poplar xylem Lambda ZAPII li... 151 6e-40
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 emb|AV423168|AV423168 AV423168 Lotus japonicus young plants (two... 63 2e-20
 emb|AW928704|AW928704 EST337492 tomato flower buds 8 mm to pre-a... 67 8e-20
 emb|AW731304|AW731304 GA_Ea0030M17 Gossypium arboreum 7-10 dpa ... 66 1e-19
 emb|AW219354|AW219354 EST301836 tomato root during/after fruit s... 64 1e-19
 60 emb|AW695746|AW695746 NF098B04ST1F1032 Developing stem Medicago ... 60 4e-19
 emb|AW729560|AW729560 GA_Ea0025G03 Gossypium arboreum 7-10 dpa ... 64 5e-19

- emb|AW774011|AW774011 EST332997 KV3 Medicago truncatula cDNA clo... 63 1e-18
emb|AW691624|AW691624 NF047B12ST1F1000 Developing stem Medicago ... 60 1e-18
emb|AW690628|AW690628 NF036F05ST1F1000 Developing stem Medicago ... 60 1e-18
5 gb|BE033948|BE033948 MG02E01 MG Mesembryanthemum crystallinum cD... 68 2e-18
emb|AW980831|AW980831 EST391984 GVN Medicago truncatula cDNA clo... 48 2e-17
emb|AW266728|AW266728 L48-63T3 Ice plant Lambda Uni-Zap XR expre... 89 4e-17
emb|AW728833|AW728833 GA_Ea0028L16 Gossypium arboreum 7-10 dpa ... 64 5e-17
10 emb|AI726953|AI726953 BNLGHi6948 Six-day Cotton fiber Gossypium ... 66 5e-17
emb|AW666733|AW666733 GA_Ea0005N06 Gossypium arboreum 7-10 dpa ... 64 7e-17
emb|AW693054|AW693054 NF059C10ST1F1081 Developing stem Medicago ... 63 1e-16
emb|AW692433|AW692433 NF055F02ST1F1000 Developing stem Medicago ... 60 2e-16
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15 emb|AW686542|AW686542 NF039C04NR1F1000 Nodulated root Medicago t... 60 4e-16
emb|AW726749|AW726749 GA_Ea0022J22 Gossypium arboreum 7-10 dpa ... 64 6e-16
emb|AW689509|AW689509 NF021E09ST1F1000 Developing stem Medicago ... 63 6e-16
emb|AV411180|AV411180 AV411180 Lotus japonicus young plants (two... 75 9e-16
emb|AW697936|AW697936 NXNV_072_C04_F Nsf Xylem Normal wood Verti... 42 1e-15
20 emb|AW692507|AW692507 NF052C09ST1F1000 Developing stem Medicago ... 60 2e-15
emb|AW685394|AW685394 NF028G11NR1F1000 Nodulated root Medicago t... 60 2e-15
emb|AI725103|AI725103 1002 PtFG2 Pinus taeda cDNA clone 8942r, ... 54 3e-15
emb|AW133056|AW133056 se13g09.yl Gm-c1013 Glycine max cDNA clone... 69 4e-15
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25 emb|AW693273|AW693273 NF064A06ST1F1000 Developing stem Medicago ... 60 7e-15
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emb|AW254916|AW254916 ML134 peppermint glandular trichome Mentha... 67 3e-14
emb|AI166906|AI166906 xylem.est.692 Poplar xylem Lambda ZAPII li... 59 5e-14
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30 emb|AW691201|AW691201 NF038H04ST1F1000 Developing stem Medicago ... 45 2e-13
emb|AW691254|AW691254 NF042G01ST1F1000 Developing stem Medicago ... 71 6e-13
emb|AI771903|AI771903 EST253003 tomato ovary, TAMU Lycopersicon ... 58 2e-12
emb|AW755537|AW755537 sl05b09.yl Gm-c1036 Glycine max cDNA clone... 43 2e-12
emb|AW690391|AW690391 NF030B07ST1F1000 Developing stem Medicago ... 49 3e-12
35 gb|BE125956|BE125956 DG1_60_B12.b1_A002 Dark Grown 1 (DG1) Sorgh... 56 2e-11
emb|AW933549|AW933549 EST359308 tomato fruit mature green, TAMU ... 46 3e-11
emb|AW573921|AW573921 EST316512 GVN Medicago truncatula cDNA clo... 59 6e-11
emb|AV425214|AV425214 AV425214 Lotus japonicus young plants (two... 54 6e-11
emb|AW621185|AW621185 EST311983 tomato root during/after fruit s... 62 1e-10
40 emb|AW720132|AW720132 LjNEST14h12r Lotus japonicus nodule librar... 57 1e-10
emb|AW697024|AW697024 NF111E05ST1F1038 Developing stem Medicago ... 43 1e-10
emb|AI727398|AI727398 BNLGHi7916 Six-day Cotton fiber Gossypium ... 66 2e-10
emb|AW317889|AW317889 sg58e01.yl Gm-c1007 Glycine max cDNA clone... 64 2e-10
emb|AI773497|AI773497 EST254597 tomato resistant, Cornell Lycope... 66 6e-10
emb|AI779047|AI779047 EST259926 tomato susceptible, Cornell Lyco... 66 6e-10
45 emb|AW160290|AW160290 EST290148 L. pennellii trichome, Cornell U... 66 6e-10
emb|AW690159|AW690159 NF028E04ST1F1000 Developing stem Medicago ... 40 9e-10
emb|AW697130|AW697130 NF112E12ST1F1098 Developing stem Medicago ... 40 9e-10
emb|AA739537|AA739537 302 PtFG2 Pinus taeda cDNA clone 8497M 3'... 57 9e-10
50 emb|AW934683|AW934683 EST353575 tomato flower buds 0-3 mm, Corne... 44 1e-09
emb|AW217676|AW217676 EST296390 tomato flower buds 8 mm to pre-a... 44 1e-09
gb|L47871|L47871 BNAF1521 Mustard flower buds Brassica rapa cDNA... 47 1e-09
emb|AI163871|AI163871 A050p31u Hybrid aspen plasmid library Popu... 59 1e-09
emb|AW728602|AW728602 GA_Ea0017E06 Gossypium arboreum 7-10 dpa ... 64 1e-09
emb|AW617945|AW617945 EST314019 L. pennellii trichome, Cornell U... 46 2e-09
55 emb|AW647996|AW647996 EST326450 tomato germinating seedlings, TA... 64 2e-09
emb|AW218271|AW218271 EST303452 tomato radicle, 5 d post-imbibit... 64 2e-09
emb|AI776062|AI776062 EST257162 tomato resistant, Cornell Lycope... 64 2e-09
emb|AW036254|AW036254 EST278333 tomato seed, TAMU Lycopersicon e... 64 2e-09
emb|AW650814|AW650814 EST329268 tomato germinating seedlings, TA... 64 2e-09
60 emb|AI443133|AI443133 sa84g05.yl Gm-c1004 Glycine max cDNA clone... 63 3e-09
emb|AW906997|AW906997 EST343224 potato stolon, Cornell Universit... 63 3e-09

emb|AI495275|AI495275 sb02h04.y1 Gm-c1004 Glycine max cDNA clone... 50 3e-09
 gb|BE053949|BE053949 GA_Ea0031D21f Gossypium arboreum 7-10 dpa ... 48 4e-09
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

20 emb|AV427887|AV427887 AV427887 Lotus japonicus young plants (two... 61 6e-17
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 emb|AI967590|AI967590 Ljirmp06-480-c9 Ljirmp Lambda HybriZap ... 68 2e-14
 emb|AW684644|AW684644 NF019C10NR1F1000 Nodulated root Medicago t... 62 9e-12
 gb|BE036389|BE036389 MO24B03 MO Mesembryanthemum crystallinum cD... 44 2e-06
 25 gb|BE034652|BE034652 ML01E04 ML Mesembryanthemum crystallinum cD... 35 0.57
 emb|AC005308|AC005308 Plasmodium falciparum chromosome 12 clone ... 35 0.57
 gb|N60116|N60116 TgESTzy01b10.r1 TgRH Tachyzoite cDNA Toxoplasma... 34 0.78
 emb|AF161334|AF161334 Raphanus raphanistrum subsp. raphanistrum ... 33 1.5
 gb|L37356|PUMPAL3A Petroselinum crispum phenylalanine ammonia-ly... 33 2.0
 30 emb|AI974840|AI974840 T113322e KV2 Medicago truncatula cDNA clon... 32 2.8
 gb|U36470|NCU36470 Neurospora crassa vacuolar ATPase 41 kDa subu... 32 2.8
 emb|AI938788|AI938788 sc60a05.y1 Gm-c1016 Glycine max cDNA clone... 32 2.8
 emb|AF114794|AF114794 Porphyra purpurea mitochondrion, complete ... 32 3.8
 emb|AI374339|AI374339 T6652 MVAT4 bloodstream form of serodeme W... 32 3.8
 35 emb|AI374387|AI374387 T6725 MVAT4 bloodstream form of serodeme W... 32 3.8
 emb|AI374381|AI374381 T6716 MVAT4 bloodstream form of serodeme W... 32 3.8
 emb|AI894927|AI894927 EST264370 tomato callus, TAMU Lycopersicon... 31 5.2
 emb|AA550548|AA550548 1711m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 31 5.2
 emb|AJ223459|ANAJ3459 Aspergillus nidulans prnA gene. 31 5.2
 40 emb|AJ390536|CAL390536 Candida albicans DNA, clone 222g9. 31 5.2
 emb|AW119888|AW119888 sd54b09.y1 Gm-c1016 Glycine max cDNA clone... 31 5.2
 emb|AI431203|AI431203 sa22f12.y2 Gm-c1006 Glycine max cDNA clone... 31 5.2
 emb|AF161331|AF161331 Sinapis arvensis S-locus related 1 (SLR1) ... 31 7.2
 emb|AF137311|AF137311 Miscanthus sinensis phytochrome B (PHYB) g... 31 7.2
 45 gb|T36711|T36711 EST101701 S. cerevisiae strain X2180-1A Sacchar... 31 7.2
 emb|AW781868|AW781868 sl97g02.y1 Gm-c1027 Glycine max cDNA clone... 31 7.2
 emb|AW755482|AW755482 sl04e07.y1 Gm-c1036 Glycine max cDNA clone... 30 9.9
 emb|AW694935|AW694935 NF081F05ST1F1046 Developing stem Medicago ... 30 9.9
 emb|AZ215370|AZ215370 Sheared DNA-56C1.TF Sheared DNA Trypanosom... 30 9.9
 50 emb|AQ945786|AQ945786 Sheared DNA-30C5.TR Sheared DNA Trypanosom... 30 9.9
 emb|AA739646|AA739646 411 PdFG2 Pinus taeda cDNA clone 8694M 3'... 30 9.9
 emb|AL034353|SPBC1271 S.pombe chromosome II cosmid c1271. 30 9.9
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments: (bits) Value

emb|AW266797|AW266797 L48-136T3 Ice plant Lambda Uni-Zap XR expr... 59 5e-08
 10 emb|AI776331|AI776331 EST257431 tomato resistant, Cornell Lycopersicon... 51 8e-06
 emb|AI938454|AI938454 sc45e10.y1 Gm-c1015 Glycine max cDNA clone... 44 0.001
 emb|AF086822|AF086822 Candida boidinii dihydroxyacetone synthase... 36 0.38
 emb|AV406828|AV406828 AV406828 Lotus japonicus young plants (two... 31 0.49
 emb|AI731942|AI731942 BNLGH11450 Six-day Cotton fiber Gossypium... 35 0.71
 15 emb|AQ255443|AQ255443 mgxb0014I21r CUGI Rice Blast BAC Library P... 35 0.71
 emb|AQ940346|AQ940346 Sheared DNA-33M2.TF Sheared DNA Trypanosom... 34 1.3
 emb|AI210373|AI210373 i0e05a1.r1 Aspergillus nidulans 24hr asexu... 34 1.8
 emb|AQ935542|AQ935542 CpG2525A CplOWAgDNA1 Cryptosporidium parvu... 33 2.5
 gb|T18147|T18147 0722c3 czapPFDd2.1, Debopam Chakrabarti Plasmod... 33 2.5
 20 emb|AW651276|AW651276 EST329730 tomato germinating seedlings, TA... 33 3.5
 emb|AI392128|AI392128 NCSM1B1T7 Subtracted Mycelial Neurospora c... 32 4.8
 emb|AW330094|AW330094 TENU4840 T.cruzi epimastigote normalized c... 32 4.8
 emb|AF055296|AF055296 Zantedeschia aethiopica geranylgeranyl red... 32 4.8
 emb|AI725804|AI725804 BNLGH113200 Six-day Cotton fiber Gossypium... 32 4.8
 25 emb|AW686984|AW686984 NF004F11RT1F1094 Developing root Medicago ... 32 6.6
 emb|AJ273808|AJ273808 AJ273808 Metarhizium anisopliae ARSEF 2575... 32 6.6
 emb|AQ943530|AQ943530 Sheared DNA-42D24.TR Sheared DNA Trypanoso... 31 9.0
 emb|AQ941987|AQ941987 Sheared DNA-42F7.TR Sheared DNA Trypanoso... 31 9.0
 emb|AW620371|AW620371 sj04d01.y1 Gm-c1032 Glycine max cDNA clone... 31 9.0
 30 emb|AI973930|AI973930 sd13g08.y1 Gm-c1020 Glycine max cDNA clone... 31 9.0
 emb|AF069470|AF069470 Phleum pratense group V allergen Phl p 5.0... 31 9.0
 emb|AL160716|P406R Leishmania major Friedlin PAC P406 right end... 31 9.0
 emb|AQ851400|AQ851400 LMAJFV1_lm40b04.y1 Leishmania major FV1 ra... 31 9.0
 emb|AF061068|AF061068 Phleum pratense clone 10029 major allergen... 31 9.0
 35 emb|AQ953188|AQ953188 Sheared DNA-50B12.TF Sheared DNA Trypanoso... 31 9.0
 emb|AW719942|AW719942 LjNEST12c6r Lotus japonicus nodule library... 31 9.0
 emb|X74735|PPLP5 P. pratense mRNA for PhlpV. 31 9.0
 emb|AW396374|AW396374 sh27d05.y1 Gm-c1016 Glycine max cDNA clone... 31 9.0
 gb|N60997|N60997 TgESTzy23f10.r1 TgRH Tachyzoite cDNA Toxoplasma... 31 9.0
 40 emb|AI164737|AI164737 A068P10U Hybrid aspen plasmid library Popu... 31 9.0
 emb|AW348348|AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3... 26 9.5
 emb|AW309665|AW309665 sf22g06.x1 Gm-c1028 Glycine max cDNA clone... 26 9.5
 emb|AW310247|AW310247 sf33d01.x1 Gm-c1028 Glycine max cDNA clone... 26 9.5
 emb|AW508196|AW508196 si50d10.y1 Gm-r1030 Glycine max cDNA clone... 27 9.6
 45 emb|AW102012|AW102012 sd81h10.y1 Gm-c1009 Glycine max cDNA clone... 26 9.8
 emb|AW309166|AW309166 sg05b01.y1 Gm-c1019 Glycine max cDNA clone... 26 9.8
 emb|AW598779|AW598779 sj46h06.y1 Gm-c1033 Glycine max cDNA clone... 26 9.8
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments: (bits) Value

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 emb|AW698685|AW698685 R125 non-glandular-haired subtracted cDNA ... 32 1.4
 5 emb|AF061282|AF061282 Sorghum bicolor 22 kDa kafirin cluster. 31 5.6
 emb|AL031854|SPBC337 S.pombe chromosome II cosmid c337. 31 5.6
 emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 31 5.6
 emb|AC006280|AC006280 Plasmodium falciparum chromosome 12 clone ... 31 5.6
 gb|M74062|YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl... 31 5.6
 10 emb|AQ947500|AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso... 31 5.6
 gb|M83307|YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl... 31 5.6
 emb|AL031856|SPBC1734 S.pombe chromosome II cosmid c1734. 31 5.6
 emb|AC073246|AC073246 Trypanosoma brucei chromosome II clone RPC... 30 7.7
 emb|AL031535|SPCC16C4 S.pombe chromosome III cosmid c16C4. 30 7.7
 15 emb|AC012647|AC012647 Trypanosoma brucei chromosome II clone RPC... 30 7.7
 gb|L28038|TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc... 30 7.7
 emb|AB004322|AB004322 Nicotiana sylvestris NsPMT1 gene for putre... 30 7.7
 emb|AQ941496|AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso... 30 7.7
 emb|AQ946940|AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom... 30 7.7
 20 emb|AQ942433|AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom... 30 7.7
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Database: plantfungal
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Searching.....done

Score E
 35 Sequences producing significant alignments: (bits) Value

emb|AQ952678|AQ952678 Sheared DNA-48H20.TF Sheared DNA Trypanoso... 35 0.32
 emb|AW698685|AW698685 R125 non-glandular-haired subtracted cDNA ... 32 1.4
 emb|AF061282|AF061282 Sorghum bicolor 22 kDa kafirin cluster. 31 5.6
 40 emb|AL031854|SPBC337 S.pombe chromosome II cosmid c337. 31 5.6
 emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 31 5.6
 emb|AC006280|AC006280 Plasmodium falciparum chromosome 12 clone ... 31 5.6
 gb|M74062|YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl... 31 5.6
 emb|AQ947500|AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso... 31 5.6
 45 gb|M83307|YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl... 31 5.6
 emb|AL031856|SPBC1734 S.pombe chromosome II cosmid c1734. 31 5.6
 emb|AC073246|AC073246 Trypanosoma brucei chromosome II clone RPC... 30 7.7
 emb|AL031535|SPCC16C4 S.pombe chromosome III cosmid c16C4. 30 7.7
 emb|AC012647|AC012647 Trypanosoma brucei chromosome II clone RPC... 30 7.7
 50 gb|L28038|TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc... 30 7.7
 emb|AB004322|AB004322 Nicotiana sylvestris NsPMT1 gene for putre... 30 7.7
 emb|AQ941496|AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso... 30 7.7
 emb|AQ946940|AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom... 30 7.7
 emb|AQ942433|AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom... 30 7.7
 55 emb|AF133529|AF133529 Candida albicans mRNA cap methyltransferas... 30 7.7

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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	emb AW399343 AW399343 EST309843 L. pennellii trichome, Cornell U...	234	2e-60
	emb AW618318 AW618318 EST320304 L. pennellii trichome, Cornell U...	177	1e-53
	emb AW310982 AW310982 sg31b02.x1 Gm-cl024 Glycine max cDNA clone...	97	1e-51
15	emb AI442277 AI442277 sa66a04.y1 Gm-cl004 Glycine max cDNA clone...	200	2e-50
	emb AW687759 AW687759 NF013B05RT1F1044 Developing root Medicago ...	160	1e-46
	emb AW684122 AW684122 NF012F06NR1F1000 Nodulated root Medicago t...	83	2e-44
	emb AW309867 AW309867 s25g10.x1 Gm-cl028 Glycine max cDNA clone...	89	5e-43
	gb BE020423 BE020423 sm40e08.y1 Gm-cl028 Glycine max cDNA clone ...	88	2e-39
20	emb AW691118 AW691118 NF041D08ST1F1000 Developing stem Medicago ...	78	2e-35
	emb AW160235 AW160235 EST290093 L. pennellii trichome, Cornell U...	120	6e-32
	emb AI960862 AI960862 sc91f07.y1 Gm-cl019 Glycine max cDNA clone...	74	5e-30
	emb AW349633 AW349633 GM210006A11B3R Gm-r1021 Glycine max cDNA 3...	89	8e-29
	emb AW775076 AW775076 EST334227 KV3 Medicago truncatula cDNA clo...	81	6e-26
25	gb BE020331 BE020331 sm40d08.y1 Gm-cl028 Glycine max cDNA clone ...	69	4e-23
	emb AW746031 AW746031 WS1_39_A03.b1_A002 Water-stressed I (WS1) ...	74	8e-23
	emb AW621546 AW621546 EST312344 tomato root during/after fruit s...	64	1e-13
	emb AW622846 AW622846 EST306916 tomato flower buds 3-8 mm, Come...	54	2e-12
	gb L43984 BLYBD Hordeum vulgare (clone ABG377) chromosome 3H STS...	69	8e-11
30	emb AW774216 AW774216 EST333367 KV3 Medicago truncatula cDNA clo...	69	1e-10
	emb AW774324 AW774324 EST333475 KV3 Medicago truncatula cDNA clo...	69	1e-10
	emb AW686169 AW686169 NF038H07NR1F1000 Nodulated root Medicago t...	68	2e-10
	emb AW160234 AW160234 EST290092 L. pennellii trichome, Cornell U...	46	2e-08
	emb AW685496 AW685496 NF030G02NR1F1000 Nodulated root Medicago t...	45	2e-07
35	emb AW684082 AW684082 NF011H08NR1F1000 Nodulated root Medicago t...	55	2e-06
	emb AW693839 AW693839 NF069F08ST1F1074 Developing stem Medicago ...	53	6e-06
	emb AI163659 AI163659 A046p04u Hybrid aspen plasmid library Popu...	53	6e-06
	emb AW033404 AW033404 EST276975 tomato callus, TAMU Lycopersicon...	49	1e-04
	emb AI054662 AI054662 coau0001K11 Cotton Boll Abscission Zone cD...	37	2e-04
40	emb AW758414 AW758414 874008A01.y1 C. reinhardtii CC-1690, Lambd...	41	0.022
	emb AW746188 AW746188 WS1_39_A03.g1_A002 Water-stressed I (WS1) ...	41	0.022
	emb Z99126 SPAC26H5 S.pombe chromosome I cosmid c26H5.	41	0.022
	emb AJ225805 EDKCHALPH Egeria densa mRNA for inward potassium ch...	39	0.14
	emb AI488725 AI488725 EST247064 tomato ovary, TAMU Lycopersicon ...	38	0.20
45	emb Z69731 SPAC6C3 S.pombe chromosome I cosmid c6C3.	36	0.71
	emb Z38061 SC9168 S.cerevisiae chromosome IX cosmid 9168.	36	0.71
	emb AW925349 AW925349 HVSMEg0001B12 Hordeum vulgare pre-anthesis...	36	0.71
	emb AW671585 AW671585 LG1_348_H11.b1_A002 Light Grown I (LG1) So...	36	0.97
	gb BE024935 BE024935 894007A03.x1 C. reinhardtii CC-1690, normal...	36	0.97
50	emb AW216501 AW216501 EST295215 tomato callus, TAMU Lycopersicon...	36	0.97
	emb AW680841 AW680841 WS1_7_E11.g1_A002 Water-stressed I (WS1) S...	35	1.3
	emb AQ911629 AQ911629 LMAJFV1_lm96c04.y1 Leishmania major FV1 ra...	35	1.3
	emb AW100578 AW100578 sd57b08.y1 Gm-cl008 Glycine max cDNA clone...	35	1.3
	emb AW010724 AW010724 ST11E02 Pine TriplEx shoot tip library Pin...	35	1.8
55	emb AL138854 SPAC23G3 S.pombe chromosome I cosmid c23G3.	35	2.5
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	emb AZ215288 AZ215288 Sheared DNA-83F7.TR Sheared DNA Trypanosom...	33 9.0
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Database: plantfungal

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50	emb AV422547 AV422547 AV422547 Lotus japonicus young plants (two...	28 0.006	
	emb AW706554 AW706554 sj58h12.y1 Gm-cl033 Glycine max cDNA clone...	28 0.010	
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55	emb AI930916 AI930916 sb44d12.y1 Gm-cl015 Glycine max cDNA clone...	28 0.031	
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	emb AW153030 AW153030 se34a10.y1 Gm-cl015 Glycine max cDNA clone...	30 0.13	
	gb BE055645 BE055645 GA_Ea0021E15f Gossypium arboreum 7-10 dpa ...	33 0.19	
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60	emb AW329270 AW329270 N200490e rootphos(-) Medicago truncatula c...	29 0.33	
	emb X02873 DCEXTG Carrot gene for extensin.	35 0.34	

	gb M11221 DAREXTA Carrot (<i>D.carota</i>) extensin mRNA, partial cds.	35	0.47
	emb AW306694 AW306694 sf47b08.y1 Gm-c1009 Glycine max cDNA clone...	27	0.54
	emb AW035648 AW035648 EST281480 tomato callus, TAMU Lycopersicon...	28	0.57
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25	gb C95684 C95684 <i>C95684</i> Marchantia polymorpha immature sex organ...	32	2.3
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	emb AW720424 AW720424 LjNEST22g2r Lotus japonicus nodule library...	32	3.2
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	gb U91982 SHU91982 <i>Stylosanthes hamata</i> EREBP-3 homolog mRNA, com...	28	3.5
	emb AV413265 AV413265 AV413265 Lotus japonicus young plants (two...	26	3.6
	gb U10398 YSCH9315 <i>Saccharomyces cerevisiae</i> chromosome VIII cosm...	27	3.6
35	emb AV412856 AV412856 AV412856 Lotus japonicus young plants (two...	26	3.7
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	emb AI495395 AI495395 sa97d11.y1 Gm-c1004 Glycine max cDNA clone...	25	4.9
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	emb AV395215 AV395215 AV395215 <i>Chlamydomonas reinhardtii</i> C9 Chla...	31	6.0
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55	emb AW717057 AW717057 h6e06nm.r1 <i>Neurospora crassa</i> morning cDNA ...	31	6.0
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5 emb|AW707173|AW707173 sk10f12.y1 Gm-c1023 Glycine max cDNA clone... 30 8.2
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10 emb|AW032140|AW032140 EST275594 tomato callus, TAMU *Lycopersicon*... 26 8.7
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Database: plantfungal
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Sequences producing significant alignments: (bits) Value

35 emb|AF029858|AF029858 *Sorghum bicolor* cytochrome P450 CYP71E1 (C... 220 e-104
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gb|BE054146|BE054146 GA_Ea0034H12f *Gossypium arboreum* 7-10 dpa ... 167 7e-50
gb|L24438|THLCYP450A *Thlaspi arvense* germline cytochrome P450 mR... 144 2e-48
40 emb|Z22545|PHFLAHYDB *P. hybrida* flavonoid 3',5'-hydroxylase mRNA. 77 9e-47
dbj|D14588|PETHF1 *Petunia hybrida* Hfl mRNA for flavonoid-3',5'-h... 77 9e-47
emb|Z22544|PHFLAHYDA *P. hybrida* flavonoid 3',5'-hydroxylase mRNA. 71 2e-44
dbj|D85184|D85184 *Gentiana triflora* mRNA for flavonoid 3',5'-hyd... 85 8e-44
emb|AW234222|AW234222 sf22f08.y1 Gm-c1028 Glycine max cDNA clone... 147 5e-43
emb|Y09423|NRCYP71A5 *Nepeta racemosa* mRNA for cytochrome P450, C... 126 8e-40
45 emb|AF122821|AF122821 *Capsicum annuum* cytochrome P450 (PepCYP) m... 127 2e-39
gb|U48435|SCU48435 *Solanum chacoense* putative cytochrome P450 ge... 136 3e-39
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emb|AF124815|AF124815 *Mentha spicata* cytochrome p450 mRNA, compl... 134 4e-39
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50 gb|U48434|SCU48434 *Solanum chacoense* cytochrome P450 mRNA, compl... 124 2e-38
emb|AW255799|AW255799 ML868 peppermint glandular trichome *Mentha*... 116 2e-38
emb|AF124816|AF124816 *Mentha x piperita* cytochrome p450 isoform ... 123 1e-37
emb|AF022460|AF022460 Glycine max cytochrome P450 monooxygenase ... 116 3e-37
emb|AW349428|AW349428 GM210007A20E11R Gm-r1021 Glycine max cDNA ... 69 8e-37
55 emb|X71658|SMCYPEG8 *S. melongena* CYP76A1 mRNA. 130 2e-36
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60 emb|AF134590|AF134590 *Papaver somniferum* (S)-N-methylcoclaurine ... 140 2e-35
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- 5 emb|X70981|SMCYPEG2 *S.melongena* CYP71A1 mRNA for P450 hydroxylase. 119 7e-34
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- emb|X71130|PHPET1 *P.hybrida* mRNA for P450 hydroxylase. 77 2e-33
- emb|AF166332|AF166332 *Nicotiana tabacum* cytochrome P450 gene, co... 127 2e-33
- emb|Y09424|NRCYP71A6 *N.racemosa* mRNA for cytochrome P450, CYP71A... 117 2e-33
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- 15 emb|AQ917284|AQ917284 T233265b *Medicago truncatula* BAC library M... 142 9e-33
- emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 115 2e-32
- emb|AF029857|AF029857 *Sorghum bicolor* cytochrome P450 CYP99A1 (C... 78 2e-32
- emb|X71654|SMCYP71B3 *S.melongena* CYP71A2 mRNA for hydroxylase. 115 3e-32
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- 20 emb|AW310655|AW310655 sg22h01.x1 *Gm-c1024* Glycine max cDNA clone... 140 3e-32
- emb|AF022459|AF022459 Glycine max cytochrome P450 monooxygenase ... 139 4e-32
- emb|AB028151|AB028151 *Antirrhinum majus* AFNS2 mRNA for cytochrom... 66 7e-32
- emb|AF150881|AF150881 *Lycopersicon esculentum* x *Lycopersicon per...* 78 3e-31
- emb|Y10493|GMC450CP7 *G.max* mRNA for putative cytochrome P450, cl... 137 3e-31
- 25 emb|AW569661|AW569661 si89h01.y1 *Gm-c1031* Glycine max cDNA clone... 137 3e-31
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- emb|AW676782|AW676782 DG1_14_D06.g1_A002 Dark Grown 1 (DG1) Sorg... 135 4e-31
- emb|AW677294|AW677294 DG1_5_H08.g1_A002 Dark Grown 1 (DG1) Sorg... 136 4e-31
- emb|AW623139|AW623139 EST321084 tomato flower buds 3-8 mm, Corne... 117 5e-31
- 30 emb|AW256491|AW256491 EST304628 KV2 *Medicago truncatula* cDNA clo... 136 6e-31
- dbj|D86351|D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,... 66 6e-31
- emb|AW922446|AW922446 DG1_19_F10.g1_A002 Dark Grown 1 (DG1) Sorg... 135 1e-30
- gb|U09610|U09610 *Berberis stolonifera* cytochrome P-450 CYP80 mRN... 125 2e-30
- emb|AW031613|AW031613 EST275067 tomato callus, TAMU Lycopersicon... 73 2e-30
- 35 emb|Y10490|GMC450CP3 *G.max* mRNA for putative cytochrome P450, cl... 133 3e-30
- emb|AF156976|AF156976 *Gerbera hybrida* flavone synthase II (CYP93... 63 3e-30
- emb|AW218579|AW218579 EST303762 tomato radicle, 5 d post-imbibit... 133 4e-30
- emb|AB028152|AB028152 *Torenia hybrida* TFNS5 mRNA for cytochrome ... 64 4e-30
- emb|A1489371|A1489371 EST247722 tomato ovary, TAMU Lycopersicon ... 111 6e-30
- 40 emb|AF000403|AF000403 *Lotus japonicus* putative cytochorome P450 ... 131 2e-29
- emb|AW394303|AW394303 sh31c01.y1 *Gm-c1017* Glycine max cDNA clone... 130 3e-29
- emb|AW560246|AW560246 EST315294 DSIR *Medicago truncatula* cDNA cl... 130 3e-29
- emb|AW458764|AW458764 sh82d02.y1 *Gm-c1016* Glycine max cDNA clone... 130 3e-29
- emb|AF135485|AF135485 Glycine max cytochrome P450 monooxygenaseC... 73 4e-29
- 45 emb|AF014800|AF014800 *Eschscholzia californica* (S)-N-methylcocla... 105 5e-29
- emb|AW923050|AW923050 DG1_48_G09.g1_A002 Dark Grown 1 (DG1) Sorg... 129 7e-29
- emb|AJ249799|CAR249799 *Cicer arietinum* partial mRNA for cytochro... 115 8e-29
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- emb|AW728587|AW728587 GA_Ea0017C12 *Gossypium arboreum* 7-10 dpa ... 101 1e-28
- 50 emb|AW922486|AW922486 DG1_19_B12.g1_A002 Dark Grown 1 (DG1) Sorg... 128 1e-28
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- emb|AW255421|AW255421 ML442 peppermint glandular trichome *Mentha*... 125 8e-28
- emb|AW256010|AW256010 MW364 peppermint glandular trichome *Mentha*... 125 8e-28
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- emb|AB006790|AB006790 *Petunia x hybrida* IMT-2 mRNA for cytochrom... 75 1e-27

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20 http://www.ncgr.org/cgi-bin/ff?pad4
(1732 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

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35 emb|AW011208|AW011208 ST18A05 Pine TriplEx shoot tip library Pin... 107 2e-23
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emb|AV423915|AV423915 AV423915 Lotus japonicus young plants (two... 98 6e-20
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 (1732 letters)

20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 25 Sequences producing significant alignments: (bits) Value

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 (848 letters)

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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35 emb|AB008200|AB008200 *Nicotiana tabacum* palB gene for phenylalan... 204 2e-51
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dbj|D43803|POPPALG4B *Populus kitakamiensis* gene for phenylalanin... 201 2e-50
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emb|X15473|PCPAL1GN P.crispum PAL-1 gene for phenylalanine ammon... 120 6e-49
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AF237955 AF237955 Rubus idaeus phenylalanine ammonia-lyase 2...	220	6e-56
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(1602 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments:

(bits) Value

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	emb AW220409 AW220409 EST302892 tomato root during/after fruit s...	53	5e-06
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 emb|AI960269|AI960269 sc81b07.y1 Gm-cl018 Glycine max cDNA clone... 27 9.1

- Query= PDF1.2_at 14621_at /id_source genbank /description
 25 gb|aac31244.1| (ac004747) putative antifungal protein [arabidopsis
 thaliana] /blast_score 1.00e-31 /ec_number /family /chip nova
 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
 post/entrez/query?db=n&form=6&dopt=g&uid=gb|pdf1| /ncgi
 http://www.ncgr.org/cgi-bin/ff?pdf1
 30 (400 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

- 35 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

- 40 emb|A26875|A26875 R.sativus AFP1 gene. 160 5e-39
 gb|U18557|RSU18557 Raphanus sativus antifungal protein 1 preprot... 159 1e-38
 gb|U59459|BNU59459 Brassica napus antifungal protein mRNA, compl... 127 6e-37
 gb|U18556|RSU18556 Raphanus sativus antifungal protein 2 preprot... 138 1e-35
 emb|X97318|RSAFP4 R.sativus mRNA for antifungal protein 4. 145 3e-34
 45 emb|X97319|RSEFP3 R.sativus mRNA for antifungal protein 3. 127 2e-31
 emb|A26963|A26963 D.merkii AMP1 sequence. 76 2e-13
 emb|X53375|HASF18 Sunflower anther-specific mRNA SF18. 75 3e-13
 emb|A27062|A27062 C.benedictus AMP2 sequence. 74 4e-13
 emb|A26906|A26906 C.benedictus AMP1 sequence. 73 7e-13
 50 gb|L47901|L47901 BNAF1712 Mustard flower buds Brassica rapa cDNA... 65 2e-10
 emb|AT001728|AT001728 AT001728 Flower bud cDNA Brassica rapa sub... 65 3e-10
 emb|A27064|A27064 C.ternatea AMP1 sequence. 58 7e-09
 emb|AT001738|AT001738 AT001738 Flower bud cDNA Brassica rapa sub... 52 2e-06
 emb|AW870017|AW870017 NXNV_122 A10 F Nsf Xylem Normal wood Verti... 35 7e-06
 55 emb|AW064751|AW064751 ST35D04 Pine, TriplEx shoot tip library Pin... 36 7e-06
 emb|X91487|PASPI1GEN P.abies mRNA for gamma-thionin protein (put... 40 1e-05
 emb|AW621708|AW621708 EST312506 tomato root during/after fruit s... 43 9e-05
 emb|AW220215|AW220215 EST302698 tomato root during/after fruit s... 43 1e-04
 emb|AW220231|AW220231 EST302714 tomato root during/after fruit s... 43 1e-04
 60 emb|AW219164|AW219164 EST301646 tomato root during/after fruit s... 43 1e-04
 emb|AW219793|AW219793 EST302275 tomato root during/after fruit s... 43 1e-04

	emb AW621529 AW621529 EST312327 tomato root during/after fruit s...	41	3e-04
	emb AW622375 AW622375 EST313174 tomato root during/after fruit s...	41	4e-04
	emb AW622390 AW622390 EST313189 tomato root during/after fruit s...	41	4e-04
	emb AW621171 AW621171 EST311969 tomato root during/after fruit s...	40	7e-04
5	dbj D29679 TOBPIT1A Tobacco pit1 mRNA (which expression is induc...	44	7e-04
	emb AW622051 AW622051 EST312849 tomato root during/after fruit s...	40	7e-04
	emb AW622079 AW622079 EST312877 tomato root during/after fruit s...	40	9e-04
	emb AW621330 AW621330 EST312128 tomato root during/after fruit s...	40	9e-04
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	emb AW220086 AW220086 EST302569 tomato root during/after fruit s...	40	0.001
	emb AW621962 AW621962 EST312760 tomato root during/after fruit s...	40	0.001
	emb AW621634 AW621634 EST312432 tomato root during/after fruit s...	37	0.005
	emb AW623112 AW623112 EST321057 tomato flower buds 3-8 mm, Corne...	40	0.006
15	emb AW683448 AW683448 NF012D04LFIF1041 Developing leaf Medicago ...	40	0.006
	emb AI487824 AI487824 EST246146 tomato ovary, TAMU Lycopersicon ...	40	0.006
	emb AI483999 AI483999 EST249870 tomato ovary, TAMU Lycopersicon ...	40	0.007
	gb U20591 SLU20591 Solanum lycopersicum flower-specific gamma-th...	40	0.007
	emb AW622923 AW622923 EST306993 tomato flower buds 3-8 mm, Corne...	40	0.007
20	emb AW929929 AW929929 EST354199 tomato flower buds 8 mm to pre-a...	40	0.007
	emb AW929939 AW929939 EST354209 tomato flower buds 8 mm to pre-a...	40	0.007
	emb AI897392 AI897392 EST266835 tomato ovary, TAMU Lycopersicon ...	40	0.008
	emb AI490243 AI490243 EST248569 tomato ovary, TAMU Lycopersicon ...	40	0.008
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25	emb AW217552 AW217552 EST296266 tomato flower buds 3-8 mm, Corne...	40	0.009
	emb AI489818 AI489818 EST248157 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AI487398 AI487398 EST245720 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AW217379 AW217379 EST296063 tomato flower buds 0-3 mm, Corne...	40	0.010
	emb AI898009 AI898009 EST267452 tomato ovary, TAMU Lycopersicon ...	40	0.010
30	emb AI897456 AI897456 EST266899 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI483612 AI483612 EST249462 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI485550 AI485550 EST243871 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI484887 AI484887 EST243150 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI484497 AI484497 EST242507 tomato ovary, TAMU Lycopersicon ...	40	0.012
35	emb AI490062 AI490062 EST248401 tomato ovary, TAMU Lycopersicon ...	40	0.012
	emb AW775186 AW775186 EST331908 GVN Medicago truncatula cDNA clo...	39	0.016
	emb AI486656 AI486656 EST244977 tomato ovary, TAMU Lycopersicon ...	38	0.024
	emb AI485044 AI485044 EST243324 tomato ovary, TAMU Lycopersicon ...	37	0.041
	emb AW399651 AW399651 EST310151 L. pennellii trichome, Cornell U...	38	0.042
40	emb A26964 A26964 D.merkii AMP2 sequence.	37	0.080
	emb X77993 HASF18A H.annuus SF18 gene.	31	0.14
	emb A27063 A27063 L.cicera AFP sequence.	34	0.74
	emb AI757757 AI757757 EtESTea34d02.y1 Eimeria S5-2 Sporozoite st...	34	0.74
	emb AW217119 AW217119 EST295833 tomato callus, TAMU Lycopersicon...	27	0.90
45	emb X95363 CAGT C.annuum gamma thionin gene.	33	1.0
	emb X95730 CAGTHIOGN Capsicum annuum defensin gene.	33	1.0
	emb AL035477 PFMAL4P4 Plasmodium falciparum chromosome 4 strain ...	33	1.0
	emb AL117384 LMFL5883 Leishmania major Friedlin chromosome 23 co...	29	1.3
	emb Z74387 SCYDR262W S.cerevisiae chromosome IV reading frame OR...	33	1.4
50	emb Z68329 SC9320A S.cerevisiae chromosome IV cosmid 9320A.	33	1.4
	emb Z70202 SC9320X S.cerevisiae chromosome IV cosmid 9320X.	33	1.4
	emb AQ846121 AQ846121 LMAJFV1_lml4f01.y1 Leishmania major FV1 ra...	29	1.7
	emb AW725876 AW725876 GA_Ea0020A08 Gossypium arboreum 7-10 dpa ...	32	1.9
	emb AV387503 AV387503 AV387503 Chlamydomonas reinhardtii C9 Chla...	32	2.6
	emb AQ947439 AQ947439 Sheared DNA-50L12.TF Sheared DNA Trypanoso...	31	3.6
55	emb AA836739 AA836739 L30-187T3 Ice plant Lambda Uni-Zap XR expr...	31	3.6
	gb M65164 PAR51C P.tetraulera 51C surface protein gene, complet...	31	3.6
	emb X16877 VUSTORED Vigna unguiculata cDNA for stored cotyledon ...	31	3.6
	emb AW736134 AW736134 EST332130 KV3 Medicago truncatula cDNA clo...	25	4.8
	emb AL034381 SPCC61 S.pombe chromosome III cosmid c61.	31	5.0
60	emb AQ642382 AQ642382 RPCI93-DpnII-29C10.TV RPCI93-DpnII Trypano...	31	5.0
	gb L01579 PEADRR230B Pea (pi39) disease resistance response prot...	31	5.0

	emb AW186932 AW186932 BNLGHi7476 Six-day Cotton fiber Gossypium ...	31	5.0
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5	gb B07260 B07260 G236T7 MVAT4 sheared genomic library Trypanosom...	31	5.0
	emb AI728815 AI728815 BNLGHi11757 Six-day Cotton fiber Gossypium...	31	5.0
	emb AI726605 AI726605 BNLGHi6250 Six-day Cotton fiber Gossypium ...	31	5.0
	gb BE033595 BE033595 MF04D10 MF Mesembryanthemum crystallinum cD...	30	6.8
	emb AW508408 AW508408 si40e08.y1 Gm-r1030 Glycine max cDNA clone...	30	6.8
	emb AW830659 AW830659 sm05b06.y1 Gm-c1027 Glycine max cDNA clone...	30	6.8
10	emb AW266371 AW266371 L30-3125T3 Ice plant Lambda Uni-Zap XR exp...	30	6.8
	emb AW266222 AW266222 L30-2930T3 Ice plant Lambda Uni-Zap XR exp...	30	6.8
	emb AW093819 AW093819 EST286999 tomato mixed elicitor, BTI Lycop...	30	6.8
	emb AI774224 AI774224 EST255419 tomato resistant, Cornell Lycopen...	30	6.8
	emb AA962873 AA962873 L30-403T3 Ice plant Lambda Uni-Zap XR expr...	30	6.8
15	emb AL034557 PFMAL4P1 Plasmodium falciparum chromosome 4 strain ...	30	6.8
	emb AQ905826 AQ905826 GSSTc010408 Trypanosome cruzi random genom...	30	6.8
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25	Database: plantfungal 661,018 sequences; 426,114,510 total letters		
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	Sequences producing significant alignments:	(bits)	Value
	gb U70666 BNU70666 Brassica napus pathogenesis-related protein P...	323	3e-88
35	gb U21849 BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds.	323	3e-88
	gb U64806 BNU64806 Brassica napus pathogenesis-related protein P...	209	4e-85
	emb AI352851 AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl...	311	4e-84
	emb AI352893 AI352893 MB72-6D PZ204.BNlib Brassica napus cDNA cl...	165	3e-62
40	emb AW217013 AW217013 EST295727 tomato callus, TAMU Lycopersicon...	152	4e-60
	emb AW219671 AW219671 EST302153 tomato root during/after fruit s...	151	1e-59
	emb AW092403 AW092403 EST285583 tomato mixed elicitor, BTI Lycop...	151	1e-59
	emb AI895090 AI895090 EST264533 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW625930 AW625930 EST319825 tomato radicle, 5 d post-imbibit...	151	1e-59
	emb AW032514 AW032514 EST276073 tomato callus, TAMU Lycopersicon...	151	1e-59
45	emb AW034260 AW034260 EST277831 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW040983 AW040983 EST283847 tomato mixed elicitor, BTI Lycop...	151	1e-59
	emb AW034206 AW034206 EST277777 tomato callus, TAMU Lycopersicon...	151	1e-59
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	emb AW092623 AW092623 EST285803 tomato mixed elicitor, BTI Lycop...	151	1e-59
50	emb AW040954 AW040954 EST283818 tomato mixed elicitor, BTI Lycop...	151	1e-59
	emb AW034454 AW034454 EST278025 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW032723 AW032723 EST276282 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW033873 AW033873 EST277444 tomato callus, TAMU Lycopersicon...	151	1e-59
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55	emb AW033593 AW033593 EST277164 tomato callus, TAMU Lycopersicon...	151	3e-59
	emb AW034724 AW034724 EST278526 tomato callus, TAMU Lycopersicon...	148	7e-59
	emb AW041033 AW041033 EST283897 tomato mixed elicitor, BTI Lycop...	148	7e-59
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	emb AW559895 AW559895 EST314943 DSIR Medicago truncatula cDNA cl...	160	1e-58
60	emb AW329241 AW329241 N200453e rootphos(-) Medicago truncatula c...	160	1e-58
	emb AW559894 AW559894 EST314942 DSIR Medicago truncatula cDNA cl...	159	5e-58

- emb|AW035820|AW035820 EST281974 tomato callus, TAMU Lycopersicon... 145 6e-58
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emb|AW034330|AW034330 EST277901 tomato callus, TAMU Lycopersicon... 144 2e-57
5 emb|AW622143|AW622143 EST312941 tomato root during/after fruit s... 149 2e-57
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emb|AI782621|AI782621 EST263500 tomato susceptible, Cornell Lyco... 144 7e-57
10 emb|AW126362|AW126362 N100469e rootphos(-) Medicago truncatula c... 160 3e-56
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emb|AW033687|AW033687 EST277258 tomato callus, TAMU Lycopersicon... 149 2e-55
emb|AI352783|AI352783 MB59-12D PZ204.BNlib Brassica napus cDNA c... 198 3e-55
emb|X14065|NTPRP1 Nicotiana tabacum gene for basic form of patho... 140 4e-55
15 emb|AW625666|AW625666 EST319573 tomato radicle, 5 d post-imbibit... 135 6e-55
emb|AW032727|AW032727 EST276286 tomato callus, TAMU Lycopersicon... 147 1e-53
emb|X52555|NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat... 116 1e-52
gb|BE034214|BE034214 MH01C07 MH Mesembryanthemum crystallinum cD... 112 4e-52
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20 emb|AW559969|AW559969 EST315017 DSIR Medicago truncatula cDNA cl... 81 4e-52
emb|AI352801|AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl... 194 1e-51
emb|X17681|NTPR1CA Tobacco gene for pathogenesis-related protein... 111 2e-51
emb|X05454|NTPR1CR Nicotiana tabacum mRNA for PR-1c protein. 111 2e-51
emb|X12487|NTPR1C Tobacco mRNA fragment for pathogenesis-related... 111 2e-51
25 emb|AJ011520|LES011520 Lycopersicon esculentum pr1a (P4) gene. 98 1e-50
gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50
emb|A22634|LEPI4GENE L.esculentum P14 gene. 98 1e-50
emb|AJ250136|STU250136 Solanum tuberosum mRNA for pathogenesis r... 99 2e-50
emb|AW218808|AW218808 EST301288 tomato root during/after fruit s... 116 3e-50
30 emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50
emb|AW094536|AW094536 EST287716 tomato mixed elicitor, BTI Lycop... 116 3e-50
emb|AW038553|AW038553 EST280236 tomato mixed elicitor, BTI Lycop... 116 3e-50
dbj|D90196|TOBPR1A Nicotiana tabacum mRNA for PR1a protein precu... 104 3e-50
emb|X05959|NTPR1AG Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
35 emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
emb|X06361|NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela... 104 4e-50
emb|X12485|NTPR1A Tobacco mRNA fragment for pathogenesis-related... 104 4e-50
emb|AW033469|AW033469 EST277040 tomato callus, TAMU Lycopersicon... 116 5e-50
emb|X06930|NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related ... 104 7e-50
40 emb|AI352858|AI352858 MB70-10D PZ204.BNlib Brassica napus cDNA c... 197 7e-50
emb|AI782416|AI782416 EST263295 tomato susceptible, Cornell Lyco... 95 7e-50
emb|AW034882|AW034882 EST279111 tomato callus, TAMU Lycopersicon... 95 1e-49
emb|AW031086|AW031086 EST274393 tomato callus, TAMU Lycopersicon... 116 1e-49
emb|X74939|HVPRIAR H. vulgare HvPR-1a mRNA for a basic PR-1-type... 114 2e-49
45 emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49
emb|AW034167|AW034167 EST277738 tomato callus, TAMU Lycopersicon... 94 2e-49
emb|X17680|NTPR1BA Tobacco gene for pathogenesis-related protein... 103 3e-49
emb|X03465|NTPRPR Nicotiana tabacum mRNA for pathogenesis-relate... 103 3e-49
dbj|D90197|TOBPR1B1 Nicotiana tabacum mRNA for PR1b protein. 103 3e-49
50 emb|Y08804|LEPR1B1 L.esculentum mRNA for PR protein. 92 6e-49
gb|M69248|TOMPRP6 Lycopersicon esculentum PR (pathogenesis relat... 92 6e-49
emb|X68738|LEP1P14A L.esculentum mRNA for ethylene-induced P1(pl... 92 6e-49
emb|AI781499|AI781499 EST262378 tomato susceptible, Cornell Lyco... 92 6e-49
emb|AI779424|AI779424 EST260303 tomato susceptible, Cornell Lyco... 92 6e-49
55 emb|AW031093|AW031093 EST274400 tomato callus, TAMU Lycopersicon... 92 6e-49
emb|AI779425|AI779425 EST260304 tomato susceptible, Cornell Lyco... 92 6e-49
emb|AI782545|AI782545 EST263424 tomato susceptible, Cornell Lyco... 92 6e-49
emb|AI782822|AI782822 EST263701 tomato susceptible, Cornell Lyco... 92 6e-49
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60 emb|AI778680|AI778680 EST259559 tomato susceptible, Cornell Lyco... 92 6e-49
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- emb|AI779287|AI779287 EST260166 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI773130|AI773130 EST254230 tomato resistant, Cornell Lycope... 92 6e-49
 emb|AI778790|AI778790 EST259669 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI778791|AI778791 EST259670 tomato susceptible, Cornell Lyco... 92 6e-49
 5 emb|AI778985|AI778985 EST259864 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AW032026|AW032026 EST275480 tomato callus, TAMU Lycopersicon... 92 6e-49
 emb|AI782288|AI782288 EST263167 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI779013|AI779013 EST259892 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI781431|AI781431 EST262298 tomato susceptible, Cornell Lyco... 92 6e-49
 10 emb|AI780973|AI780973 EST261852 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI895236|AI895236 EST264679 tomato callus, TAMU Lycopersicon... 92 6e-49

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 (1236 letters)

20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

- | | | Score | E |
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| 25 | Sequences producing significant alignments: | (bits) | Value |
| | gb M60729 HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge... | 744 | 0.0 |
| | emb A00741 A00741 A.rusticana synthetic gene (reverse complement... | 692 | 0.0 |
| | emb A00740 A00740 A.rusticana synthetic gene for peroxidase. | 692 | 0.0 |
| 30 | dbj E01651 E01651 cDNA encoding horseradish peroxidase. | 692 | 0.0 |
| | gb M37157 HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge... | 371 | e-133 |
| | emb X97349 PTXP2PER P.trichocarpa mRNA for anionic peroxidase P... | 473 | e-132 |
| | emb X97350 PTXP3PER P.trichocarpa mRNA for anionic peroxidase P... | 469 | e-131 |
| | dbj D83224 POPP01 Populus nigra mRNA for peroxidase, complete cds. | 468 | e-131 |
| 35 | gb M37156 HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge... | 363 | e-130 |
| | emb X97348 PTXP1PER P.trichocarpa mRNA for anionic peroxidase P... | 463 | e-129 |
| | dbj D30652 POPPA Populus kitakamiensis mRNA for peroxidase, part... | 441 | e-123 |
| | emb X97351 PTXP4PER P.trichocarpa mRNA for anionic peroxidase P... | 383 | e-120 |
| | dbj D30653 POPPB Populus kitakamiensis mRNA for peroxidase, part... | 356 | e-112 |
| 40 | emb AF149277 AF149277 Phaseolus vulgaris peroxidase 1 precursor ... | 227 | e-107 |
| | gb L36157 ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple... | 229 | e-107 |
| | emb AF007211 AF007211 Glycine max peroxidase precursor (GMIPER1)... | 229 | e-106 |
| | gb L07554 LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA... | 381 | e-105 |
| | emb X90692 MSRNAPE1A M.sativa mRNA for peroxidase 1A. | 211 | e-105 |
| 45 | dbj D90115 HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i... | 296 | e-103 |
| | emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod ... | 138 | 2e-97 |
| | emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor ... | 142 | 4e-97 |
| | emb X90693 MSRNAPE1B M.sativa mRNA for peroxidase 1B. | 231 | 1e-95 |
| | emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C. | 226 | 7e-94 |
| 50 | gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA. | 210 | 2e-89 |
| | emb AI959837 AI959837 sc94h07.y1 Gm-c1019 Glycine max cDNA clone... | 228 | 6e-89 |
| | emb AF244924 AF244924 Spinacia oleracea peroxidase prx15 precurs... | 208 | 9e-88 |
| | emb AW559660 AW559660 EST314772 DSIR Medicago truncatula cDNA cl... | 236 | 1e-87 |
| | emb AW774581 AW774581 EST333732 KV3 Medicago truncatula cDNA clo... | 236 | 7e-87 |
| 55 | emb AF155124 AF155124 Gossypium hirsutum bacterial-induced perox... | 215 | 2e-86 |
| | emb AW981426 AW981426 EST392579 DSIL Medicago truncatula cDNA cl... | 236 | 2e-85 |
| | emb AB042103 AB042103 Asparagus officinalis AspPOX1 mRNA for per... | 209 | 2e-85 |
| | emb AF244923 AF244923 Spinacia oleracea peroxidase prx14 precurs... | 205 | 9e-85 |
| | emb AJ250121 PAB250121 Picea abies mRNA for SPI2 protein (spi2 g... | 253 | 1e-83 |
| 60 | emb AW775762 AW775762 EST334827 DSIL Medicago truncatula cDNA cl... | 236 | 6e-83 |
| | emb Y10466 SOPR XR5 S.oleracea mRNA for peroxidase, clone PC18. | 218 | 3e-82 |

- emb|AW775425|AW775425 EST334490 *DSIL Medicago truncatula* cDNA cl... 208 1e-81
emb|AW685437|AW685437 NF029D09NR1F1000 *Nodulated root Medicago t...* 230 9e-80
emb|AB024439|AB024439 *Scutellaria baicalensis* mRNA for peroxidase... 209 2e-79
5 emb|AF244922|AF244922 *Spinacia oleracea* peroxidase prx13 precurs... 212 3e-79
emb|X57564|ARNEUPERO A.rusticana mRNA for neutral peroxidase. 115 6e-78
emb|AW776273|AW776273 EST335338 *DSIL Medicago truncatula* cDNA cl... 222 1e-77
emb|AW267813|AW267813 EST305941 *DSIR Medicago truncatula* cDNA cl... 200 1e-76
emb|X91232|MARNAPRX M.annua mRNA for peroxidase. 196 5e-76
10 emb|AF049881|AF049881 *Linum usitatissimum* peroxidase FLXPER4 (PE... 207 7e-76
emb|AW256487|AW256487 EST304624 KV2 *Medicago truncatula* cDNA clo... 200 9e-76
emb|AW775890|AW775890 EST334955 *DSIL Medicago truncatula* cDNA cl... 200 3e-74
emb|AW257195|AW257195 EST305332 KV2 *Medicago truncatula* cDNA clo... 214 5e-74
gb|M91373|CUSPREPER *Cucumis sativus* peroxidase mRNA, complete cds. 86 2e-73
gb|U41657|GMU41657 *Glycine max* seed coat peroxidase isozyme (SPO... 159 3e-73
15 emb|AB027752|AB027752 *Nicotiana tabacum* mRNA for peroxidase, com... 197 5e-73
gb|L36110|SSNPEROXIA *Stylosanthes humilis* peroxidase mRNA. 199 5e-73
gb|M37636|ARCPNC1 *Arachis hypogaea* cationic peroxidase (PNC1) mR... 204 7e-73
emb|AW685235|AW685235 NF027H10NR1F1000 *Nodulated root Medicago t...* 236 9e-73
emb|AW278775|AW278775 sf97d02.y1 *Gm-c1019 Glycine max* cDNA clone... 155 1e-72
20 emb|X71593|LECEV1A *L.esculentum* CEV1-1 mRNA. 99 2e-72
gb|J02979|TOBPXDLF *Nicotiana tabacum* lignin-forming peroxidase m... 100 2e-72
emb|AW559945|AW559945 EST314993 *DSIR Medicago truncatula* cDNA cl... 233 2e-72
emb|AW980744|AW980744 EST391897 *GVN Medicago truncatula* cDNA clo... 235 5e-70
emb|Y10467|SOPRXR6 *S.oleracea* mRNA for peroxidase, clone PC23. 105 1e-69
25 dbj|D83225|POPP02 *Populus nigra* peroxidase gene, complete cds. 196 2e-69
gb|M74103|TOBANPER *Nicotiana sylvestris* anionic peroxidase mRNA,... 205 6e-69
emb|AF043234|AF043234 *Striga asiatica* ferriprotein porphyrin-con... 211 1e-68
gb|BE034991|BE034991 MM01A12 *MM Mesembryanthemum crystallinum* cD... 202 6e-68
emb|AW574244|AW574244 EST316835 *GVN Medicago truncatula* cDNA clo... 202 1e-67
30 emb|Y10465|SOPRXR4 *S.oleracea* mRNA for peroxidase, clone PC44. 98 3e-67
emb|AW686084|AW686084 NF038B07NR1F1000 *Nodulated root Medicago t...* 236 5e-67
emb|AW561032|AW561032 EST316080 *DSIR Medicago truncatula* cDNA cl... 203 7e-67
emb|X56011|TAPERO *Wheat* mRNA for peroxidase. 111 2e-66
emb|AW185769|AW185769 se59d08.y1 *Gm-c1019 Glycine max* cDNA clone... 219 4e-65
35 emb|Y17192|CPY17192 *Cucurbita pepo* mRNA for peroxidase. 96 2e-64
gb|BE033422|BE033422 ME01E09 *ME Mesembryanthemum crystallinum* cD... 184 4e-64
emb|AB024438|AB024438 *Scutellaria baicalensis* mRNA for peroxidase... 205 7e-64
gb|M91374|CUSPREPERA *Cucumis sativus* peroxidase mRNA, complete cds. 76 2e-63
gb|L24120|LINFLXP *Linum usitatissimum* peroxidase precursor (FLXP... 167 2e-63
40 gb|M91372|CUSPREPERB *Cucumis sativus* peroxidase mRNA, complete cds. 134 2e-63
emb|AF043235|AF043235 *Striga asiatica* ferriprotein porphyrin-con... 199 3e-63
emb|AW288002|AW288002 N100846e rootphos(-) *Medicago truncatula* c... 182 7e-63
emb|AW126121|AW126121 N100318e rootphos(-) *Medicago truncatula* c... 216 1e-62
gb|L36093|BLYPRX *Barley* peroxidase mRNA, complete cds. 133 5e-62
45 emb|AW687443|AW687443 NF009F07RT1F1062 *Developing root Medicago ...* 235 1e-61
emb|AW687957|AW687957 NF001D11ST1F1000 *Developing stem Medicago ...* 236 3e-61
emb|AB024437|AB024437 *Scutellaria baicalensis* mRNA for peroxidase... 163 3e-61
emb|X58396|HVPEROXI *Barley* mRNA for peroxidase (EC=1.11.1.7). 133 5e-61
emb|AI496388|AI496388 sb04a11.y1 *Gm-c1004 Glycine max* cDNA clone... 224 6e-61
50 emb|AW686765|AW686765 NF042E07NR1F1000 *Nodulated root Medicago t...* 222 8e-61
dbj|D38050|POPP1 *Aspen* prxA3a gene for peroxidase, complete cds. 121 9e-61
emb|AW704659|AW704659 sk54h10.y1 *Gm-c1019 Glycine max* cDNA clone... 149 9e-61
emb|Y10464|SOPRXR3 *S.oleracea* mRNA for peroxidase, clone PC42. 80 3e-60
emb|AW705730|AW705730 sk51b02.y1 *Gm-c1019 Glycine max* cDNA clone... 149 8e-60
55 gb|U51191|GMU51191 *Glycine max* peroxidase precursor (sEPa1) mRNA... 100 9e-60
gb|U12314|CCU12314 *Cenchrus ciliaris* clone PX7 peroxidase mRNA, ... 105 9e-60
emb|AI938533|AI938533 sb46h09.y1 *Gm-c1015 Glycine max* cDNA clone... 145 1e-59
emb|AW705617|AW705617 sk50d03.y1 *Gm-c1019 Glycine max* cDNA clone... 149 2e-59
emb|AI781859|AI781859 EST262738 *tomato susceptible, Cornell Lyco...* 102 2e-59
60 emb|AF149278|AF149278 *Phaseolus vulgaris* peroxidase 3 precursor ... 90 3e-59
gb|U51192|GMU51192 *Glycine max* peroxidase precursor (sEPa2) mRNA... 102 4e-59

emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59
 emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 156 8e-59
 gb|M32742|CUSCUPER C.sativus peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58
 emb|AW705946|AW705946 sk52h07.y1 Gm-cl019 Glycine max cDNA clone... 224 6e-58

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 gb|aac49117.1| (u18993) tryptophan synthase alpha chain [arabidopsis
 thaliana] /blast_score 1.00e-158 /ec_number /family /chip nova
 10 /gb_link /ncgi
 (939 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

20

emb|AW730233|AW730233 GA_Ea0014B16 Gossypium arboreum 7-10 dpa ... 352 5e-98
 emb|AW649960|AW649960 EST328414 tomato germinating seedlings, TA... 308 4e-83
 emb|AW621664|AW621664 EST312462 tomato root during/after fruit s... 290 1e-77
 25 emb|AW031327|AW031327 EST274781 tomato callus, TAMU Lycopersicon... 282 3e-75
 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 271 4e-72
 emb|AW775853|AW775853 EST334918 DSIL Medicago truncatula cDNA cl... 264 9e-70
 emb|Z21642|CHASTRNA Antithamnion sp. Chloroplast trnK, trnE, trpA... 255 4e-67
 gb|BE124387|BE124387 EST393422 GVN Medicago truncatula cDNA clon... 227 9e-59
 gb|BE121873|BE121873 894015F07.y1 C. reinhardtii CC-1690, normal... 227 1e-58
 30 emb|AF022186|AF022186 Cyanidium caldarium strain RK1 chloroplast... 220 1e-56
 emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53
 emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49
 dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49
 emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49
 35 emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47
 dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46
 emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46
 dbj|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45
 gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43
 40 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42
 emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42
 emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38
 emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38
 emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32
 45 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycopen... 138 5e-32
 emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 74 3e-30
 emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26
 emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21
 emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19
 50 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17
 emb|AF084886|AF084886 Neurospora crassa 314-448A mutant tryptoph... 68 9e-11
 emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptop... 53 4e-10
 emb|AF084880|AF084880 Neurospora crassa EMSG9-9A mutant tryptoph... 66 5e-10
 emb|AF084885|AF084885 Neurospora crassa NG61-6A mutant tryptoph... 64 1e-09
 55 emb|AF084884|AF084884 Neurospora crassa 314-722A mutant tryptoph... 64 1e-09
 emb|AF084883|AF084883 Neurospora crassa 314-709A mutant tryptoph... 64 1e-09
 emb|AF084882|AF084882 Neurospora crassa 314-682A mutant tryptoph... 64 1e-09
 emb|AF084881|AF084881 Neurospora crassa 314-693A mutant tryptoph... 64 2e-09
 emb|AF084889|AF084889 Neurospora crassa 314-492-2A mutant trypto... 53 3e-09
 60 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08
 emb|AU011013|AU011013 AU011013 Schizosaccharomyces pombe late lo... 54 2e-06

	emb AW693052 AW693052 NF059C08ST1F1065 Developing stem Medicago ...	51	1e-05
	emb AV390244 AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla...	49	4e-05
	emb AW616467 AW616467 EST322878 L. hirsutum trichome, Cornell Un...	48	7e-05
	emb AL354022 P761R Leishmania major Friedlin PAC P761 right end...	44	0.002
5	gb M91656 CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1...	43	0.005
	emb AQ903789 AQ903789 GSSTc04230 Trypanosome cruzi random genom...	35	0.24
	emb AW727215 AW727215 GA_Ea0023N23 Gossypium arboreum 7-10 dpa ...	36	0.52
	gb M91654 CCITRP03 Coprinus cinereus tryptophan synthetase (TRP1...	36	0.52
	emb AW728975 AW728975 GA_Ea0018P19 Gossypium arboreum 7-10 dpa ...	35	0.64
10	emb AL139794 LMFP1105 Leishmania major Friedlin chromosome 4 PAC...	35	0.87
	emb AW926438 AW926438 HVSMEg0007D14 Hordeum vulgare pre-anthesis...	34	1.2
	emb AA965348 AA965348 e9d04a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
	gb U12630 ENU12630 Emericella nidulans R153 core histone H3 (H3)...	34	1.3
	emb AI007494 AI007494 e9c09a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
15	emb AA787433 AA787433 n3d04a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
	emb X55548 ANH3GENE A.nidulans gene for core histone for H3.	34	1.3
	emb AQ396426 AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P...	34	1.6
	emb AF262997 AF262997 Ricinus communis NADP-dependent malic prot...	34	1.6
	gb M19025 CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c...	34	1.6
20	emb AF084888 AF084888 Neurospora crassa 656-2A mutant tryptophan...	31	1.7
	emb AF084887 AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta...	31	1.7
	emb AW694774 AW694774 NF080A05ST1F1036 Developing stem Medicago ...	34	1.8
	emb Y18012 TVE18012 Trametes versicolor mRNA for laccase.	33	2.3
	emb AQ500614 AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc...	33	2.5
25	emb AW187498 AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW187530 AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW694072 AW694072 NF072B12ST1F1096 Developing stem Medicago ...	33	3.1
	emb AW186883 AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW187537 AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ...	33	3.1
30	emb AW187474 AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AA167859 AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor...	33	3.5
	emb AV421993 AV421993 AV421993 Lotus japonicus young plants (two...	33	4.3
	emb AF129874 AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp...	33	4.3
	emb AL112679 CNS01AA7 Botrytis cinerea strain T4 cDNA library un...	33	4.7
35	gb BE028433 BE028433 EtESTea78d07.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI166784 AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li...	32	5.9
	emb AQ941624 AQ941624 Sheared DNA-53E1.TF Sheared DNA Trypanosom...	32	5.9
	emb AW728623 AW728623 GA_Ea0017G06 Gossypium arboreum 7-10 dpa ...	32	5.9
	gb BE027723 BE027723 EtESTea86c08.y1 Eimeria M5-6 Merozoite stag...	32	5.9
40	emb AI757375 AI757375 EtESTea32d03.y1 Eimeria S5-2 Sporozoite st...	32	5.9
	gb BE027843 BE027843 EtESTea88c05.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI973878 AI973878 sd13a09.y1 Gm-c1020 Glycine max cDNA clone...	32	5.9
	dbj D85261 D85261 Plasmodium vivax clone TD439B DNA for merozoit...	32	5.9
	dbj D85251 D85251 Plasmodium vivax clone TD207B DNA for merozoit...	32	5.9
45	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom...	32	6.5
	emb Z71509 SCYNL233W S.cerevisiae chromosome XIV reading frame O...	32	6.5
	emb AW707662 AW707662 832011E08.y1 C. reinhardtii CC-125 nutrien...	28	7.3
	emb AF083075 AF083075 Fusarium oxysporum f. sp. lycopersici exop...	32	8.1
	emb AV411934 AV411934 AV411934 Lotus japonicus young plants (two...	32	8.1
50	emb AW703740 AW703740 sk23g09.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
	emb AW703739 AW703739 sk23g08.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
	emb AV419698 AV419698 AV419698 Lotus japonicus young plants (two...	32	8.1
	emb AV419299 AV419299 AV419299 Lotus japonicus young plants (two...	32	8.1
	emb AV420652 AV420652 AV420652 Lotus japonicus young plants (two...	32	8.1
55	emb AV408860 AV408860 AV408860 Lotus japonicus young plants (two...	32	8.1
	emb AV420989 AV420989 AV420989 Lotus japonicus young plants (two...	32	8.1
	emb AV419314 AV419314 AV419314 Lotus japonicus young plants (two...	32	8.1
	emb AW720540 AW720540 LjNEST18h4r Lotus japonicus nodule library...	32	8.1
60	emb X77895 CPGPRNL28 G.pyrenaica chloroplast trnL gene intron.	32	8.1

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gb|aaa32879.1| (m81620) tryptophan synthase beta-subunit [arabidopsis
thaliana] thaliana] /blast_score 0 /ec_number /family /chip nova
/gb_link /ncgi

5 (1526 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10 Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
15	emb AF042320 AF042320 <i>Camptotheca acuminata</i> tryptophan synthase ...	858	0.0
	emb AF047024 AF047024 <i>Chlamydomonas reinhardtii</i> tryptophan synth...	712	0.0
	gb J04594 NEUTRP3A <i>N.crassa</i> tryptophan synthetase (trp3) alpha-2...	473	e-140
	emb Z98974 SPAC19A8 <i>S.pombe</i> chromosome I cosmid c19A8.	462	e-135
	emb AW031813 AW031813 EST275267 tomato callus, TAMU <i>Lycopersicon</i> ...	429	e-119
20	emb AF121272 AF121272 <i>Gracilaria gracilis</i> putative NAD-myo-inosi...	426	e-118
	dbj D89113 D89113 <i>Schizosaccharomyces pombe</i> mRNA, partial cds, c...	310	e-114
	emb AI055312 AI055312 coau0003K07 Cotton Boll Abscission Zone cD...	404	e-112
	emb AF042321 AF042321 <i>Camptotheca acuminata</i> tryptophan synthase ...	346	e-109
	gb BE126222 BE126222 DG1_68_D09.b1_A002 Dark Grown 1 (DG1) <i>Sorgh</i> ...	379	e-104
25	emb AW650635 AW650635 EST329089 tomato germinating seedlings, TA...	372	e-102
	emb AI487343 AI487343 EST245665 tomato ovary, TAMU <i>Lycopersicon</i> ...	354	8e-97
	emb AI488733 AI488733 EST247072 tomato ovary, TAMU <i>Lycopersicon</i> ...	353	2e-96
	emb AA495663 AA495663 c313 Zhou and Ragan 1993 <i>Gracilaria gracil</i> ...	350	1e-95
	emb AW160221 AW160221 EST290079 <i>L. pennellii</i> trichome, Cornell U...	327	1e-88
30	emb V01342 SCTRP5A Yeast gene (trp5) for tryptophan synthetase.	270	6e-88
	emb Z72548 SCYGL026C <i>S.cerevisiae</i> chromosome VII reading frame O...	270	6e-88
	emb AI485149 AI485149 EST243453 tomato ovary, TAMU <i>Lycopersicon</i> ...	319	3e-86
	emb AI966766 AI966766 sc57f10.y1 <i>Gm-cl016</i> Glycine max cDNA clone...	306	3e-82
	gb M91659 CCITRP08 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	302	4e-81
35	gb BE058277 BE058277 sn13h12.y1 <i>Gm-cl016</i> Glycine max cDNA clone ...	259	6e-68
	emb AI488512 AI488512 EST246851 tomato ovary, TAMU <i>Lycopersicon</i> ...	237	2e-63
	emb AI487792 AI487792 EST246114 tomato ovary, TAMU <i>Lycopersicon</i> ...	232	8e-62
	emb AW696637 AW696637 NF109C11STIF1085 Developing stem <i>Medicago</i> ...	213	2e-59
	emb AI898827 AI898827 EST268270 tomato ovary, TAMU <i>Lycopersicon</i> ...	228	7e-59
40	emb AQ450225 AQ450225 500009D01.x1 CpIOWAM13mp18gDNA1 <i>Cryptospor</i> ...	175	3e-58
	emb AW160220 AW160220 EST290078 <i>L. pennellii</i> trichome, Cornell U...	223	3e-57
	emb AF084902 AF084902 <i>Neurospora crassa</i> TD2(4A-4A)2A mutant trypt...	214	2e-54
	emb AF084903 AF084903 <i>Neurospora crassa</i> TD71-19A mutant tryptoph...	213	3e-54
45	emb AF084904 AF084904 <i>Neurospora crassa</i> TD54-6A mutant tryptoph...	210	3e-53
	emb AI779245 AI779245 EST260124 tomato susceptible, Cornell Lyco...	208	8e-53
	emb AI487088 AI487088 EST245410 tomato ovary, TAMU <i>Lycopersicon</i> ...	149	3e-51
	emb AQ876415 AQ876415 V99F5 mTn-3xHA/lacZ Insertion Library, str...	183	4e-50
	emb AL116518 CNS01D8U <i>Botrytis cinerea</i> strain T4 cDNA library un...	160	2e-47
50	emb AW745773 AW745773 WS1_37_G06.b1_A002 Water-stressed 1 (WS1) ...	167	2e-40
	emb AF084893 AF084893 <i>Neurospora crassa</i> TD24-2A-28A mutant trypt...	130	8e-38
	emb AF084892 AF084892 <i>Neurospora crassa</i> 314-567-9A mutant trypto...	132	1e-37
	emb AF084891 AF084891 <i>Neurospora crassa</i> 314-616-2A mutant trypto...	132	1e-37
	emb AF084895 AF084895 <i>Neurospora crassa</i> TD10-8A mutant tryptoph...	130	1e-37
55	emb AF084894 AF084894 <i>Neurospora crassa</i> TD7(13A-11A)13A mutant t...	130	1e-37
	emb AF084901 AF084901 <i>Neurospora crassa</i> TD72-1-25A mutant trypto...	129	1e-37
	emb AF084900 AF084900 <i>Neurospora crassa</i> TD85-1-24A mutant trypto...	129	1e-37
	emb AF084899 AF084899 <i>Neurospora crassa</i> TD86-1-22A mutant trypto...	129	1e-37
	emb AF084898 AF084898 <i>Neurospora crassa</i> TD6(1-8A)22A mutant trypt...	129	1e-37
60	emb AF084896 AF084896 <i>Neurospora crassa</i> NG29-3A mutant tryptoph...	129	1e-37
	emb AW745836 AW745836 WS1_37_G06.g1_A002 Water-stressed 1 (WS1) ...	157	2e-37

	emb AF084897 AF084897 <i>Neurospora crassa</i> TD3-32-16A mutant trypto...	128	3e-37
	emb AI399300 AI399300 NCW07F11T3 Westergaards <i>Neurospora crassa</i> ...	145	3e-37
	emb AF084906 AF084906 <i>Neurospora crassa</i> NG40-5A mutant tryptopha...	152	8e-36
	emb AF084905 AF084905 <i>Neurospora crassa</i> NG25-4A mutant tryptopha...	152	8e-36
5	gb BE024522 BE024522 894003E01.y1 <i>C. reinhardtii</i> CC-1690, normal...	142	6e-33
	emb AJ229567 KLAJ9567 <i>Kluyveromyces lactis</i> DNA fragment for sequ...	137	3e-31
	emb AQ449630 AQ449630 500002F12.x2 CpIOWAM13mp18gDNA1 <i>Cryptospor...</i>	116	1e-27
	emb AW695848 AW695848 NF099D01ST1F1012 Developing stem <i>Medicago</i> ...	116	9e-27
10	emb AW098758 AW098758 ga01a03.y1 Moss EST library CPU <i>Ceratodon</i> ...	118	1e-25
	gb M91658 CCITRP07 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	115	8e-25
	emb AW086510 AW086510 ga01a03.x1 Moss EST library CPU <i>Ceratodon</i> ...	103	4e-21
	emb AW221168 AW221168 EST297637 tomato fruit mature green, TAMU ...	96	5e-19
	emb AW650217 AW650217 EST328671 tomato germinating seedlings, TA...	95	1e-18
15	emb AV408265 AV408265 AV408265 <i>Lotus japonicus</i> young plants (two...	77	4e-13
	emb AW688230 AW688230 NF005A01ST1F1000 Developing stem <i>Medicago</i> ...	72	1e-11
	emb AI488384 AI488384 EST246706 tomato ovary, TAMU <i>Lycopersicon</i> ...	70	4e-11
	emb AW032971 AW032971 EST276530 tomato callus, TAMU <i>Lycopersicon</i> ...	60	6e-08
	emb AW755317 AW755317 sl01e06.y1 Gm-c1036 <i>Glycine max</i> cDNA clone...	57	4e-07
20	emb AW153250 AW153250 se37h08.y1 Gm-c1015 <i>Glycine max</i> cDNA clone...	56	1e-06
	emb AQ450041 AQ450041 500007C05.x1 CpIOWAM13mp18gDNA1 <i>Cryptospor...</i>	37	2e-04
	emb AW625162 AW625162 EST319069 tomato radicle, 5 d post-imbibit...	45	0.001
	gb M91656 CCITRP05 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	45	0.002
	emb AW926725 AW926725 HVSMEg0007P16 <i>Hordeum vulgare</i> pre-anthesis...	42	0.013
25	emb X99652 ANG3PDEHY <i>A.niger</i> gpd gene.	35	0.084
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	emb AV417838 AV417838 AV417838 <i>Lotus japonicus</i> young plants (two...	38	0.17
	emb AV414417 AV414417 AV414417 <i>Lotus japonicus</i> young plants (two...	38	0.17
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30	emb AV424994 AV424994 AV424994 <i>Lotus japonicus</i> young plants (two...	38	0.17
	emb AA901537 AA901537 NCC2B7T7 <i>Conidial Neurospora crassa</i> cDNA c...	38	0.23
	gb BE060085 BE060085 HVSMEg0011G11f <i>Hordeum vulgare</i> pre-anthesis...	38	0.23
	gb U30626 SCU30626 <i>Saccharomyces cerevisiae</i> var. <i>diastaticus</i> glu...	37	0.32
	emb AJ010201 GMA010201 <i>Glycine max</i> mRNA for inosine monophosphat...	37	0.32
35	emb AW185330 AW185330 se90b04.y1 Gm-c1027 <i>Glycine max</i> cDNA clone...	37	0.32
	emb Z38061 SC9168 <i>S.cerevisiae</i> chromosome IX cosmid 9168.	37	0.32
	emb AF160799 AF160799 <i>Sporidiobolus salmonicolor</i> aldehyde reduct...	37	0.44
	emb AC016161 AC016161 <i>Leishmania major</i> chromosome 35 clone L8149...	37	0.44
	emb AW185636 AW185636 se80e06.y1 Gm-c1023 <i>Glycine max</i> cDNA clone...	37	0.44
40	emb AB030490 AB030490 <i>Glycine max</i> SG-05 gene for thiamin biosynt...	36	0.60
	emb AW278827 AW278827 sf99b01.y1 Gm-c1019 <i>Glycine max</i> cDNA clone...	36	0.60
	emb Z93048 SLZ93048 <i>S.latifolia</i> mRNA, clone CCLS 37.1.	30	0.72
	emb AV393412 AV393412 AV393412 <i>Chlamydomonas reinhardtii</i> C9 Chla...	36	0.83
	emb AL035581 SPBC1677 <i>S.pombe</i> chromosome II cosmid c1677.	36	0.83
45	emb AV425767 AV425767 AV425767 <i>Lotus japonicus</i> young plants (two...	36	0.83
	emb AI727538 AI727538 BNLGH8343 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	gb BE053957 BE053957 GA_Ea0033K12f <i>Gossypium arboreum</i> 7-10 dpa ...	35	1.1
	emb AI731384 AI731384 BNLGH8894 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	emb AW596016 AW596016 si96g09.y1 Gm-c1032 <i>Glycine max</i> cDNA clone...	35	1.1
50	emb AI730998 AI730998 BNLGH8370 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	emb AJ276509 TAE276509 <i>Triticum aestivum</i> grp1 gene for glycine-r...	28	1.3
	gb B13527 B13527 jd421 Trypanosome Shotgun M13 genomic Trypanoso...	29	1.4
	gb U56698 CPU56698 <i>Ceratodon purpureus</i> phytochrome photoreceptor...	35	2.2
	emb AF079252 AF079252 <i>Dichanthium aristatum</i> granule-bound starch...	35	2.2
55	emb AJ133604 TAE133604 <i>Triticum aestivum</i> mRNA for alpha-gliadin ...	34	4.1

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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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gb S69616 S69616 Ant18=dihydroflavonol-4-reductase [Hordeum vulg...	29	7.8	

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20 <http://www.ncgr.org/cgi-bin/ff?wt1096>
(371 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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emb AW171733 AW171733 N100627e rootphos(-) Medicago truncatula c...	36	0.099	
emb AW185514 AW185514 se80g03.y1 Gm-c1023 Glycine max cDNA clone...	36	0.099	
35 emb AI777176 AI777176 EST258141 tomato resistant, Cornell Lycopen...	35	0.26	
gb C22084 C22084 Miyagawa-wase satsuma mandarin orange (M...	35	0.26	
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emb AW218263 AW218263 EST303444 tomato radicle, 5 d post-imbibit...	35	0.26	
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40 emb AA557085 AA557085 927 Loblolly pine N Pinus taeda cDNA clone...	35	0.26	
emb AW981718 AW981718 PC15H05 Pine TriplEx pollen cone library P...	35	0.26	
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emb AF101786 AF101786 Pinus taeda clone PtaADH1 adhesive/proline...	35	0.35	
emb AA785548 AA785548 g8e04a1.f1 Aspergillus nidulans 24hr asexu...	35	0.35	
45 emb AI812646 AI812646 17D5 Pine Lambda Zap Xylem library Pinus t...	35	0.35	
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emb AW040418 AW040418 EST283282 tomato mixed elicitor, BTI Lycop...	34	0.49	
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50 emb AI490158 AI490158 EST246750 tomato resistant, Cornell Lycopen...	34	0.49	
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emb AA740016 AA740016 781 PtIFG2 Pinus taeda cDNA clone 9242M 3'...	34	0.49	
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55 emb AI416531 AI416531 sa10c07.y1 Gm-c1003 Glycine max cDNA clone...	33	0.92	
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 emb|AW011516|AW011516 ST21G04 Pine TriplEx shoot tip library Pin... 33 1.3
 emb|AW310413|AW310413 sf35f11.x1 Gm-cl028 Glycine max cDNA clone... 32 1.7
 emb|AW043248|AW043248 ST31B02 Pine TriplEx shoot tip library Pin... 32 1.7
 emb|AW255053|AW255053 ML1348 peppermint glandular trichome Menth... 32 2.4
 10 emb|AW255347|AW255347 ML358 peppermint glandular trichome Menth... 32 2.4
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 emb|AI482971|AI482971 EST242294 tomato shoot, Cornell Lycopersic... 31 3.3
 15 emb|AW568662|AW568662 si60e08.y1 Gm-r1030 Glycine max cDNA clone... 31 3.3
 emb|AI442234|AI442234 sa49d06.y1 Gm-cl004 Glycine max cDNA clone... 31 3.3
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 emb|AW218238|AW218238 EST303419 tomato radicle, 5 d post-imbibit... 31 3.3
 20 emb|AW102024|AW102024 sd82b01.y1 Gm-cl009 Glycine max cDNA clone... 31 3.3
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- 45 Database: plantfungal
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- 50 Score E
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- emb|AI771551|AI771551 EST252651 tomato ovary, TAMU Lycopersicon ... 105 1e-22
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 60 emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 105 1e-22
 emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 104 2e-22

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	emb AI899328 AI899328 EST268771 tomato ovary, TAMU Lycopersicon ...	82	2e-15
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25	emb AW831124 AW831124 sm09c06.y1 Gm-c1027 Glycine max cDNA clone...	28	0.56
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40	emb AW623982 AW623982 EST321927 tomato flower buds 3-8 mm, Corne...	29	2.5
	emb AW719534 AW719534 LjNEST5c5rW Lotus japonicus nodule library...	31	3.3
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10 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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20 emb AW729009 AW729009 GA_Ea0019F23 Gossypium arboreum 7-10 dpa ...	35	0.59
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45 Database: plantfungal
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emb AW668548 AW668548 GA_Ea0014H16 Gossypium arboreum 7-10 dpa ...	287	6e-77
emb AW668413 AW668413 GA_Ea0013N18 Gossypium arboreum 7-10 dpa ...	287	6e-77
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- emb|AI775630|AI775630 EST256730 tomato resistant, Cornell Lycopersicon... 285 3e-76
 gb|BE055389|BE055389 GA_Ea0026N20f Gossypium arboreum 7-10 dpa ... 284 5e-76
 emb|AI779420|AI779420 EST260299 tomato susceptible, Cornell Lycopersicon... 282 2e-75
 5 emb|AW349482|AW349482 GM210007A20G5R Gm-r1021 Glycine max cDNA 3... 282 2e-75
 emb|AW041006|AW041006 EST283870 tomato mixed elicitor, BTI Lycopersicon... 279 2e-74
 emb|AW597183|AW597183 sj74f03.y1 Gm-c1034 Glycine max cDNA clone... 278 3e-74
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 10 emb|AW567736|AW567736 si54c02.y1 Gm-r1030 Glycine max cDNA clone... 275 2e-73
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 emb|AW472050|AW472050 si19d05.y1 Gm-c1029 Glycine max cDNA clone... 273 8e-73
 emb|AW568096|AW568096 si68d05.y1 Gm-r1030 Glycine max cDNA clone... 273 1e-72
 emb|AW568074|AW568074 si68b05.y1 Gm-r1030 Glycine max cDNA clone... 272 1e-72
 15 emb|AW733947|AW733947 sk85e02.y1 Gm-c1035 Glycine max cDNA clone... 271 4e-72
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 emb|AW508326|AW508326 si52e11.y1 Gm-r1030 Glycine max cDNA clone... 270 7e-72
 emb|AW980703|AW980703 EST391856 GVN Medicago truncatula cDNA clone... 269 1e-71
 20 emb|AI930835|AI930835 sc47h06.y1 Gm-c1015 Glycine max cDNA clone... 269 1e-71
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 25 emb|AW101773|AW101773 sd70b02.y1 Gm-c1008 Glycine max cDNA clone... 261 4e-69
 emb|AW559683|AW559683 EST314795 DSIR Medicago truncatula cDNA clone... 260 6e-69
 emb|AW317108|AW317108 sg44d09.y1 Gm-c1025 Glycine max cDNA clone... 260 8e-69
 emb|AW397034|AW397034 sg66b12.y1 Gm-c1007 Glycine max cDNA clone... 258 3e-68
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 30 emb|AW094638|AW094638 EST287806 tomato mixed elicitor, BTI Lycopersicon... 255 3e-67
 emb|AW585325|AW585325 EST306020 KV2 Medicago truncatula cDNA clone... 251 3e-66
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 35 emb|AW756544|AW756544 sl23d11.y1 Gm-c1036 Glycine max cDNA clone... 247 6e-65
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 emb|AW279163|AW279163 sf67b11.y1 Gm-c1013 Glycine max cDNA clone... 237 8e-62
 emb|AW201089|AW201089 se97f12.y1 Gm-c1027 Glycine max cDNA clone... 236 1e-61
 40 emb|AI162549|AI162549 A019P27U Hybrid aspen plasmid library Populus... 236 2e-61
 emb|AW720300|AW720300 LjNEST20d9r Lotus japonicus nodule library... 236 2e-61
 emb|AW065021|AW065021 ST38F08 Pine TriplEx shoot tip library Pinus... 236 2e-61
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 45 emb|AW508348|AW508348 si52g09.y1 Gm-r1030 Glycine max cDNA clone... 229 2e-59
 emb|AI774108|AI774108 EST255208 tomato resistant, Cornell Lycopersicon... 227 7e-59
 emb|AI163857|AI163857 A050p05u Hybrid aspen plasmid library Populus... 226 9e-59
 emb|AW065077|AW065077 ST39D01 Pine TriplEx shoot tip library Pinus... 225 2e-58
 emb|AW704118|AW704118 sk16b03.y1 Gm-c1028 Glycine max cDNA clone... 221 4e-57
 50 emb|AI507795|AI507795 sb12g09.y1 Gm-c1004 Glycine max cDNA clone... 216 1e-55
 emb|AW289649|AW289649 NXNV003G05F Nsf Xylem Normal wood Vertical... 215 2e-55
 emb|AV422946|AV422946 AV422946 Lotus japonicus young plants (two... 122 3e-55
 gb|T14824|T14824 crs266 lambdaZAPST Ricinus communis cDNA clone ... 212 2e-54
 emb|AW443507|AW443507 EST308437 tomato mixed elicitor, BTI Lycopersicon... 207 6e-53
 55 emb|AW226029|AW226029 ST76E07 Pine TriplEx shoot tip library Pinus... 207 8e-53
 emb|AW747461|AW747461 WS1_68 B01.g1_A002 Water-stressed 1 (WS1) ... 181 1e-51
 emb|AI162776|AI162776 A023P56U Hybrid aspen plasmid library Populus... 132 7e-51
 gb|BE054071|BE054071 GA_Ea0035D19f Gossypium arboreum 7-10 dpa ... 93 4e-50
 gb|C96251|C96251 C96251 Marchantia polymorpha immature sex organ... 98 5e-50
 emb|AI442544|AI442544 sa32h03.y1 Gm-c1004 Glycine max cDNA clone... 196 2e-49
 60 emb|AI164569|AI164569 A065P13U Hybrid aspen plasmid library Populus... 180 2e-48
 emb|AW888188|AW888188 NXNV_105_F04_F Nsf Xylem Normal wood Vertical... 183 1e-45

- emb|AI855650|AI855650 sc32c06.y1 Gm-c1014 Glycine max cDNA clone... 127 3e-45
 emb|AI777234|AI777234 EST258199 tomato resistant, Cornell Lycopersicon... 148 1e-44
 emb|AI165310|AI165310 A081P03U Hybrid aspen plasmid library Popu... 152 7e-44
 emb|AW870064|AW870064 NXNV_123_F09_F Nsf Xylem Normal wood Verti... 176 1e-43
 5 emb|AI484178|AI484178 EST249331 tomato resistant, Cornell Lycopersicon... 144 2e-43
 emb|AI162101|AI162101 A012P21U Hybrid aspen plasmid library Popu... 164 3e-42
 emb|AW255890|AW255890 ML976 peppermint glandular trichome Mentha... 143 7e-42
 emb|AW733771|AW733771 sk84b01.y1 Gm-c1035 Glycine max cDNA clone... 149 7e-42
 emb|AW010084|AW010084 PC01E03 Pine TriplEx pollen cone library P... 160 7e-39
 10 emb|AI161700|AI161700 A005P46U Hybrid aspen plasmid library Popu... 150 3e-38
 emb|AW443795|AW443795 EST308725 tomato mixed elicitor, BTI Lycopersicon... 157 6e-38
 emb|AI774615|AI774615 EST255715 tomato resistant, Cornell Lycopersicon... 157 6e-38
 emb|AW651357|AW651357 EST329811 tomato germinating seedlings, TA... 157 6e-38
 emb|AW623884|AW623884 EST321829 tomato flower buds 3-8 mm, Corne... 157 6e-38
 15 emb|AI484189|AI484189 EST249342 tomato resistant, Cornell Lycopersicon... 157 9e-38
 gb|L37653|L37653 BNAESTGU Mustard flower buds Brassica rapa cDNA... 156 1e-37
 emb|AW944894|AW944894 EST336944 tomato flower buds 3-8 mm, Corne... 154 8e-37
 emb|AW726742|AW726742 GA_Ea0022J15 Gossypium arboreum 7-10 dpa ... 152 2e-36
 emb|AW694116|AW694116 NF072H11ST1F1095 Developing stem Medicago ... 150 2e-36
 20 emb|AW649234|AW649234 EST327688 tomato germinating seedlings, TA... 151 5e-36
 emb|AW725828|AW725828 GA_Ea0019N04 Gossypium arboreum 7-10 dpa ... 95 8e-36
 emb|AI777997|AI777997 EST258876 tomato susceptible, Cornell Lycopersicon... 149 3e-35
 emb|AW317704|AW317704 sg56c06.y1 Gm-c1007 Glycine max cDNA clone... 148 4e-35
 emb|AW432260|AW432260 sh71d04.y1 Gm-c1015 Glycine max cDNA clone... 143 2e-33
 25 emb|AI165031|AI165031 A073p61u Hybrid aspen plasmid library Popu... 131 6e-32
 emb|AI507718|AI507718 sb10g09.y1 Gm-c1004 Glycine max cDNA clone... 131 2e-31
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 emb|AV428084|AV428084 AV428084 Lotus japonicus young plants (two... 127 1e-28
 30 emb|AI899479|AI899479 EST268922 tomato susceptible, Cornell Lycopersicon... 124 7e-28
 emb|AI460396|AI460396 sa81a06.y1 Gm-c1004 Glycine max cDNA clone... 119 2e-26
 emb|AT002745|AT002745 AT002745 POSLM01 Pleurotus ostreatus cDNA ... 116 9e-26
 emb|AW508566|AW508566 si33e04.y1 Gm-r1030 Glycine max cDNA clone... 115 4e-25
 emb|AI166161|AI166161 B00964U Hybrid aspen plasmid library Popu... 113 1e-24

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 dehydrogenase [arabidopsis thaliana] /blast_score 0
 (3267 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

- emb|AI486200|AI486200 EST244521 tomato ovary, TAMU Lycopersicon ... 377 e-103
 50 emb|AI894899|AI894899 EST264342 tomato callus, TAMU Lycopersicon... 357 4e-97
 emb|AI488742|AI488742 EST247081 tomato ovary, TAMU Lycopersicon ... 347 2e-94
 emb|AF042184|AF042184 Brassica napus lysine-ketoglutarate reduct... 334 1e-93
 emb|AI054604|AI054604 coau0001I01 Cotton Boll Abscission Zone cD... 319 3e-92
 emb|AW034280|AW034280 EST277851 tomato callus, TAMU Lycopersicon... 316 7e-85
 55 emb|AI894874|AI894874 EST264317 tomato callus, TAMU Lycopersicon... 307 4e-82
 emb|AW932187|AW932187 EST358030 tomato fruit mature green, TAMU ... 294 2e-78
 emb|AW933092|AW933092 EST358935 tomato fruit mature green, TAMU ... 287 4e-76
 emb|AW442160|AW442160 EST311556 tomato fruit red ripe, TAMU Lycopersicon... 220 8e-74
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 60 emb|AW933411|AW933411 EST359350 tomato fruit mature green, TAMU ... 272 1e-71
 emb|AW931846|AW931846 EST357689 tomato fruit mature green, TAMU ... 264 3e-69

- emb|AI485129|AI485129 EST243433 tomato ovary, TAMU Lycopersicon ... 253 8e-66
emb|AW035300|AW035300 EST280663 tomato callus, TAMU Lycopersicon... 241 3e-62
emb|AW934545|AW934545 EST353353 tomato flower buds 0-3 mm, Corne... 230 4e-59
5 emb|AI771941|AI771941 EST253041 tomato ovary, TAMU Lycopersicon ... 228 2e-58
emb|AL022244|SPBC3B8 *S.pombe* chromosome II cosmid c3B8. 181 2e-56
emb|AW037965|AW037965 EST279609 tomato mixed elicitor, BTI Lycop... 211 2e-53
emb|AW931630|AW931630 EST357473 tomato fruit mature green, TAMU ... 208 3e-52
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10 emb|AI896768|AI896768 EST266211 tomato callus, TAMU Lycopersicon... 192 2e-47
emb|Z71665|SCYNR050C *S.cerevisiae* chromosome XIV reading frame O... 155 5e-47
emb|X77363|SCLYS9 *S.cerevisiae* LYS9 gene. 155 5e-47
emb|AW224200|AW224200 EST301107 tomato fruit red ripe, TAMU Lyco... 188 2e-46
emb|AW930672|AW930672 EST356515 tomato fruit mature green, TAMU ... 110 4e-45
emb|AI771935|AI771935 EST253035 tomato ovary, TAMU Lycopersicon ... 173 6e-42
15 emb|AI899372|AI899372 EST268815 tomato ovary, TAMU Lycopersicon ... 172 1e-41
emb|AI486726|AI486726 EST245048 tomato ovary, TAMU Lycopersicon ... 110 2e-40
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20 emb|AI488387|AI488387 EST246709 tomato ovary, TAMU Lycopersicon ... 160 6e-38
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emb|AV427683|AV427683 AV427683 *Lotus japonicus* young plants (two... 142 2e-32
emb|AI782310|AI782310 EST263189 tomato susceptible, Cornell Lyco... 139 1e-31
emb|AW432287|AW432287 sh71g03.y1 Gm-c1015 Glycine max cDNA clone... 82 6e-31
25 emb|AL111972|CNS019QK *Botrytis cinerea* strain T4 cDNA library un... 136 1e-30
emb|AU012735|AU012735 AU012735 *Schizosaccharomyces pombe* late lo... 125 5e-30
emb|AI771382|AI771382 EST252482 tomato ovary, TAMU Lycopersicon ... 132 1e-29
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30 emb|AW038858|AW038858 EST280814 tomato mixed elicitor, BTI Lycop... 114 5e-24
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emb|AI399018|AI399018 NCW10A5T3 *Westergaards Neurospora crassa* c... 63 1e-21
35 emb|AW031018|AW031018 EST274325 tomato callus, TAMU Lycopersicon... 101 4e-20
emb|AW932183|AW932183 EST358026 tomato fruit mature green, TAMU ... 72 9e-13
emb|AW096237|AW096237 EST289417 tomato mixed elicitor, BTI Lycop... 67 8e-10
emb|AA577639|AA577639 EST213 Sugarcane leaf roll *Saccharum* sp. c... 65 3e-09
emb|AW224318|AW224318 EST301045 tomato fruit red ripe, TAMU Lyco... 51 5e-05
40 emb|AI900022|AI900022 sb97g03.y1 Gm-c1012 Glycine max cDNA clone... 50 1e-04
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emb|Z38061|SC9168 *S.cerevisiae* chromosome IX cosmid 9168. 45 0.004
emb|X77362|SCLYS1 *S.cerevisiae* LYS1 gene. 45 0.004
emb|AQ448181|AQ448181 mgxb0018C10r CUGI Rice Blast BAC Library P... 41 0.041
45 gb|U13233|CAU13233 *Candida albicans* saccharopine dehydrogenase (... 40 0.078
emb|AL110979|CNS018Z0 *Botrytis cinerea* strain T4 cDNA library un... 35 0.079
emb|AL133156|SPAC227 *S.pombe* chromosome I cosmid c227. 40 0.15
emb|AF178855|AF178855 *Candida albicans* Crm1p (CRM1) gene, comple... 37 0.99
emb|AI667978|AI667978 TENG0800 *T. Cruzi* epimastigote normalised ... 36 1.4
50 emb|AW310192|AW310192 sf32e10.x1 Gm-c1028 Glycine max cDNA clone... 36 1.4
emb|AW705872|AW705872 sk52a01.y1 Gm-c1019 Glycine max cDNA clone... 35 2.6
emb|AL355930|NCB208 *Neurospora crassa* DNA linkage group II BAC c... 35 3.5
gb|N82089|N82089 TgESTzy41f01.r1 TgRH Tachyzoite cDNA *Toxoplasma*... 35 3.5
emb|AW713255|AW713255 g6f04ne.fl *Neurospora crassa* evening cDNA ... 33 4.1
55 emb|AW710105|AW710105 elc07ne.fl *Neurospora crassa* evening cDNA ... 33 4.1
emb|AW712320|AW712320 gla02ne.fl *Neurospora crassa* evening cDNA ... 33 4.2
emb|AA451583|AA451583 AJK252 Onion seedling leaf cDNA library Al... 35 4.8
emb|AQ660868|AQ660868 Sheared DNA-27G4.TF Sheared DNA *Trypanosom*... 35 4.8
emb|AI773473|AI773473 EST254573 tomato resistant, Cornell Lycop... 30 5.4
60 emb|X99000|CS39KBCIV *S.cerevisiae* 39kb DNA segment of chromosome... 34 6.7
gb|BE021261|BE021261 sm56g06.y1 Gm-c1028 Glycine max cDNA clone ... 34 6.7

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	emb Z74265 SCYDL217C S.cerevisiae chromosome IV reading frame OR...	34	6.7
	emb Z73529 SCYPL173W S.cerevisiae chromosome XVI reading frame O...	34	6.7
	emb AI486066 AI486066 EST244387 tomato ovary, TAMU Lycopersicon ...	34	6.7
5	emb AV420631 AV420631 AV420631 Lotus japonicus young plants (two...	34	6.7
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	emb AL049181 PFMAL13P4 Plasmodium falciparum chromosome 13 strai...	34	9.2
	emb AW278000 AW278000 sf89e04.y1 Gm-cl019 Glycine max cDNA clone...	34	9.2
	emb AL033391 CAC20C1 C.albicans cosmid Ca20C1.	34	9.2
10	emb AF202183 AF202183 Glycine max isoflavone reductase homolog 1...	34	9.2
	emb AW648458 AW648458 EST326912 tomato germinating seedlings, TA...	34	9.2
	emb AA051847 AA051847 Cn0025-5 Cryptococcus neoformans, Stratage...	34	9.2
	emb AI960767 AI960767 sc90b07.y1 Gm-cl019 Glycine max cDNA clone...	34	9.2
	emb Z49384 SCYJL109C S.cerevisiae chromosome X reading frame ORF...	34	9.2
15	emb AF106954 AF106954 Brassica napus galactinol synthase (GS) mR...	34	9.2
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	emb AW455238 AW455238 EST311898 tomato root during/after fruit s...	229	1e-63
	emb AW568861 AW568861 si73b10.y1 Gm-cl031 Glycine max cDNA clone...	139	3e-61
40	emb AI487264 AI487264 EST245586 tomato ovary, TAMU Lycopersicon ...	205	1e-55
	emb AI485585 AI485585 EST243906 tomato ovary, TAMU Lycopersicon ...	205	1e-54
	emb AW667985 AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ...	128	4e-54
	emb AI485223 AI485223 EST243527 tomato ovary, TAMU Lycopersicon ...	203	5e-54
	emb AI897690 AI897690 EST267133 tomato ovary, TAMU Lycopersicon ...	205	7e-54
45	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	162	1e-53
	emb AI486547 AI486547 EST244868 tomato ovary, TAMU Lycopersicon ...	150	1e-53
	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	165	1e-53
	emb AI489882 AI489882 EST248221 tomato ovary, TAMU Lycopersicon ...	205	3e-53
	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	168	5e-53
50	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	163	9e-53
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	170	8e-52
	emb AI485022 AI485022 EST243302 tomato ovary, TAMU Lycopersicon ...	205	1e-51
	emb AI484547 AI484547 EST242777 tomato ovary, TAMU Lycopersicon ...	205	1e-51
	emb AI484020 AI484020 EST249891 tomato ovary, TAMU Lycopersicon ...	205	1e-51
55	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	160	2e-51
	emb AF142596 AF142596 Nicotiana tabacum LRR receptor-like protei...	144	2e-51
	emb AW616916 AW616916 EST323327 L. hirsutum trichome, Cornell Un...	145	3e-51
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	165	1e-50
	emb AI487456 AI487456 EST245778 tomato ovary, TAMU Lycopersicon ...	139	3e-50
60	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	154	7e-50
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	164	7e-50

- emb|AF220602|AF220602 *Lycopersicon pimpinellifolium* Rio Grande 7... 96 2e-49
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5 emb|AB008191|AB008191 *Brassica rapa* mRNA for SRK29, complete cds. 154 4e-48
emb|AI898374|AI898374 EST267817 tomato ovary, TAMU *Lycopersicon* ... 192 1e-47
emb|AI484550|AI484550 EST242780 tomato ovary, TAMU *Lycopersicon* ... 191 2e-47
emb|AI967314|AI967314 Ljirmp00-017 Ljirmp Lambda HybriZap two... 89 3e-47
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10 emb|X98520|BOSFR2 *B. oleracea* mRNA for receptor-like kinase, SFR2. 153 7e-47
emb|Y18259|BOY18259 *Brassica oleracea* mRNA for SRK5 protein, par... 152 7e-47
emb|AI483733|AI483733 EST249604 tomato ovary, TAMU *Lycopersicon* ... 188 1e-46
emb|AB032474|AB032474 *Brassica oleracea* SRK60 mRNA for S60 S-loc... 127 1e-46
emb|Y18260|BOY18260 *Brassica oleracea* mRNA for SRK15 protein, pa... 150 1e-46
15 gb|U20948|ITU20948 *Ipomoea trifida* receptor protein kinase (IRK1)... 126 2e-46
gb|BE060160|BE060160 HVSMEg0011B12f *Hordeum vulgare* pre-anthesis... 151 3e-46
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emb|AF088885|AF088885 *Nicotiana tabacum* receptor-like kinase CHR... 156 6e-46
emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem *Medicago* ... 185 9e-46
20 emb|Y14286|BOY14286 *Brassica oleracea* SFR3 gene, partial. 91 1e-45
emb|AW774582|AW774582 EST333733 KV3 *Medicago truncatula* cDNA clo... 81 1e-45
emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber *Gossypium*... 81 1e-45
dbj|D38563|BOLRPKA *Brassica campestris* mRNA for receptor protein... 127 2e-45
dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 134 2e-45
25 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 145 2e-45
emb|AI898918|AI898918 EST268361 tomato ovary, TAMU *Lycopersicon* ... 183 5e-45
emb|AF131222|AF131222 *Lophopyrum elongatum* protein serine/threon... 138 2e-44
emb|AW756743|AW756743 sl26f10.y1 Gm-c1027 *Glycine max* cDNA clone... 181 2e-44
emb|AF220603|AF220603 *Lycopersicon esculentum* VFNT Cherry Pto lo... 96 2e-44
30 emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber *Gossypium* ... 132 3e-44
emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 151 4e-44
emb|AI489009|AI489009 EST247348 tomato ovary, TAMU *Lycopersicon* ... 117 7e-44
emb|AI483732|AI483732 EST249603 tomato ovary, TAMU *Lycopersicon* ... 177 4e-43
emb|AA738545|AA738545 SbRLK3 *Sorghum bicolor* cv. TX430 leaf Sorg... 153 6e-43
35 gb|U59315|LPU59315 *Lycopersicon pimpinellifolium* serine/threonin... 88 1e-42
gb|U02271|LEU02271 *Lycopersicon pimpinellifolium* Rio Grande-PtoR... 88 1e-42
emb|AJ245479|BNA245479 *Brassica napus* Sll3, slk, srk, CePP, Fmt,... 80 2e-42
emb|AI490032|AI490032 EST248371 tomato ovary, TAMU *Lycopersicon* ... 149 2e-42
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40 gb|U28007|LEU28007 *Lycopersicon esculentum* Pto kinase interactor... 83 3e-42
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emb|AW031255|AW031255 EST274630 tomato callus, TAMU *Lycopersicon*... 149 6e-42
emb|AW684940|AW684940 NF023C12NR1F1000 Nodulated root *Medicago* t... 113 6e-42
emb|AB000971|AB000971 *Brassica campestris* pseudogene for recepto... 78 8e-42
45 gb|U59316|LEU59316 *Lycopersicon esculentum* serine/threonine prot... 87 1e-41
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dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 81 2e-41
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50 emb|AB041503|AB041503 *Populus nigra* PnPK1 mRNA for protein kinas... 77 3e-41
emb|AW220489|AW220489 EST297042 tomato fruit mature green, TAMU ... 112 3e-41
emb|AI937984|AI937984 sc06e07.y1 Gm-c1012 *Glycine max* cDNA clone... 170 5e-41
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55 emb|AA738544|AA738544 SbRLK2 *Sorghum bicolor* cv. TX430 leaf Sorg... 122 1e-40
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gb|U59317|LPU59317 *Lycopersicon pimpinellifolium* serine/threonin... 93 3e-40
gb|U13923|LEU13923 *Lycopersicon pimpinellifolium* serine/threonin... 93 3e-40
emb|Z73295|CRPK1 *C. roseus* mRNA for receptor-like protein kinase. 74 5e-40
60 gb|U59318|LEU59318 *Lycopersicon esculentum* serine/threonine prot... 92 6e-40
emb|AW729859|AW729859 GA_Ea0026H04 *Gossypium arboreum* 7-10 dpa ... 81 1e-39

emb|AW982539|AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi... 129 1e-39.
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 5 emb|AW284352|AW284352 LG1_275_D12.g1_A002 Light Grown 1 (LG1) So... 165 2e-39
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 10 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 71 5e-39
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 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 73 3e-38
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 20 (2127 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AW625643 AW625643 EST319550 tomato radicle, 5 d post-imbibit...	377	e-103	
	emb AW688234 AW688234 NF005A05ST1F1000 Developing stem Medicago ...	367	e-100	
	emb AW666282 AW666282 sk34f11.y1 Gm-c1028 Glycine max cDNA clone...	360	2e-98	
35	emb AW691093 AW691093 NF041B09ST1F1000 Developing stem Medicago ...	332	5e-96	
	gb BE055044 BE055044 GA_Ea0031H08f Gossypium arboreum 7-10 dpa ...	332	9e-95	
	emb AW696933 AW696933 NF112E03ST1F1021 Developing stem Medicago ...	347	3e-94	
	emb AW926942 AW926942 HVSMEg0009B01 Hordeum vulgare pre-anthesis...	295	6e-89	
	emb AW737130 AW737130 EST338557 tomato flower buds, anthesis, Co...	325	1e-87	
	emb AW689358 AW689358 NF018C09ST1F1000 Developing stem Medicago ...	281	3e-85	
40	emb AW650696 AW650696 EST329150 tomato germinating seedlings, TA...	179	2e-84	
	emb AW625020 AW625020 EST313849 tomato radicle, 5 d post-imbibit...	301	1e-80	
	emb AI813214 AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta...	297	2e-80	
	emb AW692700 AW692700 NF054C07ST1F1000 Developing stem Medicago ...	279	6e-80	
	gb BE036418 BE036418 MO24D12 MO Mesembryanthemum crystallinum cD...	258	2e-79	
45	gb BE020170 BE020170 sm39e05.y1 Gm-c1028 Glycine max cDNA clone ...	293	3e-78	
	emb AW423801 AW423801 sh52b02.y1 Gm-c1017 Glycine max cDNA clone...	293	4e-78	
	emb AW731385 AW731385 GA_Ea0030K22 Gossypium arboreum 7-10 dpa ...	289	6e-77	
	gb BE052354 BE052354 GA_Ea0034P16f Gossypium arboreum 7-10 dpa ...	282	5e-75	
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50	emb AW926887 AW926887 HVSMEg0008N09 Hordeum vulgare pre-anthesis...	264	1e-69	
	emb AW944677 AW944677 00152 leafy spurge Lambda HybriZAP 2.1 two...	248	1e-64	
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	emb AW755716 AW755716 sl08b12.y1 Gm-c1036 Glycine max cDNA clone...	234	2e-60	
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55	gb BE060782 BE060782 HVSMEg0013F14f Hordeum vulgare pre-anthesis...	226	7e-58	
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	emb AW398821 AW398821 EST309321 L. pennellii trichome, Cornell U...	177	2e-43	
	emb AW650818 AW650818 EST329272 tomato germinating seedlings, TA...	148	2e-42	
60	emb AW697347 AW697347 NF115F08ST1F1074 Developing stem Medicago ...	168	2e-40	
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emb|AV395160|AV395160 AV395160 Chlamydomonas reinhardtii C9 Chla... 164 2e-39
emb|AW907004|AW907004 EST343231 potato stolon, Cornell Universit... 163 5e-39
5 emb|AW736943|AW736943 NXNV_081_H10_F Nsf Xylem Normal wood Vertic... 161 1e-38
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gb|L47851|L47851 BNAF1389 Mustard flower buds Brassica rapa cDNA... 155 1e-36
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10 emb|AA660997|AA660997 00894 MtRHE Medicago truncatula cDNA 5' si... 72 2e-34
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emb|AI165568|AI165568 A086P59U Hybrid aspen plasmid library Popu... 137 1e-31
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15 emb|Z97052|SPCC4G3 S.pombe chromosome III cosmid c4G3. 82 7e-30
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emb|AA840711|AA840711 CAN22 Anther cDNA library of Hot pepper Ca... 93 5e-28
emb|AW688606|AW688606 NF009E07ST1F1000 Developing stem Medicago ... 124 2e-27
20 emb|AC005761|AC005761 Leishmania major chromosome 3 clone L952 s... 78 5e-27
emb|AL157811|SPAC186 S.pombe chromosome I cosmid c186. 90 2e-26
gb|U18839|SCE9747 Saccharomyces cerevisiae chromosome V cosmids ... 80 2e-23
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emb|Z37997|SC9877 S.cerevisiae chromosome IX cosmid 9877. 80 2e-22
25 emb|AW689996|AW689996 NF026G01ST1F1000 Developing stem Medicago ... 91 7e-20
emb|AL031180|SPUNK4 S.pombe chromosome I cosmid c2E11. 99 2e-19
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gb|U43503|SCU43503 Saccharomyces cerevisiae chromosome XVI cosmi... 84 3e-15
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35 emb|AI486949|AI486949 EST245271 tomato ovary, TAMU Lycopersicon ... 83 1e-14
emb|Z71550|SCYNL274C S.cerevisiae chromosome XIV reading frame O... 83 1e-14
emb|AW442114|AW442114 EST311510 tomato fruit red ripe, TAMU Lyco... 83 1e-14
emb|AW030822|AW030822 EST274077 tomato callus, TAMU Lycopersicon... 83 1e-14
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40 emb|AW442123|AW442123 EST311519 tomato fruit red ripe, TAMU Lyco... 83 1e-14
emb|AW651324|AW651324 EST329778 tomato germinating seedlings, TA... 83 1e-14
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emb|Z21493|MISTFDHD S.tuberosum mRNA for formate dehydrogenase. 83 1e-14
emb|AI822999|AI822999 L30-850T3 Ice plant Lambda Uni-Zap XR expr... 82 1e-14
45 emb|AW693443|AW693443 NF065D03ST1F1000 Developing stem Medicago ... 71 2e-14
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emb|AT000538|AT000538 AT000538 Brassica rapa guard cell Brassica... 80 7e-14
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emb|AW037837|AW037837 EST279466 tomato mixed elicitor, BTI Lycop... 75 2e-12
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15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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20 Score E
 Sequences producing significant alignments: (bits) Value

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 25 emb|AI485780|AI485780 EST244101 tomato ovary, TAMU Lycopersicon ... 242 2e-86
 emb|AI485695|AI485695 EST244016 tomato ovary, TAMU Lycopersicon ... 261 5e-86
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 emb|AI897089|AI897089 EST266532 tomato ovary, TAMU Lycopersicon ... 226 8e-58
 35 emb|AW774994|AW774994 EST334145 KV3 *Medicago truncatula* cDNA clo... 182 3e-56
 emb|AW559604|AW559604 EST314652 *DSIR Medicago truncatula* cDNA cl... 177 4e-53
 emb|AI485284|AI485284 EST243588 tomato ovary, TAMU Lycopersicon ... 206 5e-52
 emb|AI485664|AI485664 EST243985 tomato ovary, TAMU Lycopersicon ... 198 2e-49
 emb|AW774741|AW774741 EST333892 KV3 *Medicago truncatula* cDNA clo... 90 2e-48
 40 emb|AI487608|AI487608 EST245930 tomato ovary, TAMU Lycopersicon ... 187 3e-46
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 45 emb|AW775688|AW775688 EST334753 *DSIL Medicago truncatula* cDNA cl... 108 8e-34
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 emb|AW257207|AW257207 EST305344 KV2 *Medicago truncatula* cDNA clo... 75 2e-24
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	emb AI771644 AI771644 EST252744 tomato ovary, TAMU Lycopersicon ...	104	4e-21
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	emb AW616540 AW616540 EST322951 L. hirsutum trichome, Cornell Un...	98	2e-19
	emb AL110506 SPBC577 S.pombe chromosome II cosmid c577.	74	2e-18
	emb AW126841 AW126841 ga16f04.y1 Moss EST library PPU Physcomitr...	94	4e-18
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10	emb AW687035 AW687035 NF005C05RT1F1037 Developing root Medicago ...	73	2e-17
	emb AW685930 AW685930 NF036F03NR1F1000 Nodulated root Medicago t...	73	2e-17
	emb AV415287 AV415287 AV415287 Lotus japonicus young plants (two...	90	5e-17
	gb BE124605 BE124605 EST393640 GVN Medicago truncatula cDNA clon...	65	6e-15
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	emb AW666237 AW666237 sk34b04.y1 Gm-c1028 Glycine max cDNA clone...	77	5e-13
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25	emb AZ048449 AZ048449 PSB67 Barley PstI genomic clones Hordeum v...	67	8e-10
	emb AW760518 AW760518 sl51d02.y1 Gm-c1027 Glycine max cDNA clone...	66	1e-09
	emb AW332143 AW332143 S4G7 AGS-1 Pneumocystis carinii f. sp. car...	36	1e-09
	emb AW687790 AW687790 NF013E04RT1F1034 Developing root Medicago ...	65	3e-09
	emb AI486692 AI486692 EST245014 tomato ovary, TAMU Lycopersicon ...	54	3e-09
30	emb AW333870 AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c...	36	5e-09
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	emb AW127178 AW127178 M110117 GVN Medicago truncatula cDNA clone...	63	1e-08
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45	emb AQ655271 AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso...	38	0.004
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	emb AW437996 AW437996 ST83C09 Pine TriplEx shoot tip library Pin...	42	0.016
	emb AI440709 AI440709 sa62e11.y1 Gm-c1004 Glycine max cDNA clone...	31	0.045
	emb AW979881 AW979881 EST341528 tomato root deficiency, Cornell ...	37	0.54
50	emb AF263282 AF263282 Filobasidiella neoformans var. neoformans ...	34	0.64
	emb AW702543 AW702543 TgESTzz85a12.y1 TgRH*-Tachyzoite cDNA Toxo...	32	0.69
	emb AZ214873 AZ214873 Sheared DNA-109E2.TR Sheared DNA Trypanoso...	37	0.74
	emb AQ939979 AQ939979 Sheared DNA-42A15.TF Sheared DNA Trypanoso...	37	0.74
	emb AQ651205 AQ651205 Sheared DNA-30N15.TF Sheared DNA Trypanoso...	37	0.74
55	emb AQ945454 AQ945454 Sheared DNA-54H22.TF Sheared DNA Trypanoso...	37	0.74
	emb AW774740 AW774740 EST333891 KV3 Medicago truncatula cDNA clo...	36	1.4
	emb Z38060 SC5610 S.cerevisiae chromosome IX sequence derived fr...	36	1.4
	emb AL049183 PFMAL13P6 Plasmodium falciparum chromosome 13 strai...	35	2.6
	gb M28064 PFAHRKP Plasmodium brasilianum DNA homologous to the h...	35	2.6
60	emb AI482770 AI482770 EST242093 tomato shoot, Cornell Lycopersic...	35	2.6
	emb AQ653909 AQ653909 Sheared DNA-1G20.TR Sheared DNA Trypanosom...	35	2.6

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 (938 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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15	Sequences producing significant alignments:				
	gb U68763	GMU68763	Glycine max putative transcription factor SCO...	71	1e-35
	emb Y18788	MSY18788	Medicago sativa mRNA for putative TFIIIA (or...	71	3e-35
	emb AF053077	AF053077	Nicotiana tabacum osmotic stress-induced z...	70	3e-33
20	emb AW729218	AW729218	GA_Ea0024G18 Gossypium arboreum 7-10 dpa ...	71	5e-33
	emb AW781249	AW781249	sk67b08.y1 Gm-c1016 Glycine max cDNA clone...	70	7e-31
	dbj D26086	PETZFP4	Petunia zinc-finger protein gene.	68	3e-30
	emb AW560934	AW560934	EST315982 DSIR Medicago truncatula cDNA cl...	68	8e-30
	emb AW775559	AW775559	EST334624 DSIL Medicago truncatula cDNA cl...	70	1e-29
	gb BE123920	BE123920	EST394045 DSIL Medicago truncatula cDNA clp...	70	1e-29
25	emb AI988657	AI988657	sd06b03.y1 Gm-c1020 Glycine max cDNA clone...	70	9e-29
	emb AW102472	AW102472	sd88f02.y1 Gm-c1009 Glycine max cDNA clone...	64	1e-28
	dbj D26084	PETZFDB2	Petunia mRNA for zinc-finger DNA binding pro...	69	1e-28
	dbj D26083	PETZFDB1	Petunia hybrida gene for zinc-finger DNA bin...	68	4e-28
	emb AI988290	AI988290	sc98f10.y1 Gm-c1020 Glycine max cDNA clone...	64	3e-27
30	emb AW706944	AW706944	sk08e10.y1 Gm-c1023 Glycine max cDNA clone...	69	2e-26
	emb AW153229	AW153229	se37f05.y1 Gm-c1015 Glycine max cDNA clone...	69	3e-26
	emb AW616587	AW616587	EST322998 L. hirsutum trichome, Cornell Un...	68	5e-26
	gb BE095284	BE095284	00345 leafy spurge Lambda HybriZAP 2.1 two...	69	5e-26
	emb AW278572	AW278572	sf46c03.y1 Gm-c1009 Glycine max cDNA clone...	65	8e-26
35	emb AI487287	AI487287	EST245609 tomato ovary, TAMU Lycopersicon ...	68	9e-26
	dbj D26085	PETZFDB3	Petunia zinc-finger DNA binding protein gene.	60	1e-25
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	emb AW279005	AW279005	sg04d04.y1 Gm-c1019 Glycine max cDNA clone...	67	2e-25
	emb AW164639	AW164639	se74f02.y1 Gm-c1023 Glycine max cDNA clone...	67	2e-25
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	emb AI488218	AI488218	EST246540 tomato ovary, TAMU Lycopersicon ...	62	9e-24
	emb AW037956	AW037956	EST279600 tomato mixed elicitor, BTI Lycop...	59	4e-23
	emb Y16131	Y16131	Y16131 young root nodules Medicago sativa subs...	67	8e-23
	emb AW030858	AW030858	EST274148 tomato callus, TAMU Lycopersicon...	66	9e-23
50	emb AW032112	AW032112	EST275566 tomato callus, TAMU Lycopersicon...	68	5e-22
	emb AW625323	AW625323	EST319146 tomato radicle, 5 d post-imbibit...	59	8e-21
	emb AW033257	AW033257	EST276828 tomato callus, TAMU Lycopersicon...	66	2e-20
	emb AI485651	AI485651	EST243972 tomato ovary, TAMU Lycopersicon ...	62	2e-20
	emb AW033574	AW033574	EST277145 tomato callus, TAMU Lycopersicon...	66	2e-20
55	emb AI896031	AI896031	EST265474 tomato callus, TAMU Lycopersicon...	66	3e-20
	emb AI771191	AI771191	EST252387 tomato ovary, TAMU Lycopersicon ...	66	3e-20
	emb AW032357	AW032357	EST275811 tomato callus, TAMU Lycopersicon...	66	3e-20
	emb AW219736	AW219736	EST302218 tomato root during/after fruit s...	59	1e-19
	emb AW219517	AW219517	EST301915 tomato root during/after fruit s...	59	2e-19
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	gb BE021759 BE021759 sm62a09.y1 Gm-c1028 Glycine max cDNA clone ... 71 3e-17
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon... 55 4e-17
	emb AW720367 AW720367 LjNEST21g11r Lotus japonicus nodule librar... 64 6e-17
5	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA... 59 9e-17
	emb AB000455 AB000455 Petunia hybrida mRNA for PETHy;ZPT4-1, com... 60 1e-16
	gb BE058334 BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone ... 62 1e-16
	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon... 55 2e-16
10	emb AV422432 AV422432 AV422432 Lotus japonicus young plants (two... 66 3e-16
	emb AW277333 AW277333 sf80a11.y1 Gm-c1019 Glycine max cDNA clone... 64 4e-16
	emb AI900061 AI900061 sb98d02.y1 Gm-c1012 Glycine max cDNA clone... 64 5e-16
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	emb AI960244 AI960244 sc80g07.y1 Gm-c1018 Glycine max cDNA clone... 64 7e-16
	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD... 62 1e-15
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	emb AI894999 AI894999 EST264442 tomato callus, TAMU Lycopersicon... 68 9e-15
	emb AW622660 AW622660 EST313460 tomato root during/after fruit s... 68 9e-15
	emb AW755973 AW755973 sl11h06.y1 Gm-c1036 Glycine max cDNA clone... 64 4e-14
20	emb AI938565 AI938565 sb55e03.y1 Gm-c1018 Glycine max cDNA clone... 64 4e-14
	emb AB035133 AB035133 Petunia x hybrida gene for C2H2 zinc-finge... 52 1e-13
	emb AB006605 AB006605 Petunia x hybrida mRNA for ZPT3-3, complet... 52 1e-13
	emb AB035132 AB035132 Petunia x hybrida gene for C2H2 zinc-finge... 50 4e-13
	emb AB006597 AB006597 Petunia x hybrida mRNA for ZPT2-10, comple... 50 4e-13
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	emb AW776204 AW776204 EST335269 DSIL Medicago truncatula cDNA cl... 65 1e-12
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	emb AW738399 AW738399 EST339826 tomato flower buds, anthesis, Co... 59 2e-11
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60 (1352 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments: (bits) Value

10	emb AJ000728 LEAJ728 Lycopersicon esculentum mRNA for MAP kinase... 555 e-157
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	emb AW945105 AW945105 EST337156 tomato flower buds 3-8 mm, Corne... 318 6e-86
	emb AW756736 AW756736 sl26f02.y1 Gm-c1027 Glycine max cDNA clone... 174 9e-75
	dbj D31964 TOBNPK2 Tobacco mRNA for protein kinase (NPK2), compl... 183 8e-65
	gb BE054500 BE054500 GA_Ea0031F11f Gossypium arboreum 7-10 dpa ... 165 1e-59
15	emb AW220008 AW220008 EST302491 tomato root during/after fruit s... 228 6e-59
	emb AW624623 AW624623 EST322568 tomato flower buds 3-8 mm, Corne... 215 9e-55
	emb AI438023 AI438023 sa34h10.y1 Gm-c1004 Glycine max cDNA clone... 208 7e-53
	emb AW617901 AW617901 EST296829 L. hirsutum trichome, Cornell Un... 203 2e-51
	emb AJ007393 YLI7393 Yarrowia lipolytica ste7 gene. 92 4e-49
20	emb AW931392 AW931392 EST357235 tomato fruit mature green, TAMU ... 189 3e-47
	emb AW039087 AW039087 EST281060 tomato mixed elicitor, BTI Lycop... 183 2e-45
	emb Z99259 SPAC2C4 S.pombe chromosome I cosmid c2C4. 85 6e-43
	emb AW032808 AW032808 EST276367 tomato callus, TAMU Lycopersicon... 175 9e-43
	gb U07801 UMU07801 Ustilago maydis serine/threonine/tyrosine kin... 121 2e-42
25	emb AJ009609 BNA9609 Brassica napus mRNA for MAP4K alpha2 protein. 87 1e-41
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35	gb L19195 YSASTKIN Candida albicans (clone pKB66) serine/threoni... 128 2e-37
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	gb U43703 SCU43703 Saccharomyces cerevisiae chromosome XVI cosmi... 68 2e-37
	emb X62631 SPWIS1 S.pombe wis1 gene for protein kinase. 68 3e-37
	emb AW625928 AW625928 EST319823 tomato radicle, 5 d post-imbibit... 90 8e-37
40	emb AW348493 AW348493 GM210002B12A8R Gm-r1021 Glycine max cDNA 3... 154 1e-36
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	emb Z49403 SCYJL128C S.cerevisiae chromosome X reading frame ORF... 78 5e-35
45	gb U12237 SCU12237 Saccharomyces cerevisiae suppressor of fluori... 78 5e-35
	gb J02946 YSCPBS2 Saccharomyces cerevisiae putative protein kina... 78 5e-35
	emb AJ243184 LIN243184 Leishmania infantum mkk gene for putative... 78 2e-34
	emb AW032663 AW032663 EST276222 tomato callus, TAMU Lycopersicon... 82 2e-34
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60	emb AW981083 AW981083 EST392236 GVN Medicago truncatula cDNA clo... 88 3e-31
	gb BE036317 BE036317 MO23C02 MO Mesembryanthemum crystallinum cD... 82 1e-30

- emb|AF069777|AF069777 *Cryptonectria parasitica* mitogen-activated... 66 2e-30
 emb|AW099876|AW099876 sd17g06.y2 *Gm-c1012 Glycine max* cDNA clone... 80 3e-30
 emb|AF249887|AF249887 *Pneumocystis carinii* map kinase kinase (mk... 72 6e-30
 emb|AW622016|AW622016 EST312814 tomato root during/after fruit s... 97 7e-29
 5 emb|Z69239|SPAC1D4 *S.pombe* chromosome I cosmid c1D4. 116 2e-28
 emb|X07445|SPBYR1 *Fission yeast* byr1 gene. 116 2e-28
 emb|Z67750|SC41KCIV *S.cerevisiae* DNA (cosmid 31A2; chromosome IV... 77 7e-28
 emb|X97751|SCIV23 *S.cerevisiae* chrIV genes STE7, CLB3, MSH5, RPC... 77 7e-28
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 10 gb|M14097|YSCSTE7 *Yeast (S.cerevisiae)* regulatory gene STE7, com... 77 8e-28
 dbj|D26601|TOBPK Tobacco mRNA for protein kinase, complete cds. 54 1e-27
 dbj|E05289|E05289 DNA encoding a protein kinase that is homologo... 54 1e-27
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 emb|AQ849880|AQ849880 LMAJFV1_lm51a11.x1 *Leishmania major* FV1 ra... 104 1e-26
 emb|AW564378|AW564378 LG1_292_H08.b1_A002 Light Grown 1 (LG1) So... 121 1e-26
 emb|AC005140|AC005140 *Plasmodium falciparum* chromosome 12 clone ... 88 2e-26
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 20 emb|Z28126|SCYKL126W *S.cerevisiae* chromosome XI reading frame OR... 84 5e-26
 gb|M21307|YSCPKN *Yeast (S.cerevisiae)* protein kinase (YPK1) gene... 84 7e-26
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 gb|M24929|YSCYKR2A *Saccharomyces cerevisiae* protein kinase (YKR2... 85 9e-26
 25 emb|AJ779511|AJ779511 EST260390 tomato susceptible, Cornell Lycò... 118 1e-25
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 emb|Z97211|SPBC2F12 *S.pombe* chromosome II cosmid c2F12. 56 2e-24
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 emb|AJ238845|BNA238845 *Brassica napus* mRNA for MAP3K epsilon 1 p... 78 3e-24
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 40 gb|U73457|CAU73457 *Candida albicans* Cst20p (CST20) gene, complet... 86 8e-24
 emb|AJ005079|AJKL5079 *Kluyveromyces lactis* BCK1 gene, complete CDS. 51 8e-24
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 dbj|D82023|D82023 *Schizosaccharomyces pombe* mkk1+ gene for MAP k... 73 2e-23
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 45 emb|AQ501953|AQ501953 V11H7 mTn-3xHA/lacZ Insertion Library Sacc... 72 2e-23
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 gb|U22371|SPU22371 *Schizosaccharomyces pombe* Pak1p (PAK1) mRNA, ... 87 5e-23
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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5	emb AW728196 AW728196 GA_Ea0014P01 Gossypium arboreum 7-10 dpa ...	257	1e-76
	emb AW737982 AW737982 EST339409 tomato flower buds, anthesis, Co...	287	2e-76
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	emb AW622517 AW622517 EST313317 tomato root during/after fruit s...	287	2e-76
10	emb AW623663 AW623663 EST321608 tomato flower buds 3-8 mm, Corne...	287	2e-76
	emb AW622008 AW622008 EST312806 tomato root during/after fruit s...	287	2e-76
	emb AI777165 AI777165 EST258130 tomato resistant, Cornell Lycope...	287	2e-76
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	emb AW774377 AW774377 EST333528 KV3 Medicago truncatula cDNA clo...	242	4e-71
	emb AW620616 AW620616 sj07e05.y1 Gm-c1032 Glycine max cDNA clone...	230	3e-69
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	emb AI776227 AI776227 EST257327 tomato resistant, Cornell Lycope...	244	3e-63
	emb AI899451 AI899451 EST268894 tomato susceptible, Cornell Lyco...	242	9e-63
	gb BE125791 BE125791 DG1_57_D06.b1_A002 Dark Grown 1 (DG1) Sorgh...	241	2e-62
30	emb AI482787 AI482787 EST242110 tomato shoot, Cornell Lycopersic...	241	2e-62
	gb BE123902 BE123902 EST394027 DSIL Medicago truncatula cDNA clo...	231	2e-62
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35	emb AW255550 AW255550 ML584 peppermint glandular trichome Menth...	237	4e-61
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40	emb AW755523 AW755523 sl05a05.y1 Gm-c1036 Glycine max cDNA clone...	223	4e-57
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	emb AW201709 AW201709 sf06d02.y1 Gm-c1027 Glycine max cDNA clone...	216	6e-55
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60	emb AW287668 AW287668 LG1_244_H12.b1_A002 Light Grown 1 (LG1) So...	180	4e-44
	emb AW625474 AW625474 EST319381 tomato radicle, 5 d post-imbibit...	156	1e-41

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gb|BE125862|BE125862 DG1_58_G08.b1_A002 Dark Grown 1 (DG1) Sorgh... 155 1e-36
10 emb|AV417826|AV417826 AV417826 Lotus japonicus young plants (two... 121 7e-36
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15 emb|AI482794|AI482794 EST242117 tomato shoot, Cornell Lycopersic... 146 5e-34
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25 emb|AW093288|AW093288 EST286468 tomato mixed elicitor, BTI Lycop... 136 4e-31
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30 emb|AW349246|AW349246 GM210004B21F9R Gm-r1021 Glycine max cDNA 3... 134 1e-30
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35 emb|AW925882|AW925882 HVSMeg0005M05 Hordeum vulgare pre-anthesis... 133 3e-30
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40 emb|AW754728|AW754728 PC07B03 Pine TriplEx pollen cone library P... 127 3e-28
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Database: plantfungal
50 661,018 sequences; 426,114,510 total letters

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Score E
55 Sequences producing significant alignments: (bits) Value

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gb|M96549|TOMHSC80P Tomato heat shock cognate protein 80 gene, 3... 577 0.0
gb|U55859|TAU55859 Triticum aestivum heat shock protein 80 mRNA,... 575 0.0
60 emb|X98582|TAX98582 T.aestivum mRNA for HSP80-2 protein. 572 0.0
emb|X63195|NTHSP82 N.tabacum mRNA for heat shock protein 82. 601 0.0

	emb AF123259 AF123259 <i>Lycopersicon esculentum</i> heat shock protein...	483	0.0
	emb AF165818 AF165818 <i>Guillardia theta</i> nucleomorph 5S ribosomal ...	505	0.0
	emb AF042329 AF042329 <i>Eimeria tenella</i> heat shock protein 90 (hsp...	514	0.0
5	gb M57386 THEHSP90 <i>T. parva</i> heat shock protein 90 (hsp90) mRNA, c...	500	0.0
	emb Z29667 PFHESHP <i>P. falciparum</i> (7) mRNA for heat-shock protein.	507	0.0
	gb U45449 EBU45449 <i>Eimeria bovis</i> heat shock protein 90 (hsp90) m...	495	0.0
	emb AF151114 AF151114 <i>Tetrahymena thermophila</i> strain B2086 hsp82...	486	0.0
	emb AF136649 AF136649 <i>Babesia bovis</i> heat shock protein 90 (HSP90...	487	0.0
10	gb M15346 TRBHSC <i>T. cruzi</i> tandemly repeated gene encoding an 85 k...	457	0.0
	emb X14176 TBHSP83 <i>Trypanosoma brucei</i> HSP83 gene.	452	0.0
	gb M73492 LEIHSP90 <i>Leishmania donovani</i> heat shock protein 90 mRN...	456	0.0
	emb X87770 LIHSP83GN <i>L. infantum</i> hsp83 gene.	454	0.0
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	gb U92465 AFU92465 <i>Aspergillus fumigatus</i> heat shock protein (Hsp...	458	e-165
15	emb AF212996 AF212996 <i>Neurospora crassa</i> heat shock protein 80 ge...	473	e-165
	emb AL110469 SPAC926 <i>S. pombe</i> chromosome I cosmid c926.	460	e-165
	gb L35550 YSPHSP90X <i>Schizosaccharomyces pombe</i> heat shock protein...	460	e-162
	gb U81165 PAU81165 <i>Podospira anserina</i> suppressor of vegetative i...	292	e-161
	emb Z67751 SC38KCXVI <i>S. cerevisiae</i> DNA (chromosome XVI; 38 kb).	448	e-159
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	emb X81025 CAHSP90 <i>C. albicans</i> hsp90 gene.	451	e-159
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25	emb AF221856 AF221856 <i>Euphorbia esula</i> heat-shock protein 80 mRNA...	292	e-158
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30	emb AW982575 AW982575 HVSMeg0003K07f <i>Hordeum vulgare</i> pre-anthesi...	471	e-131
	emb AW774793 AW774793 EST333944 KV3 <i>Medicago truncatula</i> cDNA clo...	459	e-128
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35	emb AW650299 AW650299 EST328753 tomato germinating seedlings, TA...	455	e-127
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40	emb AW621485 AW621485 EST312283 tomato root during/after fruit s...	445	e-124
	emb AW905909 AW905909 EST342082 potato stolon, Cornell Universit...	331	e-124
	emb AW618647 AW618647 EST320633 <i>L. pennellii</i> trichome, Cornell U...	439	e-122
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	emb AW931002 AW931002 EST356845 tomato fruit mature green, TAMU ...	436	e-121
45	emb AW186517 AW186517 se68g12.y1 <i>Gm-c1019 Glycine max</i> cDNA clone...	432	e-120
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	emb AW216642 AW216642 EST295356 tomato callus, TAMU <i>Lycopersicon</i> ...	423	e-117
	emb AW217696 AW217696 EST296410 tomato flower buds 8 mm to pre-a...	422	e-117
50	emb AW011081 AW011081 ST16E03 Pine TriplEx shoot tip library Pin...	421	e-116
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	emb AW693965 AW693965 NF071A06ST1F1040 Developing stem <i>Medicago</i> ...	408	e-113
	emb AW690869 AW690869 NF036A07ST1F1000 Developing stem <i>Medicago</i> ...	390	e-113
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60	emb AW983321 AW983321 HVSMeg0010D10f <i>Hordeum vulgare</i> pre-anthesi...	354	e-112
	emb AI726426 AI726426 BNLGHi5602 Six-day Cotton fiber <i>Gossypium</i> ...	407	e-112

- emb|AW930252|AW930252 EST340709 tomato fruit mature green, TAMU ... 406 e-112
 emb|AW979717|AW979717 EST341337 tomato root deficiency, Cornell ... 404 e-111
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 10 emb|AW220869|AW220869 EST297338 tomato fruit mature green, TAMU ... 398 e-109
 emb|AW616417|AW616417 EST322828 L. hirsutum trichome, Cornell Un... 397 e-109
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 15 emb|AW693115|AW693115 NF060C10ST1F1081 Developing stem Medicago ... 226 e-107
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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- emb|AW931781|AW931781 EST357624 tomato fruit mature green, TAMU ... 189 3e-47
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emb|AW906840|AW906840 EST342963 potato stolon, Cornell Universit... 140 2e-32
emb|AB014484|AB014484 Nicotiana tabacum NtHSF2 mRNA for heat sho... 140 3e-32
35 emb|AF208544|AF208544 Lycopersicon peruvianum heat stress transc... 139 4e-32
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40 emb|AV415736|AV415736 AV415736 Lotus japonicus young plants (two... 138 1e-31
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emb|AW569138|AW569138 si63g09.y1 Gm-r1030 Glycine max cDNA clone... 134 1e-30
45 emb|AW569256|AW569256 si64g09.y1 Gm-r1030 Glycine max cDNA clone... 134 1e-30
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55 emb|AQ579554|AQ579554 T135016b shotgun sub-library of BAC clone ... 113 4e-24
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5 emb|AW924303|AW924303 WS1_52_H11.b1_A002 Water-stressed 1 (WS1) ... 99 7e-20
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10 emb|X55149|KLHSFG K. lactis HSF gene for heat shock transcriptio... 76 2e-17
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 40 emb|AW306872|AW306872 sf49g05.y1 Gm-c1009 Glycine max cDNA clone... 128 2e-33
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Database: plantfungal
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35	emb AJ277900 VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas...	284	e-104	
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45	gb U22147 HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1) ...	265	1e-95	
	emb X54456 NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana...	106	3e-95	
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Database: plantfungal
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 (965 letters)

Database: plantfungal
 15 661,018 sequences; 426,114,510 total letters

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	emb Z54233 VVCCOAMT V.vinifera mRNA for caffeoyl-CoA O-methyltr...	136 9e-67
	gb M69184 PUMCCOAMT Petroselinum crispum caffeoyl-CoA 3-O-methyl...	133 2e-66
	gb U27116 PTU27116 Populus tremuloides caffeoyl-CoA 3-O-methyltr...	135 3e-66
	emb AJ224894 PBTJA4894 Populus balsamifera subsp. trichocarpa mR...	135 3e-66
30	gb U13151 ZEU13151 Zinnia elegans S-adenosyl-L-methionine:trans...	136 4e-66
	emb AI489305 AI489305 EST247644 tomato ovary, TAMU Lycopersicon ...	139 4e-66
	emb AJ224895 PBTJA4895 Populus balsamifera subsp. trichocarpa mR...	136 6e-66
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	emb AF168780 AF168780 Eucalyptus globulus caffeoyl-CoA O-methyltr...	133 8e-66
35	emb AF053553 AF053553 Mesembryanthemum crystallinum caffeoyl-CoA...	132 1e-65
	emb AF240466 AF240466 Populus tomentosa caffeoyl-CoA O-methyltra...	135 1e-65
	emb A22706 A22706 Caffeoyl-CoA-3-O-Methyltransferase gene.	129 3e-65
	gb U62734 NTU62734 Nicotiana tabacum caffeoyl-CoA O-methyltransf...	134 5e-65
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40	gb U62736 NTU62736 Nicotiana tabacum caffeoyl-CoA O-methyltransf...	136 5e-65
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	emb Y12228 EG12228 E.gunnii mRNA for caffeoyl-CoA O-methyltransf...	133 7e-65
	gb L22203 SLASADEN Stellaria longipes S-adenosyl-L-methionine:tr...	124 8e-65
	emb AF046122 AF046122 Eucalyptus globulus caffeoyl-CoA 3-O-methy...	133 9e-65
45	gb U62735 NTU62735 Nicotiana tabacum caffeoyl-CoA O-methyltransf...	134 3e-64
	emb AF036095 AF036095 Pinus taeda caffeoyl-CoA O-methyltransfera...	130 6e-64
	emb AF060180 AF060180 Nicotiana tabacum caffeoyl-coenzyme A trun...	90 9e-60
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	emb AI486500 AI486500 EST244821 tomato ovary, TAMU Lycopersicon ...	139 2e-55
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15 emb|AI898952|AI898952 EST268395 tomato ovary, TAMU Lycopersicon ... 139 2e-51
emb|AW424002|AW424002 sh59c10.y1 Gm-c1015 Glycine max cDNA clone... 115 2e-51
emb|AW707192|AW707192 sk22a02.y1 Gm-c1028 Glycine max cDNA clone... 132 3e-50
emb|AI899227|AI899227 EST268670 tomato ovary, TAMU Lycopersicon ... 139 3e-50
emb|AW980337|AW980337 EST391490 GVN Medicago truncatula cDNA clo... 127 3e-50
20 emb|AW648499|AW648499 EST326953 tomato germinating seedlings, TA... 99 7e-50
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emb|AW695176|AW695176 NF092D12ST1F1101 Developing stem Medicago ... 142 1e-47
25 emb|AW684885|AW684885 NF022F07NR1F1000 Nodulated root Medicago t... 142 2e-47
emb|AA660318|AA660318 00189 MtRHE Medicago truncatula cDNA 5' si... 144 2e-47
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30 emb|AW620537|AW620537 sj06d09.y1 Gm-c1032 Glycine max cDNA clone... 133 1e-46
emb|AI775483|AI775483 EST256583 tomato resistant, Cornell Lycope... 139 2e-46
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35 emb|AW707224|AW707224 sk22c12.y1 Gm-c1028 Glycine max cDNA clone... 140 9e-46
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40 emb|AW686370|AW686370 NF040G10NR1F1000 Nodulated root Medicago t... 127 4e-44
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45 gb|BE059325|BE059325 sn31c09.y1 Gm-c1016 Glycine max cDNA clone ... 140 3e-43
emb|AW831448|AW831448 sm23c03.y1 Gm-c1028 Glycine max cDNA clone... 140 6e-43
emb|AI938893|AI938893 sc62d08.y1 Gm-c1016 Glycine max cDNA clone... 134 2e-42
emb|AW257069|AW257069 EST305206 KV2 Medicago truncatula cDNA clo... 142 2e-42
emb|AW695899|AW695899 NF100E02ST1F1017 Developing stem Medicago ... 125 5e-42
50 emb|AW774697|AW774697 EST333848 KV3 Medicago truncatula cDNA clo... 84 8e-42
emb|AW683492|AW683492 NF012H09LF1F1079 Developing leaf Medicago ... 134 2e-41
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gb|BE022002|BE022002 sm65c10.y1 Gm-c1028 Glycine max cDNA clone ... 137 3e-41
55 emb|AI488060|AI488060 EST246382 tomato ovary, TAMU Lycopersicon ... 100 7e-41
emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40
emb|AW625461|AW625461 EST319368 tomato radicle, 5 d post-imbibit... 99 1e-40
emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40
emb|AI960196|AI960196 sc80a08.y1 Gm-c1018 Glycine max cDNA clone... 132 5e-40
60 emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39
emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39

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(925 letters)

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 10 661,018 sequences; 426,114,510 total letters

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15	Sequences producing significant alignments:	(bits)	Value
	emb AJ012689 CAR012689 Cicer arietinum mRNA for ribonuclease T2.	384	e-106
	gb U13256 NAU13256 Nicotiana alata RNase NE mRNA, complete cds.	361	4e-99
	gb U19924 ZEU19924 Zinnia elegans wounding-induced ribonuclease ...	358	4e-98
20	emb AB034638 AB034638 Nicotiana tabacum mRNA for RNase, complete...	353	1e-96
	emb X79337 LERNALX L.esculentum mRNA for ribonuclease le.	212	2e-93
	dbj D49529 D49529 Pyrus pyrifolia mRNA for ribonuclease, complet...	335	4e-91
	emb AI486253 AI486253 EST244574 tomato ovary, TAMU Lycopersicon ...	212	2e-89
	emb AI485206 AI485206 EST243510 tomato ovary, TAMU Lycopersicon ...	212	1e-81
25	gb U19923 ZEU19923 Zinnia elegans ribonuclease mRNA, complete cds.	232	3e-80
	emb X79338 LERNALX L.esculentum mRNA for ribonuclease lx.	177	1e-73
	emb AB032257 AB032257 Nicotiana glutinosa NGR3 mRNA for RNase NG...	176	7e-70
	emb AI484830 AI484830 EST243091 tomato ovary, TAMU Lycopersicon ...	212	7e-70
	emb AW684365 AW684365 NF016B03NR1F1000 Nodulated root Medicago t...	251	7e-66
30	emb AI489460 AI489460 EST247799 tomato ovary, TAMU Lycopersicon ...	212	3e-63
	emb Y17444 LES17444 Lycopersicon esculentum RNALE gene, exons 1 ...	152	2e-57
	emb AI772676 AI772676 EST253776 tomato resistant, Cornell Lycope...	152	2e-57
	emb AI775352 AI775352 EST256452 tomato resistant, Cornell Lycope...	212	3e-56
	gb BE037115 BE037115 MP15C03 MP Mesembryanthemum crystallinum cD...	153	4e-55
35	emb AF000939 AF000939 Hordeum vulgare aleurone ribonuclease mRNA...	89	7e-55
	gb M83668 NELSTORAGE Nelumbo nucifera storage protein mRNA, comp...	127	2e-54
	emb AI812905 AI812905 22D1 Pine Lambda Zap Xylem library Pinus t...	165	3e-54
	emb AI488432 AI488432 EST246771 tomato ovary, TAMU Lycopersicon ...	211	5e-54
	emb AW775298 AW775298 EST334363 DSIL Medicago truncatula cDNA cl...	200	7e-54
40	emb AW279538 AW279538 sf90h05.y1 Gm-c1019 Glycine max cDNA clone...	188	6e-47
	emb AF000940 AF000940 Hordeum vulgare ribonuclease gene, complet...	116	2e-44
	gb BE060583 BE060583 HVSMEg0012L03f Hordeum vulgare pre-anthesis...	74	5e-42
	emb Y17445 LES17445 Lycopersicon esculentum RNALE gene, exons 1 ...	122	6e-42
	emb AI777654 AI777654 EST258449 tomato susceptible, Cornell Lyco...	152	2e-41
45	emb AW596890 AW596890 sj84b03.y1 Gm-c1034 Glycine max cDNA clone...	162	3e-39
	gb BE060118 BE060118 HVSMEg0011I10f Hordeum vulgare pre-anthesis...	89	6e-37
	gb BE060590 BE060590 HVSMEg0012L10f Hordeum vulgare pre-anthesis...	89	2e-36
	emb AW704136 AW704136 sk16e03.y1 Gm-c1028 Glycine max cDNA clone...	145	4e-34
	emb AW289659 AW289659 NXNV003D07F Nsf Xylem Normal wood Vertical...	109	8e-32
50	gb U19794 MDU19794 Malus domestica S-like RNase gene, partial cds.	76	2e-25
	emb AI967855 AI967855 Ljirmp14-054-a9 Ljirmp Lambda HybriZap ...	109	4e-23
	emb Y17446 LES17446 Lycopersicon esculentum RNALX gene, exons 1 ...	104	1e-21
	dbj D64012 LUFRNLC2 Luffa cylindrica mRNA for ribonuclease (RNas...	95	1e-20
	emb AW053670 AW053670 L30-1447T3 Ice plant Lambda Uni-Zap XR exp...	45	2e-20
55	gb BE020073 BE020073 sm38f09.y1 Gm-c1028 Glycine max cDNA clone ...	45	7e-20
	emb AW039494 AW039494 EST281775 tomato mixed elicitor, BTI Lycop...	43	6e-19
	emb AW216541 AW216541 EST295255 tomato callus, TAMU Lycopersicon...	43	6e-19
	dbj D64011 LUFRNLC1 Luffa cylindrica mRNA for ribonuclease (RNas...	89	8e-19
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60	emb AW980478 AW980478 EST391631 GVN Medicago truncatula cDNA clo...	44	4e-18
	gb BE124916 BE124916 EST393951 GVN Medicago truncatula cDNA clon...	44	4e-18

- emb|AB032256|AB032256 *Nicotiana glutinosa* NGR2 mRNA for RNase NG... 41 9e-18
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 5 emb|AB034248|AB034248 *Volvox carteri* vml mRNA for S-like RNase,... 58 8e-17
 emb|AF176533|AF176533 *Solanum chacoense* self-incompatibility rib... 82 2e-16
 emb|AI416638|AI416638 sa17c06.y1 *Gm-c1004 Glycine max* cDNA clone... 45 6e-16
 emb|X96465|AHS2RNASE *A.hispanicum* mRNA for S2-Rnase. 60 2e-15
 emb|AB028153|AB028153 *Prunus avium* mRNA for S1-RNase, complete cds. 56 3e-15
 10 emb|AW223027|AW223027 EST299838 tomato fruit red ripe, TAMU Lyco... 43 4e-15
 emb|AW224120|AW224120 EST300931 tomato fruit red ripe, TAMU Lyco... 43 5e-15
 emb|AW223831|AW223831 EST300642 tomato fruit red ripe, TAMU Lyco... 43 5e-15
 emb|AF191732|AF191732 *Solanum chacoense* self-incompatibility rib... 82 6e-15
 emb|AB010306|AB010306 *Prunus avium* mRNA for S3-RNase, complete cds. 57 2e-14
 15 emb|X76065|LPSRNASE *L.peruvianum* mRNA for S-RNase S3. 60 2e-14
 emb|AB010304|AB010304 *Prunus avium* mRNA for S2-RNase, partial cds. 60 4e-14
 emb|AI729649|AI729649 BNLGHI13860 Six-day Cotton fiber *Gossypium*... 45 9e-14
 emb|AI729386|AI729386 BNLGHI13239 Six-day Cotton fiber *Gossypium*... 45 1e-13
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 20 gb|S61768|S61768 S (S5)=self-incompatibility {3' region} [*Lycopersicon*... 60 1e-13
 emb|X56897|SCSIAP3 *S.chacoense* mRNA for self-incompatibility ass... 63 1e-13
 emb|AW563386|AW563386 LG1_214_C01.b1_A002 Light Grown 1 (LG1) So... 45 1e-13
 emb|AB011470|AB011470 *Prunus dulcis* mRNA for Sc-RNase, complete ... 60 3e-13
 emb|AB011469|AB011469 *Prunus dulcis* mRNA for Sb-RNase, complete ... 57 4e-13
 25 emb|AW623083|AW623083 EST321028 tomato flower buds 3-8 mm, *Corne*... 43 8e-13
 emb|AW034883|AW034883 EST279112 tomato callus, TAMU *Lycopersicon*... 43 8e-13
 emb|AF232304|AF232304 *Solanum chacoense* gametophytic self-incomp... 58 1e-12
 emb|Z26583|LPSLGS6 *L.peruvianum* (Mill) self-incompatibility glyc... 56 1e-12
 emb|AB011471|AB011471 *Prunus dulcis* mRNA for Sd-RNase, partial cds. 57 1e-12
 30 emb|AV427528|AV427528 AV427528 *Lotus japonicus* young plants (two... 74 2e-12
 emb|AF148465|AF148465 *Prunus dulcis* Sa-S-RNase gene, partial cds. 73 3e-12
 emb|AB026982|AB026982 *Prunus salicina* mRNA for Sb-RNase, partial... 60 5e-12
 dbj|E01266|E01266 cDNA encoding S2-protein linked to part of its... 56 1e-11
 gb|M24600|TOBGPS *N.alata* stylar glycoprotein 2 mRNA, complete cds. 56 1e-11
 35 dbj|E01267|E01267 cDNA encoding S2-protein linked to its signal ... 56 1e-11
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 gb|L25930|TOBRNASESB *Nicotiana alata* RNase S mRNA. 56 1e-11
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 emb|AI724132|AI724132 RHIZ1_7_B07.y2_A001 Rhizome1 *Sorghum halep*... 70 2e-11
 40 emb|AJ271062|PHY271062 *Petunia hybrida* mRNA for Sv-ribonuclease ... 62 2e-11
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 emb|X96464|AHS5RNASE *A.hispanicum* mRNA for S5-Rnase. 57 4e-11
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 45 emb|X96466|AHS4RNASE *A.hispanicum* mRNA for S4-Rnase. 46 7e-11
 gb|M81686|PETSXPB *Petunia hybrida* Sx-protein (self-incompatibi... 58 1e-10
 emb|Z26581|LPSLGSC *L.peruvianum* (Mill) mRNA for self-incompatabi... 51 2e-10
 emb|X56896|SCSIAP *S.chacoense* mRNA for self-incompatibility asso... 62 3e-10
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 50 emb|AI460477|AI460477 sa79g07.y1 *Gm-c1004 Glycine max* cDNA clone... 42 3e-10
 emb|Z26582|LPSLGS7 *L.peruvianum* (Mill) self-incompatibility glyc... 61 3e-10
 dbj|D63887|D63887 *Nicotiana alata* mRNA for ribonuclease, complet... 61 3e-10
 emb|AF105363|AF105363 *Lycium andersonii* self-incompatibility rib... 66 4e-10
 gb|U07362|PHU07362 *Petunia hybrida* S1 self-incompatibility ribon... 62 4e-10
 55 gb|L40542|POTDSCS *Solanum carolinense* self-incompatibility ribon... 65 7e-10

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 (1480 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

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Sequences producing significant alignments:

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	emb AI782831 AI782831 EST263710 tomato susceptible, Cornell Lyco...	270	1e-71
10	emb AW093706 AW093706 EST286886 tomato mixed elicitor, BTI Lycop...	256	4e-67
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20	emb AW761120 AW761120 sl63e05.y1 Gm-cl027 Glycine max cDNA clone...	127	9e-32
	gb BE037096 BE037096 MP14H01 MP Mesembryanthemum crystallinum cD...	86	2e-30
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	emb AW782240 AW782240 sm03c06.y1 Gm-cl027 Glycine max cDNA clone...	80	2e-15
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40	emb AW034079 AW034079 EST277574 tomato callus, TAMU Lycopersicon...	77	3e-13
	emb AW991119 AW991119 SsS0174 Suaeda salsa ZAP cDNA library Suae...	58	7e-10
	emb X95732 NPZEAXANT N.plumbaginifolia mRNA for zeaxanthin epoxi...	63	6e-09
	emb AV418279 AV418279 AV418279 Lotus japonicus young plants (two...	48	8e-09
	emb X91491 CAXANEPOX C.annuum mRNA for xanthophyll epoxidase.	61	2e-08
45	emb Z83835 LEZEAXAN L.esculentum mRNA for zeaxanthin epoxidase.	59	1e-07
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	dbj D38415 AED4ABH Agaricus bisporus DNA for 4-aminobenzoate hyd...	47	3e-04
50	emb AQ274524 AQ274524 mgxb0022E01r CUGI Rice Blast BAC Library P...	47	3e-04
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	emb Z35859 SCYBL098W S.cerevisiae chromosome II reading frame OR...	39	0.12
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60	emb AL115728 CNS01CMW Botrytis cinerea strain T4 cDNA library un...	36	0.80
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- emb|AI496271|AI496271 sb01f06.y1 Gm-c1004 Glycine max cDNA clone... 36 0.80
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 emb|AW185727|AW185727 se58h04.y1 Gm-c1019 Glycine max cDNA clone... 35 1.5
 5 emb|AW279175|AW279175 sf67d04.y1 Gm-c1013 Glycine max cDNA clone... 35 1.5
 emb|AF211986|AF211986 Acleisanthes anisophylla 18S ribosomal RNA... 35 1.5
 emb|AW348744|AW348744 GM210003A22C7R Gm-r1021 Glycine max cDNA 3... 35 2.1
 emb|AZ217020|AZ217020 Sheared DNA-75G4.TF Sheared DNA Trypanosom... 35 2.1
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 emb|Z73040|SCYGR255C S.cerevisiae chromosome VII reading frame O... 35 2.1
 10 emb|AW680385|AW680385 WS1_52_D05.g1_A002 Water-stressed 1 (WS1) ... 35 2.1
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 emb|AL114377|CNS01BLD Botrytis cinerea strain T4 cDNA library un... 35 2.1
 15 gb|BE122310|BE122310 894019A08.y1 C. reinhardtii CC-1690, normal... 35 2.1
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 emb|AJ011587|KLA011587 Kluyveromyces lactis mufl gene. 34 2.9
 20 emb|AI068756|AI068756 mgae0004aD11f Magnaporthe grisea Appressor... 34 2.9
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 emb|AF068686|AF068686 Glycine max geranylgeranyl hydrogenase (Gg... 34 2.9
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 emb|Z74950|BO13G61C B.oleracea mRNA (unknown). 34 3.9
 30 emb|AW477291|AW477291 ga44f01.y1 Moss EST library PPU Physcomitr... 34 3.9
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 40 emb|AC004145|AC004145 Leishmania major chromosome 3 clone L5801 ... 33 5.4
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 45 emb|AL160727|P417R Leishmania major Friedlin PAC P417 right end... 33 5.4
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- emb|AI896318|AI896318 EST265761 tomato callus, TAMU Lycopersicon... 182 5e-65
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 gb|U93048|DCU93048 *Daucus carota* somatic embryogenesis receptor... 128 5e-51
 5 emb|AW432288|AW432288 sh71g05.y1 *Gm-c1015* Glycine max cDNA clone... 200 5e-50
 emb|AI730535|AI730535 BNLGH7007 Six-day Cotton fiber *Gossypium* ... 152 1e-49
 emb|AF085168|AF085168 *Triticum aestivum* receptor-like protein ki... 77 2e-46
 emb|AF085166|AF085166 *Hordeum vulgare* receptor-like kinase gene,... 86 2e-45
 emb|AF085167|AF085167 *Hordeum vulgare* receptor-like kinase ARK1A... 85 3e-45
 10 gb|U51330|TAU51330 *Triticum aestivum* leaf rust resistance kinase... 82 8e-45
 emb|AF100771|AF100771 *Hordeum vulgare* receptor-like kinase (Hv3A... 100 2e-44
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 25 dbj|D38564|BOLRPKB *Brassica campestris* mRNA for receptor protein... 82 9e-41
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 30 emb|Y14285|BOY14285 *Brassica oleracea* mRNA for SFR1 protein. 78 5e-39
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 35 emb|AB024422|AB024421S2 *Brassica oleracea* SRK13-b gene, exon 2, ... 84 2e-38
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 40 gb|M97667|BNASTKR *Brassica napus* ssp. *oleifera* serine/threonine ... 82 3e-38
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 45 gb|U00443|BNU00443 *Brassica napus* cultivar T2 S-receptor kinase ... 81 6e-38
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 55 emb|AW030223|AW030223 EST273478 tomato callus, TAMU Lycopersicon... 92 2e-36
 emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 118 2e-36
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 60 emb|AJ245479|BNA245479 *Brassica napus* Sll3, silk, srk, CePP, Fmt,... 82 4e-36
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- emb|AW687349|AW687349 NF008F08RT1F1074 Developing root Medicago ... 80 9e-36
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 10 emb|AW597214|AW597214 si71g06.y1 Gm-c1031 Glycine max cDNA clone... 126 2e-34
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 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 74 2e-34
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 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 74 3e-34
 15 emb|AW934655|AW934655 EST353547 tomato flower buds 0-3 mm, Corne... 93 3e-34
 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 67 3e-34
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 25 emb|AA738547|AA738547 SbRLK5 Sorghum bicolor cv. TX430 leaf Sorg... 115 2e-33
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- emb|AI483399|AI483399 EST241520 tomato shoot, Cornell Lycopersic... 289 2e-89
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- emb|AI731648|AI731648 BNLGHi10360 Six-day Cotton fiber *Gossypium*... 182 2e-61
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10 emb|AW648007|AW648007 EST326461 tomato germinating seedlings, TA... 100 2e-38
emb|AI773256|AI773256 EST254356 tomato resistant, Cornell *Lycopersicon*... 99 5e-38
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15 emb|AL096874|SPBC1539 *S.pombe* chromosome II cosmid c1539. 57 5e-29
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25 emb|X07071|ANTRPC *Aspergillus niger* trpC gene. 64 3e-09
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emb|X02390|ANTRPC1 *Aspergillus nidulans* trpC gene. 62 7e-09
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30 emb|A11156|A11156 MOX structural gene and it's 5'and 3'-flanking... 58 1e-07
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gb|J01252|NEUTRP1 *n.crassa* trifunctional tryptophan biosynthesis... 57 3e-07
35 emb|X56047|PDTRPC *P. chrysosporium* trpC gene for trifunctional p... 55 1e-06
emb|X75951|SC6ORF *S.cerevisiae* URA1, SAC1, RSD1 and TRP3 genes a... 50 1e-06
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40 gb|M74901|CPCTRP1 *Cryptococcus neoformans* phosphoribosyl anthran... 40 0.042
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45 gb|U33057|SCD9717 *Saccharomyces cerevisiae* chromosome IV cosmids... 34 2.6
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50 emb|AJ133598|PSA133598 *Pisum sativum* chloroplast gF16P gene, exo... 33 5.0
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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	gb U74630 RCU74630 Ricinus communis calreticulin mRNA, complete ...	575	e-163
	emb AF052040 AF052040 Berberis stolonifera calreticulin mRNA, co...	571	e-162
	emb X85382 NTRNATCAL N.tabacum mRNA for calreticulin.	570	e-161
20	emb AF134733 AF134733 Prunus armeniaca calcium-binding protein c...	565	e-160
	gb L27349 BLYCRH2A Hordeum vulgare calreticulin (CRH2) mRNA, par...	560	e-159
	gb L27348 BLYCRH1A Hordeum vulgare calreticulin (CRH1) mRNA, par...	560	e-159
	emb AF019376 AF019376 Brassica napus calreticulin mRNA, complete...	465	e-156
	emb X80756 CAPCRTC C.annuum PCRTC mRNA.	344	e-154
25	gb U74631 RCU74631 Ricinus communis calreticulin gene, complete ...	149	e-123
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	emb AI728389 AI728389 BNLGHi10665 Six-day Cotton fiber Gossypium...	438	e-122
	emb AI782264 AI782264 EST263143 tomato susceptible, Cornell Lyco...	418	e-116
	emb AB018243 AB018243 Solanum melongena EEF22 mRNA for calreticu...	402	e-111
30	emb AW667951 AW667951 GA_Ea0012A11 Gossypium arboreum 7-10 dpa ...	402	e-111
	emb AW216727 AW216727 EST295441 tomato callus, TAMU Lycopersicon...	391	e-108
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5 emb|AW035959|AW035959 EST282818 tomato callus, TAMU Lycopersicon... 303 3e-81
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10 emb|AW727696|AW727696 GA_Ea0015K01 Gossypium arboreum 7-10 dpa ... 258 8e-79
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25 emb|AW033083|AW033083 EST276642 tomato callus, TAMU Lycopersicon... 275 8e-73
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emb|AF162779|AF162779 Trypanosoma cruzi Tc45-calreticulin precur... 143 2e-60
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60 (757 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments:

(bits) Value

	gb U70666 BNU70666 Brassica napus pathogenesis-related protein P...	323	3e-89
10	gb U21849 BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds.	323	3e-89
	gb U64806 BNU64806 Brassica napus pathogenesis-related protein P...	209	4e-86
	emb AI352851 AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl...	311	5e-84
	emb AI352893 AI352893 MB72-6D PZ204.BNlib Brassica napus cDNA cl...	165	3e-62
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	emb AW219671 AW219671 EST302153 tomato root during/after fruit s...	151	1e-59
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	emb AI895090 AI895090 EST264533 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW625930 AW625930 EST319825 tomato radicle, 5 d post-imbibit...	151	1e-59
	emb AW032514 AW032514 EST276073 tomato callus, TAMU Lycopersicon...	151	1e-59
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	emb AW219480 AW219480 EST301878 tomato root during/after fruit s...	151	1e-59
	emb AW092623 AW092623 EST285803 tomato mixed elicitor, BTI Lycop...	151	1e-59
25	emb AW040954 AW040954 EST283818 tomato mixed elicitor, BTI Lycop...	151	1e-59
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40	emb AW034330 AW034330 EST277901 tomato callus, TAMU Lycopersicon...	144	2e-57
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	emb AW032727 AW032727 EST276286 tomato callus, TAMU Lycopersicon...	147	1e-53
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55	emb AW053720 AW053720 L30-1612T3 Ice plant Lambda Uni-Zap XR exp...	112	4e-52
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	emb AI352801 AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl...	194	1e-51
	emb X17681 NTPR1CA Tobacco gene for pathogenesis-related protein...	111	2e-51
	emb X05454 NTPR1CR Nicotiana tabacum mRNA for PR-1c protein.	111	2e-51
60	emb X12487 NTPR1C Tobacco mRNA fragment for pathogenesis-related...	111	2e-51
	emb AJ011520 LES011520 Lycopersicon esculentum pr1a (P4) gene.	98	1e-50

- gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50
 emb|A22634|LEPI4GENE L.esculentum P14 gene. 98 1e-50
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 5 emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50
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 10 emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
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 20 emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49
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 25 emb|Y08804|LEPR1B1 L.esculentum mRNA for PR protein. 92 7e-49
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55 Database: plantfungal
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- emb|AF079872|AF079872 Nicotiana tabacum cyclic nucleotide-gated ... 380 0.0
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emb|AW038928|AW038928 EST280884 tomato mixed elicitor, BTI Lycop... 190 2e-80
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emb|AW033272|AW033272 EST276843 tomato callus, TAMU Lycopersicon... 260 2e-68
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45 emb|AW037755|AW037755 EST279384 tomato mixed elicitor, BTI Lycop... 122 1e-26
emb|AW508715|AW508715 si35e10.y1 Gm-r1030 Glycine max cDNA clone... 117 3e-25
emb|AW350588|AW350588 GM210009A10H2R Gm-r1021 Glycine max cDNA 3... 106 1e-24
emb|AW350847|AW350847 GM210009B20G5R Gm-r1021 Glycine max cDNA 3... 106 2e-24
50 emb|AI776960|AI776960 EST251986 tomato callus, TAMU Lycopersicon... 111 2e-23
emb|AW781088|AW781088 sl88h09.y1 Gm-c1037 Glycine max cDNA clone... 111 3e-23
emb|AW039011|AW039011 EST280984 tomato mixed elicitor, BTI Lycop... 111 3e-23
emb|AW617273|AW617273 EST323684 L. hirsutum trichome, Cornell Un... 106 7e-22
55 gb|BE022211|BE022211 sm72b10.y1 Gm-c1028 Glycine max cDNA clone ... 106 7e-22
emb|AW668188|AW668188 GA_Ea0013B18 Gossypium arboreum 7-10 dpa ... 105 2e-21
emb|AA824914|AA824914 CT202.SK Tomato Leaf cDNA from cv. VFNT ch... 93 6e-21
emb|AT000374|AT000374 AT000374 Apple peel cDNA library Malus x d... 102 1e-20
emb|AW623583|AW623583 EST321528 tomato flower buds 3-8 mm, Corne... 69 7e-20
60 emb|AI495394|AI495394 sa97d10.y1 Gm-c1004 Glycine max cDNA clone... 98 2e-19
emb|AI725563|AI725563 BNLGHi12127 Six-day Cotton fiber Gossypium... 67 5e-18

emb|AW119379|AW119379 sd45d12.y1 Gm-c1016 Glycine max cDNA clone... 74 3e-17
 emb|AW617083|AW617083 EST323494 L. hirsutum trichome, Cornell Un... 65 7e-17
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 5 emb|AI776961|AI776961 EST251987 tomato callus, TAMU Lycopersicon... 67 5e-12
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 emb|AW688833|AW688833 NF012B10ST1F1000 Developing stem Medicago ... 58 1e-09
 emb|AW164084|AW164084 Ljirnp19-528-f6 Ljirnp Lambda HybriZap ... 56 1e-06
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 10 emb|AW184978|AW184978 se85a09.y1 Gm-c1023 Glycine max cDNA clone... 54 4e-06
 emb|AW091651|AW091651 EST284747 tomato mixed elicitor, BTI Lycop... 51 3e-05
 emb|AW041519|AW041519 EST284383 tomato mixed elicitor, BTI Lycop... 51 3e-05
 emb|AF145272|AF145272 Samanea saman pulvinus inward-rectifying c... 49 1e-04
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 15 emb|AW928912|AW928912 EST337700 tomato flower buds 8 mm to pre-a... 48 2e-04
 emb|AW756344|AW756344 sl19e03.y1 Gm-c1036 Glycine max cDNA clone... 47 6e-04
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 20 emb|AW256736|AW256736 EST304873 KV2 Medicago truncatula cDNA clo... 40 0.016
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 emb|AL163552|LMFL5075 Leishmania major Friedlin chromosome 14 co... 38 0.25
 25 emb|AQ847838|AQ847838 LMAJFV1_lm42a03.y1 Leishmania major FV1 ra... 38 0.25
 emb|AI748348|AI748348 sb51d12.y1 Gm-c1016 Glycine max cDNA clone... 38 0.35
 emb|AL031530|SPCC970 S.pombe chromosome III cosmid c970. 38 0.35
 gb|U33057|SCD9717 Saccharomyces cerevisiae chromosome IV cosmids... 37 0.48
 gb|M84796|YSCEUG1 Saccharomyces cerevisiae endoplasmic reticulum... 37 0.48
 30 emb|AF099095|AF099095 Samanea saman pulvinus inward-rectifying c... 37 0.66
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 emb|AF053314|AF053314 Exophiala dermatitidis chitin synthase 3 (... 36 1.2
 emb|AQ947260|AQ947260 Sheared DNA-45L23.TR Sheared DNA Trypanoso... 31 1.5
 emb|AC016528|AC016528 Leishmania major chromosome 35 clone L4123... 35 1.7
 35 emb|AI781524|AI781524 EST262403 tomato susceptible, Cornell Lyco... 31 2.0
 gb|U28374|YSCD9740 Saccharomyces cerevisiae chromosome IV cosmid... 35 2.3
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 gb|BE034738|BE034738 ML03G05 ML Mesembryanthemum crystallinum cD... 35 2.3
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 40 emb|AW648153|AW648153 EST326607 tomato germinating seedlings, TA... 35 2.3
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 emb|AW728887|AW728887 GA_Ea0018B11 Gossypium arboreum 7-10 dpa ... 34 4.4
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 (827 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

50

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

55

emb|AI489346|AI489346 EST247685 tomato ovary, TAMU Lycopersicon ... 79 2e-28
 emb|AW350323|AW350323 GM210007B20E12R Gm-r1021 Glycine max cDNA ... 80 2e-27
 emb|AW509006|AW509006 si38h07.y1 Gm-r1030 Glycine max cDNA clone... 79 2e-26
 emb|AW685404|AW685404 NF028H10NR1F1000 Nodulated root Medicago t... 74 2e-24
 60 emb|AW781320|AW781320 sk68d07.y1 Gm-c1016 Glycine max cDNA clone... 86 2e-24
 emb|AI897832|AI897832 EST267275 tomato ovary, TAMU Lycopersicon ... 78 1e-23

- emb|AW102460|AW102460 sd88d10.y1 Gm-c1009 Glycine max cDNA clone... 70 2e-22
emb|AI490284|AI490284 EST248610 tomato ovary, TAMU Lycopersicon ... 103 2e-22
emb|AI487362|AI487362 EST245684 tomato ovary, TAMU Lycopersicon ... 72 3e-20
5 gb|BE125690|BE125690 DG1_54_A02.g1_A002 Dark Grown 1 (DG1) Sorgh... 96 3e-19
emb|X80231|LTCAMA L.tarentolae CAM A gene for calmodulin. 73 1e-18
emb|AL115248|CNS01C9K Botrytis cinerea strain T4 cDNA library un... 65 4e-18
dbj|D10521|TETCALW T.pyrifomis mRNA for calmodulin. 73 7e-18
gb|M76407|SLECALMODU Stylonychia lemnae calmodulin gene, complet... 74 9e-18
10 emb|AF007889|AF007889 Symbiodinium microadriaticum calmodulin (S... 74 1e-17
emb|AF078679|AF078679 Olea europaea calcium-binding protein (PCA... 57 2e-17
emb|X56511|TBCALUBG T. brucei genes for calmodulin, EFH5 and ubi... 77 2e-17
emb|X52096|TCCALB2 Trypanosoma cruzi CalA2 calmodulin gene. 77 2e-17
emb|AF030033|AF030033 Phaseolus vulgaris calmodulin (CaM) mRNA; ... 75 2e-17
15 emb|X90560|PPCAMPROT Physcomitrella patens mRNA for calmodulin. 71 2e-17
gb|U91642|POU91642 Pleurotus ostreatus calmodulin mRNA, complete... 75 2e-17
emb|AF078680|AF078680 Olea europaea calcium-binding protein (PCA... 57 2e-17
emb|X85091|MPCAM M.pyrifera mRNA for calmodulin. 74 2e-17
gb|M83535|PHTCALPIA P.infestans calmodulin (calA) gene, complete... 75 2e-17
emb|Y08373|TGCM T.gondii mRNA for calmodulin. 74 2e-17
20 gb|C96396|C96396 C96396 Marchantia polymorpha immature sex organ... 73 3e-17
emb|AL113315|CNS01ARV Botrytis cinerea strain T4 cDNA library un... 72 3e-17
emb|AB044286|AB044286 Chara corallina ccam mRNA for calmodulin, ... 75 4e-17
emb|AB041712|AB041712 Chara corallina cccam2 mRNA for calmodulin... 75 4e-17
emb|AB041711|AB041711 Chara corallina cccam1 mRNA for calmodulin... 75 4e-17
25 gb|J05116|ACKCAL A.klebsiana calmodulin gene, complete cds. 75 4e-17
emb|X70923|NCCALMOE N.crassa mRNA for calmodulin. 74 6e-17
emb|AI328739|AI328739 a6d02ne.fl Neurospora crassa evening cDNA ... 74 6e-17
emb|AF034964|AF034964 Glomerella cingulata calmodulin (cam) mRNA... 74 6e-17
30 gb|U12505|HCCMD Histoplasma capsulatum 186AS calmodulin mRNA, co... 74 8e-17
gb|M34540|PARCAM P.tetraurelia calmodulin gene, complete cds. 74 8e-17
gb|S68025|S68025 CAM=calmodulin [Paramecium tetraurelia, Genomic... 74 8e-17
emb|AW164773|AW164773 se77e12.y1 Gm-c1023 Glycine max cDNA clone... 64 8e-17
emb|AW719875|AW719875 LjNEST11d4r Lotus japonicus nodule library... 57 8e-17
emb|AW830090|AW830090 sm22a12.y1 Gm-c1028 Glycine max cDNA clone... 64 8e-17
35 emb|AW126204|AW126204 N100049e rootphos(-) Medicago truncatula c... 57 8e-17
emb|X52242|TTCALM T.thermophila mRNA for calmodulin. 73 1e-16
gb|L02963|NEUCLMDLN Neurospora crassa calmodulin mRNA, complete ... 74 1e-16
emb|AW625406|AW625406 EST319229 tomato radicle, 5 d post-imbibit... 62 1e-16
gb|K02944|TRBCMRSB Trypanosoma brucei gambiense calmodulin genes... 73 2e-16
40 gb|M88307|BNACALM Brassica juncea calmodulin mRNA, complete cds. 73 2e-16
gb|U10150|BNU10150 Brassica napus Naehan calmodulin (bcm1) mRNA,... 73 2e-16
emb|X89890|BPCALMGEM B.pilosa mRNA for calmodulin. 73 2e-16
emb|AW099396|AW099396 sd39h01.y1 Gm-c1016 Glycine max cDNA clone... 76 2e-16
emb|AW101324|AW101324 sd77e09.y1 Gm-c1009 Glycine max cDNA clone... 59 2e-16
45 emb|AL112713|CNS01AB5 Botrytis cinerea strain T4 cDNA library un... 73 2e-16
emb|AL114582|CNS01BR2 Botrytis cinerea strain T4 cDNA library un... 74 2e-16
emb|AL112170|CNS019W2 Botrytis cinerea strain T4 cDNA library un... 74 2e-16
emb|AL114124|CNS01BEC Botrytis cinerea strain T4 cDNA library un... 74 2e-16
emb|AL115056|CNS01C48 Botrytis cinerea strain T4 cDNA library un... 73 2e-16
50 emb|AL116760|CNS01DFK Botrytis cinerea strain T4 cDNA library un... 73 2e-16
emb|AW573768|AW573768 EST316359 GVN Medicago truncatula cDNA clo... 72 2e-16
emb|Y13784|MSCALMODU Mougeotia scalaris mRNA for calmodulin. 70 3e-16
emb|AI727960|AI727960 BNLGHi9833 Six-day Cotton fiber Gossypium ... 73 3e-16
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55 emb|AW164628|AW164628 se74e01.y1 Gm-c1023 Glycine max cDNA clone... 60 3e-16
emb|AF150059|AF150059 Brassica napus calmodulin (CaM1) mRNA, com... 72 3e-16
emb|AW738989|AW738989 gb23c06.y1 Moss EST library PPN Physcomitr... 73 3e-16
gb|U48693|TAU48693 Triticum aestivum calmodulin TaCaM3-1 mRNA, c... 73 4e-16
gb|M27303|BLYCAMA Barley cam gene encoding calmodulin, complete ... 73 4e-16
60 gb|BE033450|BE033450 ME02B08 ME Mesembryanthemum crystallinum cD... 73 4e-16
emb|AF064552|AF064552 Apium graveolens calmodulin mRNA, complete... 73 4e-16

- gb|S81594|S81594 auxin-regulated calmodulin [*Vigna radiata*=mung ... 73 4e-16
 gb|L20691|VIRCALMOD *Vigna radiata* calmodulin mRNA, complete cds. 73 4e-16
 emb|AW730911|AW730911 GA_Ea0029I11 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 gb|BE036340|BE036340 MO23E04 *MO Mesembryanthemum crystallinum* cD... 73 4e-16
 5 emb|AF030032|AF030032 *Phaseolus vulgaris* calmodulin (CaM) mRNA, ... 73 4e-16
 gb|L01431|SOYSCAM2X Soybean calmodulin (SCaM-2) mRNA, complete cds. 73 4e-16
 emb|Y09853|CACAM *Cicer arietinum* mRNA for CaM protein. 73 4e-16
 gb|L01432|SOYSCAM3X Soybean calmodulin (SCaM-3) mRNA, complete cds. 73 4e-16
 gb|U49104|TAU49104 *Triticum aestivum* calmodulin TaCaM3-3 mRNA, c... 73 4e-16
 10 gb|U49105|TAU49105 *Triticum aestivum* calmodulin TaCaM4-1 mRNA, c... 73 4e-16
 emb|AF030034|AF030034 *Phaseolus vulgaris* calmodulin (CaM) mRNA, ... 73 4e-16
 emb|AW728030|AW728030 GA_Ea0029H21 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 gb|L20507|VIRCALMODU *Vigna radiata* (clone pMBCaM-1) calmodulin m... 73 4e-16
 gb|U48242|TAU48242 *Triticum aestivum* calmodulin TaCaM1-1 mRNA, c... 73 4e-16
 15 gb|M80836|PETCAM81 *Petunia hybrida* CAM81 mRNA, 73 4e-16
 gb|U49103|TAU49103 *Triticum aestivum* calmodulin TaCaM3-2 mRNA, c... 73 4e-16
 emb|X52398|MSCAL1 Alfalfa call mRNA for calmodulin. 73 4e-16
 gb|U48688|TAU48688 *Triticum aestivum* calmodulin TaCaM1-2 mRNA, c... 73 4e-16
 gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16
 20 emb|AW927068|AW927068 HVSMEg0009G21 *Hordeum vulgare* pre-anthesis... 73 4e-16
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 emb|AW348582|AW348582 GM210002B22C3R *Gm-r1021* Glycine max cDNA 3... 73 4e-16
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 25 emb|AW775754|AW775754 EST334819 DSIL *Medicago truncatula* cDNA cl... 73 4e-16
 gb|BE052400|BE052400 GA_Ea0001L24f *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 emb|AW666735|AW666735 GA_Ea0005N08 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 gb|U13882|PSU13882 *Pisum sativum* Alaska calmodulin mRNA, complet... 73 4e-16
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 30 emb|AW666619|AW666619 GA_Ea0005C16 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 emb|AW108833|AW108833 gate0001L24f *Gossypium arboreum* 7-10 dpa f... 73 4e-16
 emb|Z12839|LLCALMOD *Lilium longiflorum* mRNA encoding calmodulin. 73 4e-16
 gb|L18912|LILCALMODU *Lilium longiflorum* calmodulin mRNA, complet... 73 4e-16

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 gp|u58314|1491939 [arabidopsis thaliana] /blast_score 0
 (2661 letters)

40 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

45 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

- gb|U58314|CBU58314 *Clarkia breweri* S-linalool synthase (Lis) mRN... 146 e-171
 50 emb|AF067603|AF067603 *Clarkia breweri* linalool synthase 2 (LIS2)... 149 e-154
 emb|AF067602|AF067602 *Clarkia concinna* linalool synthase gene, c... 112 1e-53
 emb|AF097310|AF097310 *Stevia rebaudiana* kaurene synthase (KS1-1)... 88 5e-31
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 emb|AF067604|AF067604 *Oenothera arizonica* linalool synthase-like... 75 5e-24
 55 emb|AF067601|AF067601 *Clarkia breweri* linalool synthase 1 (LIS1)... 86 1e-17
 gb|U43904|CMU43904 *Cucurbita maxima* ent-kaurene synthase B mRNA,... 63 5e-17
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 emb|AI485623|AI485623 EST243944 tomato ovary, TAMU *Lycopersicon* ... 55 9e-14
 gb|U92267|AGU92267 *Abies grandis* gamma-humulene synthase mRNA, c... 45 2e-10
 60 gb|U50768|AGU50768 *Abies grandis* abietadiene synthase (ac22) mRN... 58 6e-10
 emb|AW255432|AW255432 ML454 peppermint glandular trichome *Mentha*... 56 1e-08

	emb AW255334 AW255334 ML343 peppermint glandular trichome Mentha...	56	1e-08
	emb AF233894 AF233894 Perilla citriodora limonene synthase mRNA,...	62	2e-08
	gb U87909 AGU87909 Abies grandis pinene synthase (AG3.18) mRNA, ...	61	5e-08
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5	emb AF006195 AF006195 Abies grandis E-alpha-bisabolene synthase ...	55	7e-08
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10	gb U63652 PSU63652 Pisum sativum ent-kaurene synthase A (LS) mRN...	60	1e-07
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	emb AI491074 AI491074 EST241783 tomato shoot, Cornell Lycopersic...	38	1e-07
	emb AW617193 AW617193 EST323604 L. hirsutum trichome, Cornell Un...	40	2e-07
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	emb AW616908 AW616908 EST323319 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AW617347 AW617347 EST323758 L. hirsutum trichome, Cornell Un...	39	3e-07
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	emb AW617665 AW617665 EST324076 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AW617376 AW617376 EST323787 L. hirsutum trichome, Cornell Un...	39	3e-07
	emb AF049905 AF049905 Cucurbita maxima copalyl diphosphate synth...	58	3e-07
	emb AW616328 AW616328 EST322739 L. hirsutum trichome, Cornell Un...	38	5e-07
30	emb AW624730 AW624730 EST322675 tomato flower buds 3-8 mm, Come...	37	6e-07
	emb AB042424 AB042424 Croton sublyratus cps mRNA for copalyl dip...	57	7e-07
	emb AW254843 AW254843 ML1265 peppermint glandular trichome Mentha...	57	7e-07
	emb AW254789 AW254789 ML1071 peppermint glandular trichome Mentha...	57	7e-07
	emb AW254821 AW254821 ML1244 peppermint glandular trichome Mentha...	57	7e-07
35	emb AW255149 AW255149 ML145 peppermint glandular trichome Mentha...	57	7e-07
	emb AW255044 AW255044 ML1227 peppermint glandular trichome Mentha...	57	7e-07
	emb AF139207 AF139207 Abies grandis (-)-limonene/(-)-alpha-pinen...	57	9e-07
	emb AW616366 AW616366 EST322777 L. hirsutum trichome, Cornell Un...	36	2e-06
	emb AW255042 AW255042 ML1225 peppermint glandular trichome Mentha...	55	2e-06
40	emb AW255052 AW255052 ML1347 peppermint glandular trichome Mentha...	55	2e-06
	emb AW254888 AW254888 ML1312 peppermint glandular trichome Mentha...	55	2e-06
	emb AW687409 AW687409 NF009C09RT1F1069 Developing root Medicago ...	54	5e-06
	emb AB015675 AB015675 Lycopersicon esculentum CPS mRNA for copal...	54	5e-06
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45	emb AF175323 AF175323 Mentha longifolia limonene synthase mRNA, ...	54	6e-06
	gb L13459 MHC4SLSP Mentha spicata 4S-limonene synthase mRNA, com...	54	6e-06
	emb AW255678 AW255678 ML735 peppermint glandular trichome Mentha...	53	1e-05
	emb AF139205 AF139205 Abies grandis beta-phellandrene synthase (...)	52	2e-05
	emb AW617714 AW617714 EST324125 L. hirsutum trichome, Cornell Un...	33	2e-05
50	emb AF154125 AF154125 Artemisia annua (3R)-linalool synthase (QH...	51	4e-05
	emb AF049906 AF049906 Cucurbita maxima copalyl diphosphate synth...	51	4e-05
	emb AW684730 AW684730 NF020C02NR1F1000 Nodulated root Medicago t...	51	4e-05
	gb U87908 AGU87908 Abies grandis myrcene synthase (AG2.2) mRNA, ...	51	6e-05
	emb AW255083 AW255083 ML1378 peppermint glandular trichome Mentha...	51	6e-05
55	emb AW254876 AW254876 ML1300 peppermint glandular trichome Mentha...	49	2e-04
	gb U48796 TBU48796 Taxus brevifolia taxadiene synthase (TDC1) mR...	49	2e-04
	emb AF051899 AF051899 Salvia officinalis 1,8-cineole synthase mR...	48	4e-04
	emb AF006193 AF006193 Abies grandis (-)-4S-limonene synthase mRN...	47	5e-04
	emb AF154124 AF154124 Artemisia annua (3R)-linalool synthase (QH...	46	0.001
60	emb AF139206 AF139206 Abies grandis terpinolene synthase (agc9) ...	45	0.004
	emb AW687308 AW687308 NF008C02RT1F1008 Developing root Medicago ...	44	0.005

	emb AF051900 AF051900 <i>Salvia officinalis</i> (+)-bornyl diphosphate ...	43	0.009
	emb AF212433 AF212433 <i>Capsicum annuum</i> UV-induced sesquiterpene c...	43	0.009
	emb AF061285 AF061285 <i>Capsicum annuum</i> sesquiterpene cyclase mRNA...	43	0.009
	emb AW685590 AW685590 NF029D03NR1F1000 Nodulated root <i>Medicago t...</i>	34	0.014
5	emb AW125997 AW125997 N100193e rootphos(-) <i>Medicago truncatula</i> c...	34	0.015
	emb AW622483 AW622483 EST313271 tomato root during/after fruit s...	42	0.018
	emb AW254970 AW254970 ML1141 peppermint glandular trichome <i>Menth...</i>	41	0.034
	emb AB006530 AB006530 <i>Citrullus lanatus</i> Sat gene for serine acet...	41	0.046
	emb AW559431 AW559431 EST314479 DSIR <i>Medicago truncatula</i> cDNA cl...	32	0.065
10	emb AW255471 AW255471 ML495 peppermint glandular trichome <i>Mentha...</i>	40	0.087
	emb AB005744 AB005744 <i>Perilla frutescens</i> DNA for 1-limonene synt...	40	0.087
	emb AW616571 AW616571 EST322982 <i>L. hirsutum</i> trichome, Cornell Un...	30	0.17
	emb AW617415 AW617415 EST323826 <i>L. hirsutum</i> trichome, Cornell Un...	30	0.17
	gb U20189 HMU20189 <i>Hyoscyamus muticus</i> clone cVS2 vetispiradiene ...	39	0.23
15	emb AF042382 AF042382 <i>Solanum tuberosum</i> vetispiradiene synthase ...	38	0.31
	emb AF043300 AF043300 <i>Solanum tuberosum</i> putative vetispiradiene ...	38	0.31
	emb AB022720 AB022720 <i>Solanum tuberosum</i> PVS3 mRNA for vetispirad...	38	0.31
	gb L32134 RCCCASSYNT <i>Ricinus communis</i> casbene synthase mRNA.	38	0.43
	emb AW043070 AW043070 ST28H10 Pine TriplEx shoot tip library Pin...	38	0.43
20	emb AI940878 AI940878 sb79b02.y1 Gm-c1010 <i>Glycine max</i> cDNA clone...	38	0.43
	emb AB022719 AB022719 <i>Solanum tuberosum</i> PVS2 mRNA for vetispirad...	37	0.58
	emb AF043298 AF043298 <i>Solanum tuberosum</i> putative vetispiradiene ...	37	0.58
	emb AF043299 AF043299 <i>Solanum tuberosum</i> putative vetispiradiene ...	37	0.58
	emb AJ001452 FVAJ1452 <i>Fragaria vesca</i> partial mRNA for putative s...	30	0.70
25	emb AB022598 AB022598 <i>Solanum tuberosum</i> PVS1 mRNA for vetispirad...	36	1.1
	emb AB023816 AB023816 <i>Solanum tuberosum</i> PVS4 mRNA for vetispirad...	36	1.1

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(1580 letters)

35 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	emb AB001379 AB001379 <i>Glycyrrhiza echinata</i> CYP81E1 mRNA for cyto...	376	e-149	
	emb AB022732 AB022732 <i>Glycyrrhiza echinata</i> CYP Ge-31 mRNA for cy...	376	e-149	
	emb AJ238439 CAR238439 <i>Cicer arietinum</i> mRNA for a cytochrome P45...	377	e-147	
45	emb AJ012581 CAR012581 <i>Cicer arietinum</i> mRNA for cytochrome P450.	376	e-147	
	emb AJ239051 CAR239051 <i>Cicer arietinum</i> mRNA for cytochrome P450 ...	255	e-145	
	emb AB025016 AB025016 <i>Lotus japonicus</i> mRNA for cytochrome P450, ...	340	e-142	
	emb AJ249800 CAR249800 <i>Cicer arietinum</i> partial mRNA for cytochro...	352	3e-96	
	emb AJ000478 HTCYP81L <i>Helianthus tuberosus</i> mRNA for cytochrome P...	225	4e-84	
50	emb AJ000477 HTCYP81C <i>Helianthus tuberosus</i> mRNA for cytochrome P...	225	4e-84	
	emb AW185361 AW185361 se90e02.y1 Gm-c1027 <i>Glycine max</i> cDNA clone...	302	5e-81	
	emb AJ249801 CAR249801 <i>Cicer arietinum</i> partial mRNA for cytochro...	298	6e-80	
	emb AF082028 AF082028 <i>Hemerocallis</i> hybrid cultivar senescence-as...	209	4e-76	
	emb AW733691 AW733691 sk83g07.y1 Gm-c1016 <i>Glycine max</i> cDNA clone...	277	2e-73	
55	emb AW307234 AW307234 sf54d12.y1 Gm-c1009 <i>Glycine max</i> cDNA clone...	275	6e-73	
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60	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber <i>Gossypium</i> ...	188	2e-62	
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- emb|AW329224|AW329224 N200436e rootphos(-) *Medicago truncatula* c... 228 1e-58
emb|AW932147|AW932147 EST357990 tomato fruit mature green, TAMU ... 226 3e-58
emb|AW100311|AW100311 sd22g12.y2 Gm-c1012 *Glycine max* cDNA clone... 218 8e-56
emb|AF014802|AF014802 *Eschscholzia californica* (S)-N-methylcocla... 177 9e-56
5 emb|AI774414|AI774414 EST255514 tomato resistant, Cornell Lycopen... 152 9e-56
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10 emb|AV412147|AV412147 AV412147 *Lotus japonicus* young plants (two... 204 2e-51
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dbj|D83968|SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... 116 5e-50
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emb|AI731081|AI731081 BNLGHI8648 Six-day Cotton fiber *Gossypium* ... 198 1e-49
emb|AW257188|AW257188 EST305325 KV2 *Medicago truncatula* cDNA clo... 152 2e-49
15 emb|AW309826|AW309826 sf25c03.x1 Gm-c1028 *Glycine max* cDNA clone... 196 5e-49
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20 emb|X71657|SMCYPEG7 *S.melongena* CYP76A2 mRNA for hydroxylase. 160 4e-47
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emb|X71658|SMCYPEG8 *S.melongena* CYP76A1 mRNA. 161 7e-47
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25 emb|Y10982|GMP450CP6 *Glycine max* mRNA for cytochrome P450-like p... 159 9e-47
emb|Y09920|HT7ECODET *Helianthus tuberosus* mRNA for 7-ethoxycouma... 156 1e-46
emb|Y10098|HTCYP76B1 *H.tuberosus* mRNA for 7-ethoxycoumarin O-dec... 156 1e-46
emb|AF124372|AF124372 *Nicotiana tabacum* NT7 mRNA, partial cds. 145 1e-46
emb|AW728802|AW728802 GA_Ea0028I12 *Gossypium arboreum* 7-10 dpa ... 168 2e-46
30 emb|AF156976|AF156976 *Gerbera hybrida* flavone synthase II (CYP93... 103 2e-46
emb|X96784|NTP450GEN *N.tabacum* cytochrome P-450 gene. 162 6e-46
dbj|D14590|D14590 *Campanula medium* mRNA for flavonoid 3',5'-hydr... 157 1e-45
emb|AW616482|AW616482 EST322893 *L. hirsutum* trichome, Cornell Un... 124 2e-45
emb|AW617814|AW617814 EST324213 *L. hirsutum* trichome, Cornell Un... 124 2e-45
35 emb|AF155332|AF155332 *Petunia x hybrida* flavonoid 3'-hydroxylase... 183 2e-45
emb|AW616075|AW616075 EST296834 *L. hirsutum* trichome, Cornell Un... 124 5e-45
gb|U72654|EGU72654 *Eustoma grandiflorum* flavonoid 3',5'-hydroxyla... 160 6e-45
gb|M32885|AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... 160 8e-45
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40 emb|AW102198|AW102198 sd84f03.y1 Gm-c1009 *Glycine max* cDNA clone... 181 1e-44
dbj|D14589|D14589 *Eustoma russellianum* mRNA for flavonoid 3',5'-... 160 2e-44
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45 emb|AW309498|AW309498 sf20c05.x1 Gm-c1028 *Glycine max* cDNA clone... 178 1e-43
emb|AF135485|AF135485 *Glycine max* cytochrome P450 monooxygenaseC... 100 1e-43
gb|U29333|PSU29333 *Pisum sativum* novel wound-inducible cytochrom... 157 1e-43
emb|AW616143|AW616143 EST296912 *L. hirsutum* trichome, Cornell Un... 128 1e-43
emb|AW616066|AW616066 EST296823 *L. hirsutum* trichome, Cornell Un... 122 1e-43
50 emb|AW255096|AW255096 ML139 peppermint glandular trichome *Mentha*... 162 2e-43
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emb|AW651341|AW651341 EST329795 tomato germinating seedlings, TA... 156 9e-43
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55 emb|AB023636|AB023636 *Glycyrrhiza echinata* CYP Ge-8 mRNA for cyt... 107 4e-42
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60 emb|AI731481|AI731481 BNLGHI9879 Six-day Cotton fiber *Gossypium* ... 171 9e-42
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 5 emb|AB022733|AB022733 Glycyrrhiza echinata CYP Ge-51 mRNA for cy... 104 4e-41
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 15 emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 168 9e-41
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| 35 | gb U64925 NTU64925 Nicotiana tabacum geranylgeranylated protein ... | 260 | 1e-68 | |
| | emb AW625701 AW625701 EST319608 tomato radicle, 5 d post-imbibit... | 228 | 6e-59 | |
| | emb AW720227 AW720227 LjNEST17c4r Lotus japonicus nodule library... | 219 | 4e-56 | |
| | emb AW220184 AW220184 EST302667 tomato root during/after fruit s... | 208 | 7e-53 | |
| | emb AI774580 AI774580 EST255680 tomato resistant, Cornell Lycopersicon... | 173 | 2e-42 | |
| 40 | emb AW685484 AW685484 NF030E02NR1F1000 Nodulated root Medicago t... | 171 | 2e-41 | |
| | emb AI443867 AI443867 sa44d09.y1 Gm-c1004 Glycine max cDNA clone... | 170 | 3e-41 | |
| | emb AW397252 AW397252 sg76f06.y1 Gm-c1007 Glycine max cDNA clone... | 168 | 1e-40 | |
| | emb AW033368 AW033368 EST276939 tomato callus, TAMU Lycopersicon... | 162 | 5e-39 | |
| | emb AV417858 AV417858 AV417858 Lotus japonicus young plants (two... | 153 | 4e-36 | |
| 45 | emb AI780050 AI780050 EST260929 tomato susceptible, Cornell Lyco... | 138 | 9e-32 | |
| | emb AW039095 AW039095 EST281068 tomato mixed elicitor, BTI Lycopersicon... | 111 | 2e-23 | |
| | emb AI780139 AI780139 EST261018 tomato susceptible, Cornell Lyco... | 86 | 7e-16 | |
| | emb AW164180 AW164180 Ljirmp21-672-c8 Ljirmp Lambda HybriZap ... | 84 | 2e-15 | |
| | emb AI781596 AI781596 EST262475 tomato susceptible, Cornell Lyco... | 75 | 1e-12 | |
| 50 | emb AW774764 AW774764 EST333915 KV3 Medicago truncatula cDNA clo... | 62 | 7e-09 | |
| | emb AW348781 AW348781 GM210003A22H11R Gm-r1021 Glycine max cDNA ... | 54 | 2e-06 | |
| | emb AI491210 AI491210 EST241919 tomato shoot, Cornell Lycopersicon... | 29 | 0.010 | |
| | emb AW651526 AW651526 EST329980 tomato germinating seedlings, TA... | 29 | 0.011 | |
| | emb AW220594 AW220594 EST296979 tomato fruit mature green, TAMU ... | 29 | 0.011 | |
| 55 | emb AW926585 AW926585 HVSMEg0007J19 Hordeum vulgare pre-anthesis... | 29 | 0.025 | |
| | emb AW032321 AW032321 EST275775 tomato callus, TAMU Lycopersicon... | 28 | 0.026 | |
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	emb AW727289 AW727289 GA_Ea0011H24 Gossypium arboreum 7-10 dpa ...	35	1.9
	gb L36856 PEAIAP34A Pisum sativum GTP-binding protein (IAP34) mR...	28	2.1
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	emb AW256896 AW256896 EST305033 KV2 Medicago truncatula cDNA clo...	28	2.3
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35	emb AF124792 AF124792 Sporothrix schenckii protein kinase C (PCK...	29	4.7
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	gb L25088 YSCMEF2MIT Saccharomyces cerevisiae nuclear-encoded mi...	33	6.8
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50	emb AW738509 AW738509 EST339936 tomato flower buds, anthesis, Co...	32	9.4
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	emb Y11565 NC11565 N.crassa acu-15 gene.	32	9.4
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5 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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15	emb AI485780 AI485780 EST244101 tomato ovary, TAMU Lycopersicon ...	242	1e-85
	emb AI485695 AI485695 EST244016 tomato ovary, TAMU Lycopersicon ...	261	3e-85
	emb AI485239 AI485239 EST243543 tomato ovary, TAMU Lycopersicon ...	291	1e-77
	emb AI899197 AI899197 EST268640 tomato ovary, TAMU Lycopersicon ...	161	1e-77
	emb AW034573 AW034573 EST278257 tomato callus, TAMU Lycopersicon...	272	8e-72
20	emb AI488812 AI488812 EST247151 tomato ovary, TAMU Lycopersicon ...	251	1e-65
	emb AW687082 AW687082 NF005G09RT1F1071 Developing root Medicago ...	182	6e-65
	emb AI898248 AI898248 EST267691 tomato ovary, TAMU Lycopersicon ...	204	1e-63
	emb AI483614 AI483614 EST249464 tomato ovary, TAMU Lycopersicon ...	238	1e-61
	emb AI897089 AI897089 EST266532 tomato ovary, TAMU Lycopersicon ...	226	7e-58
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	emb AW559604 AW559604 EST314652 DSIR Medicago truncatula cDNA cl...	177	3e-53
	emb AI485284 AI485284 EST243588 tomato ovary, TAMU Lycopersicon ...	204	3e-51
	emb AI485664 AI485664 EST243985 tomato ovary, TAMU Lycopersicon ...	195	8e-49
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	emb AI485008 AI485008 EST243271 tomato ovary, TAMU Lycopersicon ...	157	2e-37
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35	emb AI967736 AI967736 Ljirnp11-837-a7 Ljirnp Lambda HybriZap ...	147	4e-34
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40	emb X94335 SC130KBXV S.cerevisiae 130kb DNA fragment from chromo...	51	1e-29
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	emb X79743 SCBPPS S.cerevisiae BET1, PAN1 PRI1 and STS1 genes.	72	2e-27
	emb Z38062 SC9687 S.cerevisiae chromosome IX cosmid 9687.	72	2e-27
45	emb AI488810 AI488810 EST247149 tomato ovary, TAMU Lycopersicon ...	121	3e-26
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	emb AW257207 AW257207 EST305344 KV2 Medicago truncatula cDNA clo...	75	2e-24
	emb AV406995 AV406995 AV406995 Lotus japonicus young plants (two...	67	2e-23
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	emb AI771644 AI771644 EST252744 tomato ovary, TAMU Lycopersicon ...	104	3e-21
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5 emb|AQ644913|AQ644913 RPCI93-EcoRI-2C7.TV RPCI93-EcoRI Trypanoso... 53 1e-13
emb|AA495505|AA495505 c430 Zhou and Ragan 1993 Gracilaria gracil... 49 4e-13
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emb|AW666237|AW666237 sk34b04.y1 Gm-c1028 Glycine max cDNA clone... 77 4e-13
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15 emb|AW695904|AW695904 NF099H04ST1F1043 Developing stem Medicago ... 49 2e-10
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20 emb|AW333870|AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c... 36 4e-09
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25 emb|AW693686|AW693686 NF068A05ST1F1036 Developing stem Medicago ... 62 2e-08
emb|AW208046|AW208046 M111077e DSIR Medicago truncatula cDNA clo... 61 4e-08
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30 emb|AI781410|AI781410 EST262277 tomato susceptible, Cornell Lyco... 52 2e-05
emb|AW617564|AW617564 EST323975 L. hirsutum trichome, Cornell Un... 49 2e-04
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35 emb|AQ655271|AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso... 38 0.004
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emb|AW437996|AW437996 ST83C09 Pine TriplEx shoot tip library Pin... 42 0.014
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40 gb|M28064|PFAHRKP Plasmodium brasilianum DNA homologous to the h... 37 0.45
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emb|AW774740|AW774740 EST333891 KV3 Medicago truncatula cDNA clo... 36 1.2
50 emb|Z38060|SC5610 S.cerevisiae chromosome IX sequence derived fr... 36 1.2
emb|AL031745|PFMAL1P2 Plasmodium falciparum chromosome 1 strain ... 35 2.2

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55 emb|cab52675.1| (aj010971) glucose-6-phosphate 1-dehydrogenase
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Database: plantfungal
60 661,018 sequences; 426,114,510 total letters

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	emb AF012862 AF012862	Petroselinum crispum cytosolic glucose-6-p...	841 0.0
	emb AJ001770 NTTCG9	Nicotiana tabacum mRNA for cytosolic glucose...	893 0.0
	gb U18238 MSU18238	Medicago sativa glucose-6-phosphate dehydroge...	900 0.0
10	emb AF012863 AF012863	Petroselinum crispum cytosolic glucose-6-p...	887 0.0
	emb AJ001769 NTTCG6	Nicotiana tabacum mRNA cytosolic glucose-6-p...	895 0.0
	emb AF097663 AF097663	Mesembryanthemum crystallinum cytoplasmic ...	754 0.0
	emb AB011441 AB011441	Triticum aestivum WESR5 mRNA for glucose-6...	500 e-141
	emb X70373 KLLTZWF	K.lactis LET1 gene and ZWF gene for glucose...	231 e-138
15	emb Z69381 SCCXIV39K	S.cerevisiae 38,855 bp segment of chromosom...	244 e-136
	gb M34709 YSCG6PD	S.cerevisiae glucose-6-phosphate dehydrogenase...	244 e-136
	emb X57336 SCMET19	S. cerevisiae MET19 gene for glucose-6-phosph...	244 e-136
	emb Z71517 SCYNL241C	S.cerevisiae chromosome XIV reading frame O...	244 e-136
	emb AJ010712 STU010712	Solanum tuberosum mRNA for glucose-6-phos...	240 e-136
20	emb X99405 NTG6PD	N.tabacum mRNA for chloroplast glucose-6-phosp...	242 e-135
	emb AF012861 AF012861	Petroselinum crispum plastidic glucose-6-p...	248 e-135
	emb AI730607 AI730607	BNLGH17371 Six-day Cotton fiber Gossypium ...	481 e-135
	emb X87942 ANG6PDHSE	A.niger mRNA for glucose-6-phosphate dehydr...	225 e-132
	emb AW686120 AW686120	NF038D09NR1F1000 Nodulated root Medicago t...	472 e-132
25	emb AJ132346 DBI132346	Dunaliella bioculata mRNA for plastidic g...	235 e-132
	emb AW925642 AW925642	HVSMEg0005C04 Hordeum vulgare pre-anthesis...	465 e-130
	emb AJ001772 NTTPG18	Nicotiana tabacum mRNA for plastidic glucos...	243 e-129
	emb AW930385 AW930385	EST340938 tomato fruit mature green, TAMU ...	444 e-124
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30	emb X83923 STG6PDHPI	S.tuberosum mRNA for glucose-6-phosphate de...	249 e-118
	emb AJ000182 SO000182	Spinacia oleracea mRNA for glucose-6-phosp...	242 e-117
	emb AJ001771 NTTPG16	Nicotiana tabacum mRNA for plastidic glucos...	247 e-116
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35	emb AW233801 AW233801	sf26h03.y1 Gm-c1028 Glycine max cDNA clone...	415 e-115
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40	emb AJ006246 CCA6246	Cyanidium caldarium mRNA for glucose-6-phos...	239 e-102
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	emb AJ000183 SO000183	Spinacia oleracea mRNA for glucose-6-phosp...	190 3e-99
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	emb AW560329 AW560329	EST315377 DSIR Medicago truncatula cDNA cl...	323 2e-87
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	emb AW219903 AW219903	EST302386 tomato root during/after fruit s...	305 7e-82
	emb AW180861 AW180861	MgA1030f MgA Library Mycosphaerella gramin...	226 5e-80
	emb AW616585 AW616585	EST322996 L. hirsutum trichome, Cornell Un...	175 7e-80
	emb AW309937 AW309937	sf26h03.x1 Gm-c1028 Glycine max cDNA clone...	294 1e-78
55	emb AW031447 AW031447	EST274901 tomato callus, TAMU Lycopersicon...	166 6e-78
	emb AI894720 AI894720	EST264163 tomato callus, TAMU Lycopersicon...	291 1e-77
	emb AW690515 AW690515	NF030E09ST1F1000 Developing stem Medicago ...	174 3e-77
	emb AW736245 AW736245	EST332231 KV3 Medicago truncatula cDNA clo...	278 7e-76
	emb AW455246 AW455246	EST311906 tomato root during/after fruit s...	155 6e-75
60	emb AW980010 AW980010	EST310488 tomato root deficiency, Cornell ...	153 3e-74
	emb AL023595 SPCC794	S.pombe chromosome III cosmid c794.	177 1e-73

- emb|AW255521|AW255521 ML551 peppermint glandular trichome Mentha... 270 3e-71
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 5 emb|AW737104|AW737104 EST338531 tomato flower buds, anthesis, Co... 141 1e-64
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 emb|AW737079|AW737079 EST338506 tomato flower buds, anthesis, Co... 141 3e-64
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 emb|AW617385|AW617385 EST323796 L. hirsutum trichome, Cornell Un... 141 2e-57
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 15 emb|X77829|ANNGSDA A.niger (N400) gsdA gene. 131 4e-55
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 25 emb|AJ279688|BPE279688 Betula pendula partial mRNA for Glucose-6... 93 7e-47
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 30 emb|AW980083|AW980083 EST341594 tomato root deficiency, Cornell ... 133 2e-42
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 Sequences producing significant alignments: (bits) Value

60 emb|AW725454|AW725454 GA_Ea0018A14 Gossypium arboreum 7-10 dpa ... 238 8e-81
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- gb|U34860|SCU34860 *Saccharomyces cerevisiae* origin recognition c... 122 2e-33
 dbj|D38172|YSCTEM1P Yeast gene for GTP-binding protein Tem1p, co... 122 2e-33
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 emb|Y12314|SPSPG1GEN *S.pombe* spg1 gene. 67 9e-20
 5 emb|AJ001587|SPAJ1587 *Schizosaccharomyces pombe* sid3 gene. 67 9e-20
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 gb|L08691|YSCGSP2X Yeast GTP-binding protein (GSP2) gene, comple... 32 2e-06
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 emb|X71945|SCCNR1A *S.cerevisiae* CNR1 gene. 32 2e-06
 dbj|D17748|TETTRAN *Tetrahymena thermophila* mRNA for Ran/TC4, com... 33 3e-06
 15 dbj|D21825|TETPRAN *Tetrahymena pyriformis* mRNA for Ran/TC4, comp... 33 3e-06
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 35 emb|AW930158|AW930158 EST340615 tomato fruit mature green, TAMU ... 36 0.33
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 40 emb|AW040005|AW040005 EST282496 tomato mixed elicitor, BTI Lycop... 35 0.56
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 emb|AW705209|AW705209 sk43a11.y1 Gm-c1019 Glycine max cDNA clone... 35 0.57
 45 emb|AV414769|AV414769 AV414769 *Lotus japonicus* young plants (two... 35 0.62
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 50 emb|AV413108|AV413108 AV413108 *Lotus japonicus* young plants (two... 35 0.62
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 emb|AI937960|AI937960 sc06b11.y1 Gm-c1012 Glycine max cDNA clone... 35 0.62
 emb|Z73961|LJRAC1 *L.japonicus* mRNA for small GTP-binding protein... 35 0.62
 emb|AI162198|AI162198 A013P52U Hybrid aspen plasmid library Popu... 35 0.62
 55 emb|AW694335|AW694335 NF075C06ST1F1049 Developing stem *Medicago ...* 35 0.62
 emb|AW109094|AW109094 gate0002P07f *Gossypium arboreum* 7-10 dpa f... 35 0.62
 gb|L19093|PEARHOGTPP *Pisum sativum* rho (ras-related) GTP-binding... 35 0.62
 emb|AW565277|AW565277 LG1_332_G03.b1_A002 Light Grown 1 (LG1) So... 35 0.62
 emb|AV412205|AV412205 AV412205 *Lotus japonicus* young plants (two... 35 0.62
 60 gb|BE054534|BE054534 GA_Ea0033M19f *Gossypium arboreum* 7-10 dpa ... 35 0.62
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	emb AF146341 AF146341 Physcomitrella patens Rac-like GTP binding...	35	0.85
	emb AI731831 AI731831 BNLGHI11032 Six-day Cotton fiber Gossypium...	35	0.85
20	emb AF051223 AF051223 Picea mariana Rac-like GTP binding protein...	35	0.85
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	emb AW217573 AW217573 EST296287 tomato flower buds 3-8 mm, Corne...	34	1.6
	emb Z36133 SCYBR264C S.cerevisiae chromosome II reading frame OR...	34	1.6
	emb X70529 SCCIIORF S. cerevisiae chromosome II sequence for ORF...	34	1.6
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	gb BE036577 BE036577 MP01F02 MP Mesembryanthemum crystallinum cD...	34	2.2
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	gb U18556 RSU18556 Raphanus sativus antifungal protein 2 preprot...	160	1e-38
	emb X97319 RSEFP3 R.sativus mRNA for antifungal protein 3.	133	8e-37
	gb U59459 BNU59459 Brassica napus antifungal protein mRNA, compl...	135	2e-36
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	emb A27062 A27062 C.benedictus AMP2 sequence.	73 1e-12
	emb X53375 HASF18 Sunflower anther-specific mRNA SF18.	72 3e-12
	emb A26906 A26906 C.benedictus AMP1 sequence.	72 3e-12
	emb AT001738 AT001738 AT001738 Flower bud cDNA Brassica rapa sub...	69 2e-11
5	emb A27064 A27064 C.ternatea AMP1 sequence.	58 8e-10
	emb X91487 PASPI1GEN P.abies mRNA for gamma-thionin protein (put...	40 1e-05
	emb AW870017 AW870017 NXNV_122_A10_F Nsf Xylem Normal wood Verti...	35 6e-05
	emb AW064751 AW064751 ST35D04 Pine TriplEx shoot tip library Pin...	36 7e-05
	emb AW775186 AW775186 EST331908 GVN Medicago truncatula cDNA clo...	41 0.001
10	dbj D29679 TOBPIT1A Tobacco pit1 mRNA (which expression is induc...	41 0.003
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	emb AW623112 AW623112 EST321057 tomato flower buds 3-8 mm, Corne...	40 0.008
	emb AW220231 AW220231 EST302714 tomato root during/after fruit s...	36 0.008
15	emb AW219164 AW219164 EST301646 tomato root during/after fruit s...	36 0.008
	emb AW219793 AW219793 EST302275 tomato root during/after fruit s...	36 0.009
	emb AI487824 AI487824 EST246146 tomato ovary, TAMU Lycopersicon ...	40 0.009
	emb AI483999 AI483999 EST249870 tomato ovary, TAMU Lycopersicon ...	40 0.010
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20	emb AW622923 AW622923 EST306993 tomato flower buds 3-8 mm, Corne...	40 0.010
	emb AW929929 AW929929 EST354199 tomato flower buds 8 mm to pre-a...	40 0.010
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25	emb AW217379 AW217379 EST296063 tomato flower buds 0-3 mm, Corne...	40 0.012
	emb AI484887 AI484887 EST243150 tomato ovary, TAMU Lycopersicon ...	40 0.012
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	emb AW622375 AW622375 EST313174 tomato root during/after fruit s...	35 0.026
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	emb AW622051 AW622051 EST312849 tomato root during/after fruit s...	34 0.053
45	emb AI485044 AI485044 EST243324 tomato ovary, TAMU Lycopersicon ...	37 0.059
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	emb AW621634 AW621634 EST312432 tomato root during/after fruit s...	31 0.32
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55	emb Y15139 BOY15139 Bixa orellana chloroplast rbcL gene.	34 0.54
	emb Y15149 ABY15149 Aquilaria beccariana rbcL gene.	34 0.54
	emb AF022128 AF022128 Bixa orellana ribulose 1,5-bisphosphate ca...	34 0.54
	emb AF022125 AF022125 Theobroma cacao ribulose 1,5-bisphosphate ...	34 0.54
	gb L12568 AKARBC Akania bidwillii ribulosebisphosphate carboxyla...	34 0.54
60	emb A27063 A27063 L.cicera AFP sequence.	34 0.54
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- gb|BE124525|BE124525 EST393560 GVN Medicago truncatula cDNA clon... 31 0.68
 emb|AW725876|AW725876 GA_Ea0020A08 Gossypium arboreum 7-10 dpa ... 34 0.75
 gb|L01579|PEADRR230B Pea (pi39) disease resistance response prot... 34 0.75
 emb|AI757757|AI757757 EtESTea34d02.y1 Eimeria S5-2 Sporozoite st... 34 0.75
 5 gb|L14293|HDOCPRBCL Hydrolea ovata chloroplast ribulosebisphosph... 33 1.0
 emb|AL138618|LMFL2954 Leishmania major Friedlin chromosome 23 co... 33 1.4
 emb|AJ233156|PPAJ3156 Pentace polyantha chloroplast rbcL gene, p... 33 1.4
 gb|L01961|TEPCPRBCL Thespesia populnea ribulose 1,5-bisphosphate... 33 1.4
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 15 emb|AJ012208|AAU012208 Abroma angusta chloroplast rbcL gene. 33 1.4
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 http://www3.ncbi.nlm.nih.gov/htbin-
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- Database: plantfungal
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- emb|Y10156|BNMYAP12 B.napus for myrosinase-associated protein, c... 224 e-163
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 emb|AW774945|AW774945 EST334096 KV3 Medicago truncatula cDNA clo... 46 5e-13
 60 emb|AW685185|AW685185 NF025E06NR1F1000 Nodulated root Medicago t... 62 1e-10
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	emb AW757161 AW757161 sl29h09.y1 Gm-c1027 Glycine max cDNA clone...	46	3e-07
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	emb AW624906 AW624906 EST313735 tomato radicle, 5 d post-imbibit...	35	5e-04
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	emb AW109570 AW109570 gate0004H20f Gossypium arboreum 7-10 dpa f...	45	7e-04
	emb AW279386 AW279386 sf66f11.y1 Gm-c1013 Glycine max cDNA clone...	37	7e-04
	emb AW720472 AW720472 LjNEST19f4r Lotus japonicus nodule library...	35	7e-04
	emb AW458524 AW458524 sh10c06.y1 Gm-c1016 Glycine max cDNA clone...	37	8e-04
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	emb AI729137 AI729137 BNLGHi12747 Six-day Cotton fiber Gossypium...	46	8e-04
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	emb AI728284 AI728284 BNLGHi10336 Six-day Cotton fiber Gossypium...	45	0.001
	emb AW160215 AW160215 EST290073 L. pennellii trichome, Cornell U...	45	0.002
55	emb AI729089 AI729089 BNLGHi12599 Six-day Cotton fiber Gossypium...	45	0.002
	gb H74345 H74345 249 Deletion-treated Brassica napus cDNA clone ...	37	0.002
	emb AW733443 AW733443 sk73f03.y1 Gm-c1016 Glycine max cDNA clone...	37	0.002
	emb AW509209 AW509209 sh92f05.y1 Gm-c1016 Glycine max cDNA clone...	38	0.002
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60	emb AW459861 AW459861 sh96c01.y1 Gm-c1016 Glycine max cDNA clone...	37	0.002
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emb|AW733540|AW733540 sk74h07.y1 *Gm-c1016* Glycine max cDNA clone... 37 0.003
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emb|AW396681|AW396681 sh29d09.y1 *Gm-c1017* Glycine max cDNA clone... 44 0.003
5 gb|BE023812|BE023812 sm92g03.y1 *Gm-c1015* Glycine max cDNA clone ... 44 0.003
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emb|AW127455|AW127455 M110643 DSIL *Medicago truncatula* cDNA clon... 36 0.003
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emb|AW648494|AW648494 EST326948 tomato germinating seedlings, TA... 43 0.005
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emb|AW666820|AW666820 GA_Ea0006B14 *Gossypium arboreum* 7-10 dpa ... 35 0.006
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emb|AW667892|AW667892 GA_Ea0011E24 *Gossypium arboreum* 7-10 dpa ... 42 0.007
25 emb|AW667522|AW667522 GA_Ea0009J12 *Gossypium arboreum* 7-10 dpa ... 42 0.007
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emb|AW100112|AW100112 sd20e02.y2 *Gm-c1012* Glycine max cDNA clone... 30 0.012
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gb|t04815, gb|t45993, gb|r30138, gb|ai099570 and gb|t22281 come from
35 this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family
/chip nova /gb_link
http://www3.ncbi.nlm.nih.gov/htbin-
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http://www.ncgr.org/cgi-bin/ff?ac006577
40 (1194 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

45 Searching.....done

Score E
Sequences producing significant alignments: (bits) Value

50 emb|Y10156|BNMYAP12 *B.napus* for myrosinase-associated protein, c... 224 e-163
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gb|U39289|BNU39289 *Brassica napus* myrosinase-associated protein ... 227 e-156
gb|U39319|BNU39319 *Brassica napus* myrosinase-associated protein ... 176 e-127
emb|AJ223307|BNAJ3307 *Brassica napus* gene encoding induced myros... 176 6e-99
55 emb|AW568594|AW568594 si78g03.y1 *Gm-c1031* Glycine max cDNA clone... 47 1e-13
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emb|AW774945|AW774945 EST334096 KV3 *Medicago truncatula* cDNA clo... 46 5e-13
emb|AW685185|AW685185 NF025E06NR1F1000 Nodulated root *Medicago* t... 62 1e-10
emb|AW922141|AW922141 LG1_323_G11.b1_A002 Light Grown 1 (LG1) So... 65 5e-10
60 emb|AW687872|AW687872 NF014D07RT1F1061 Developing root *Medicago* ... 46 2e-09
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30 emb|AW564505|AW564505 LG1_295_D11.b1_A002 Light Grown 1 (LG1) So... 49 9e-05
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25 emb|AT000294|AT000294 AT000294 Apple young fruit cDNA library Ma... 42 0.010
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30 Query= AC006577.16_f_at 12779_f_at /id_source genbank /description
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this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family
35 /chip nova /gb_link /ncgi
(1194 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

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50 emb|AJ223307|BNAJ3307 Brassica napus gene encoding induced myros... 176 6e-99
emb|AW568594|AW568594 si78g03.y1 Gm-c1031 Glycine max cDNA clone... 47 1e-13
emb|AW288014|AW288014 N100858e rootphos(-) Medicago truncatula c... 67 3e-13
emb|AW774945|AW774945 EST334096 KV3 Medicago truncatula cDNA clo... 46 5e-13
emb|AW685185|AW685185 NF025E06NR1F1000 Nodulated root Medicago t... 62 1e-10
55 emb|AW922141|AW922141 LG1_323_G11.b1_A002 Light Grown 1 (LG1) So... 65 5e-10
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60 emb|AW164470|AW164470 se73a09.y1 Gm-c1023 Glycine max cDNA clone... 58 2e-07
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25	emb AW127684 AW127684 M110431 DSLC Medicago truncatula cDNA clon...	38	3e-05
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30	emb AW459066 AW459066 sh18h02.y1 Gm-c1016 Glycine max cDNA clone...	40	2e-04
	emb AW926586 AW926586 HVSMEg0007J20 Hordeum vulgare pre-anthesis...	47	2e-04
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	emb AW720472 AW720472 LjNEST19f4r Lotus japonicus nodule library...	35	7e-04
	emb AW458524 AW458524 sh10c06.y1 Gm-c1016 Glycine max cDNA clone...	37	8e-04
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 emb|AT000294|AT000294 AT000294 Apple young fruit cDNA library Ma... 42 0.010
 emb|AW100112|AW100112 sd20e02.y2 Gm-c1012 Glycine max cDNA clone... 30 0.012
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 gb|aa042519 come from this gene. [arabidopsis thaliana]" /blast_score
 30 0 /ec_number /family /chip nova /gb_link /ncgi
 (1335 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

35

Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

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gb|L27349|BLYCRH2A Hordeum vulgare calreticulin (CRH2) mRNA, par... 669 0.0

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emb|AW773947|AW773947 EST332933 KV3 Medicago truncatula cDNA clo... 469 e-131

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- emb|AW622049|AW622049 EST312847 tomato root during/after fruit s... 467 e-131
- emb|AW216727|AW216727 EST295441 tomato callus, TAMU Lycopersicon... 460 e-128
- emb|AW731454|AW731454 GA_Ea0030H17 Gossypium arboreum 7-10 dpa ... 456 e-127
- emb|AI735991|AI735991 sb21e08.y1 Gm-c1007 Glycine max cDNA clone... 450 e-125
- 5 emb|Y09078|DBCALLKPR D.bioculata mRNA for calreticulin-like prot... 228 e-124
- emb|AA660877|AA660877 00772 MtrHE Medicago truncatula cDNA 5' si... 310 e-123
- emb|AW668560|AW668560 GA_Ea0014K06 Gossypium arboreum 7-10 dpa ... 441 e-123
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- 10 gb|BE059929|BE059929 sn38h08.y1 Gm-c1016 Glycine max cDNA clone ... 431 e-120
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- emb|AW695765|AW695765 NF098D02ST1F1016 Developing stem Medicago ... 421 e-118
- emb|AW626316|AW626316 EST320223 tomato radicle, 5 d post-imbibit... 422 e-117
- emb|AA660477|AA660477 00363 MtrHE Medicago truncatula cDNA 5' si... 421 e-117
- 15 emb|AW727433|AW727433 GA_Ea0012B12 Gossypium arboreum 7-10 dpa ... 421 e-117
- emb|AW650460|AW650460 EST328914 tomato germinating seedlings, TA... 419 e-116
- emb|AW621571|AW621571 EST312369 tomato root during/after fruit s... 419 e-116
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- 20 emb|AW738476|AW738476 EST339903 tomato flower buds, anthesis, Co... 412 e-114
- emb|AW685878|AW685878 NF031C11NR1F1000 Nodulated root Medicago t... 411 e-114
- emb|AW933869|AW933869 EST359712 tomato fruit mature green, TAMU ... 407 e-113
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- emb|AW649817|AW649817 EST328271 tomato germinating seedlings, TA... 402 e-111
- emb|AW773817|AW773817 EST332803 KV3 Medicago truncatula cDNA clo... 399 e-110
- emb|AI495184|AI495184 sa89b11.y1 Gm-c1004 Glycine max cDNA clone... 398 e-110
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- 30 emb|AW035959|AW035959 EST282818 tomato callus, TAMU Lycopersicon... 396 e-109
- emb|AW932476|AW932476 EST358319 tomato fruit mature green, TAMU ... 395 e-109
- emb|AW979917|AW979917 EST341567 tomato root deficiency, Cornell ... 395 e-109
- emb|AW649196|AW649196 EST327650 tomato germinating seedlings, TA... 391 e-108
- emb|AI960982|AI960982 sc93e09.y1 Gm-c1019 Glycine max cDNA clone... 386 e-106
- 35 emb|AW033083|AW033083 EST276642 tomato callus, TAMU Lycopersicon... 385 e-106
- emb|AW596414|AW596414 sj12b07.y1 Gm-c1032 Glycine max cDNA clone... 384 e-106
- emb|AW648010|AW648010 EST326464 tomato germinating seedlings, TA... 382 e-105
- emb|AW725587|AW725587 GA_Ea0018N14 Gossypium arboreum 7-10 dpa ... 379 e-104
- emb|AW725609|AW725609 GA_Ea0018P14 Gossypium arboreum 7-10 dpa ... 379 e-104
- 40 emb|AW727696|AW727696 GA_Ea0015K01 Gossypium arboreum 7-10 dpa ... 303 e-103
- emb|AW705880|AW705880 sk52a09.y1 Gm-c1019 Glycine max cDNA clone... 372 e-102
- emb|AW306403|AW306403 se50b10.y1 Gm-c1017 Glycine max cDNA clone... 369 e-101
- emb|AW720057|AW720057 LjNEST13b1r Lotus japonicus nodule library... 367 e-101
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- 45 emb|AW933031|AW933031 EST358874 tomato fruit mature green, TAMU ... 366 e-100
- emb|AW649360|AW649360 EST327814 tomato germinating seedlings, TA... 366 e-100
- emb|AW035234|AW035234 EST280496 tomato callus, TAMU Lycopersicon... 364 1e-99
- emb|AW907386|AW907386 EST343509 potato stolon, Cornell Universit... 361 9e-99
- emb|AW756722|AW756722 sl26d08.y1 Gm-c1027 Glycine max cDNA clone... 359 3e-98
- 50 emb|AW760501|AW760501 sl51b04.y1 Gm-c1027 Glycine max cDNA clone... 358 6e-98
- emb|AI726591|AI726591 BNLGHi6198 Six-day Cotton fiber Gossypium ... 354 8e-97
- emb|AW201052|AW201052 se97c10.y1 Gm-c1027 Glycine max cDNA clone... 347 1e-94
- emb|Y09816|EGCALRPR E.gracilis mRNA for calreticulin precursor. 255 1e-93
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- 55 emb|AI437497|AI437497 sa34a12.y1 Gm-c1004 Glycine max cDNA clone... 329 4e-89
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- emb|AI896365|AI896365 EST265808 tomato callus, TAMU Lycopersicon... 325 6e-88
- emb|AW043340|AW043340 ST32B12 Pine TripleEx shoot tip library Pin... 324 1e-87
- emb|AI812952|AI812952 22G9 Pine Lambda Zap Xylem library Pinus t... 255 1e-86
- 60 emb|AW648456|AW648456 EST326910 tomato germinating seedlings, TA... 316 3e-85
- emb|AI899646|AI899646 EST269089 tomato susceptible, Cornell Lyco... 316 3e-85

- emb|AW624478|AW624478 EST322423 tomato flower buds 3-8 mm, Corne... 312 3e-84
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 10 emb|AW728940|AW728940 GA_Ea0018J21 Gossypium arboreum 7-10 dpa ... 291 1e-77
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 15 emb|AW560421|AW560421 EST315469 DSIR Medicago truncatula cDNA cl... 270 1e-74
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 emb|AW043146|AW043146 ST29H08 Pine TriplEx shoot tip library Pin... 273 2e-73

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Score E
 Sequences producing significant alignments: (bits) Value

- emb|AJ249799|CAR249799 Cicer arietinum partial mRNA for cytochro... 308 e-114
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 40 gb|U72654|EGU72654 Eustoma grandiflorum flavonoid 3'5'-hydroxyla... 179 8e-85
 emb|AI897763|AI897763 EST267206 tomato ovary, TAMU Lycopersicon ... 305 7e-82
 emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. 278 3e-81
 emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 269 6e-81
 emb|Y09920|HT7ECODET Helianthus tuberosus mRNA for 7-ethoxycouma... 300 2e-80
 45 emb|Y10098|HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dec... 300 2e-80
 dbj|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 121 9e-79
 emb|X70824|SMPEG1 S.melongena pEG1 mRNA for hydroxylase P450. 171 1e-77
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 50 emb|AF134590|AF134590 Papaver somniferum (S)-N-methylcoclaurine ... 223 6e-75
 emb|AF191772|AF191772 Papaver somniferum (S)-N-methylcoclaurine ... 221 1e-74
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 emb|AI484957|AI484957 EST243220 tomato ovary, TAMU Lycopersicon ... 280 3e-74
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 10 emb|AW730128|AW730128 GA_Ea0027P19 *Gossypium arboreum* 7-10 dpa ... 184 6e-63
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 25 gb|BE054146|BE054146 GA_Ea0034H12F *Gossypium arboreum* 7-10 dpa ... 234 2e-60
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 dbj|D14588|PETHF1 *Petunia hybrida* Hfl mRNA for flavonoid-3',5'-h... 182 3e-60
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 30 emb|AF122821|AF122821 *Capsicum annuum* cytochrome P450 (PepCYP) m... 231 8e-60
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 40 emb|AF124816|AF124816 *Mentha x piperita* cytochrome p450 isoform ... 146 2e-57
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 10 emb|AJ010324|PAJ10324 Populus trichocarpa cv trichobel mRNA for ... 93 4e-51
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 emb|AB025016|AB025016 Lotus japonicus mRNA for cytochrome P450, ... 152 6e-51
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	emb AW650703 AW650703 EST329157 tomato germinating seedlings, TA...	88	2e-28
	emb AW648696 AW648696 EST327066 tomato germinating seedlings, TA...	85	7e-25
40	emb AT000481 AT000481 AT000481 Brassica rapa guard cell Brassica...	62	3e-23
	emb AI895460 AI895460 EST264903 tomato callus, TAMU Lycopersicon...	77	2e-22
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25	gb BE059498 BE059498 sn32h03.y1 Gm-cl016 Glycine max cDNA clone ...	42	0.013
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	emb AW930573 AW930573 EST341030 tomato fruit mature green, TAMU ...	42	0.013
	emb AW310205 AW310205 sf32g08.x1 Gm-cl028 Glycine max cDNA clone...	42	0.013
	gb L35779 L35779 BNAESTG Mustard flower buds Brassica rapa cDNA ...	42	0.013
30	emb AW233985 AW233985 sf32g08.y1 Gm-cl028 Glycine max cDNA clone...	42	0.013
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	emb AW032373 AW032373 EST275827 tomato callus, TAMU Lycopersicon...	41	0.017
	emb AI490542 AI490542 EST249096 tomato ovary, TAMU Lycopersicon ...	41	0.017
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	emb AI489915 AI489915 EST248254 tomato ovary, TAMU Lycopersicon ...	41	0.017
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 5 emb|AW733406|AW733406 sk73b02.y1 Gm-c1016 Glycine max cDNA clone... 40 0.060
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 emb|AI774760|AI774760 EST255860 tomato resistant, Cornell Lycopersicon... 39 0.083
 10 emb|AW559645|AW559645 EST314757 DSIR Medicago truncatula cDNA cl... 39 0.083
 emb|AW458207|AW458207 sh79g06.y1 Gm-c1016 Glycine max cDNA clone... 39 0.083

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20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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25 Score E
 Sequences producing significant alignments: (bits) Value

emb|X61488|BNCHITIN B.napus mRNA for chitinase. 453 e-166
 gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 212 1e-95
 30 gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 211 4e-95
 emb|X57187|PVCHITIN P.vulgaris mRNA for chitinase. 135 8e-86
 dbj|D45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 136 5e-82
 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 185 5e-81
 emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 182 8e-80
 35 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 156 4e-79
 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 156 4e-79
 dbj|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 119 4e-78
 dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 119 7e-78
 dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 119 1e-77
 40 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase class 4 (p... 103 6e-77
 gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 105 1e-75
 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 84 7e-73
 gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 140 1e-72
 gb|BE034428|BE034428 MH04G02 MH Mesembryanthemum crystallinum cD... 139 3e-72
 45 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 133 2e-70
 gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 131 1e-69
 emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 239 1e-66
 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 130 2e-66
 emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 177 5e-66
 50 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 167 9e-65
 emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 172 2e-64
 gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 165 4e-64
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 55 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 93 4e-63
 gb|U52848|DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 161 1e-62
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 60 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 147 3e-57
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- emb|AI776153|AI776153 EST257241 tomato resistant, Cornell Lycopersicon... 177 5e-56
- emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon... 141 2e-55
- gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 86 3e-55
- emb|AW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 140 6e-55
- 5 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon... 138 3e-54
- emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 137 4e-54
- emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 98 1e-53
- emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 134 2e-53
- emb|AW924422|AW924422 WS1_69_C06.b1_A002 Water-stressed I (WS1) ... 139 4e-53
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- gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 86 8e-53
- emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 116 2e-52
- gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 116 1e-51
- gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 116 1e-51
- 15 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 117 9e-51
- emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 124 2e-50
- gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 141 6e-50
- emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 149 1e-49
- emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon... 165 4e-49
- 20 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 120 4e-49
- emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 115 9e-49
- emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 112 1e-48
- gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 112 1e-48
- emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 115 1e-48
- 25 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed I (WS1) ... 140 2e-48
- gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 83 3e-48
- gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 112 5e-48
- emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 112 5e-48
- emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 139 9e-48
- 30 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed I (WS1) ... 139 9e-48
- emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 118 3e-47
- emb|AF061806|AF061806 Elaeagnus umbellata basic chitinase mRNA, ... 118 4e-47
- gb|M94105|ALCCHITIN Allium sativum chitinase mRNA, 3' end. 116 7e-47
- emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 120 2e-46
- 35 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 116 3e-46
- emb|AW922596|AW922596 DG1_46_C01.b1_A002 Dark Grown 1 (DG1) Sorg... 79 3e-46
- emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 116 3e-46
- gb|BE034267|BE034267 MH02D06 MH Mesembryanthemum crystallinum cD... 74 3e-46
- gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 122 4e-46
- 40 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 116 4e-46
- emb|X88800|VURNACHII V.unguiculata mRNA for chitinase clase 1 (p... 112 7e-46
- emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 121 9e-46
- emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 109 1e-45
- emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 112 2e-45
- 45 emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 135 2e-45
- gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 116 2e-45
- gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 109 2e-45
- gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 116 3e-45
- gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 109 6e-45
- 50 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 108 8e-45
- emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 147 2e-44
- gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 141 4e-44
- emb|AA739579|AA739579 344 PiIFG2 Pinus taeda cDNA clone 8562M 3'... 107 1e-43
- emb|AW560048|AW560048 EST315096 DSIR Medicago truncatula cDNA cl... 116 1e-43
- 55 emb|A23396|A23396 B.vulgaris gene for chitinase 76. 105 3e-43
- emb|AW267781|AW267781 EST305909 DSIR Medicago truncatula cDNA cl... 115 4e-43
- emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 108 8e-43
- emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 125 1e-42
- emb|AI352718|AI352718 MB46-29 PZ204.BNlib Brassica napus cDNA cl... 144 4e-42
- 60 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 80 5e-42
- emb|AI729668|AI729668 BNLGH13889 Six-day Cotton fiber Gossypium... 111 2e-41

- emb|AF061805|AF061805 Elaeagnus umbellata acidic chitinase mRNA,... 116 3e-41
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 emb|Z15138|LECHI14 L.esculentum mRNA for chitinase (partial). 114 1e-40
 gb|U30465|LEU30465 Lycopersicon esculentum class II chitinase (C... 114 2e-40
 5 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 100 1e-39

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 (1116 letters)

15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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25	emb AW671006 AW671006 LG1_278_H12.b1_A002 Light Grown 1 (LG1) So...	81	6e-28	
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	emb Z74916 SCYOR008C S.cerevisiae chromosome XV reading frame OR...	37	0.31	
	gb U39481 SCU39481 Saccharomyces cerevisiae Slglp (SLG1) gene, c...	37	0.31	
	emb AA680906 AA680906 LmFrAm0494 Leishmania major Amastigote ful...	33	1.0	
30	emb AF193903 AF193903 Cafeteria roenbergensis mitochondrial DNA,...	35	1.1	
	emb AF229795 AF229795 Vigna radiata beta galactosidase mRNA, com...	35	1.5	
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	emb AC005802 AC005802 Leishmania major chromosome 3 clone L6202 ...	34	2.1	
	emb AC005893 AC005893 Leishmania major chromosome 3 clone L822 s...	34	2.1	
35	emb AA520166 AA520166 TgESTzz39b08.s1 TgME49 invivo Bradyzoite c...	34	2.9	
	emb AW618793 AW618793 EST320779 L. pennellii trichome, Cornell U...	34	2.9	
	emb AW306460 AW306460 se51a02.y1 Gm-cl017 Glycine max cDNA clone...	34	2.9	
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40	emb AF017430 AF017430 Hordeum vulgare EEA1 mRNA, complete cds.	33	3.9	
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	emb AW925272 AW925272 HVSMEg0001G19 Hordeum vulgare pre-anthesis...	33	5.4	
55	emb AA783066 AA783066 alh02c9.r1 Aspergillus nidulans 24hr asexu...	26	5.7	
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	emb AW277786 AW277786 sf86e12.y1 Gm-cl019 Glycine max cDNA clone...	32	7.4	

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5 emb|AW277436|AW277436 sf82a10.y1 Gm-c1019 Glycine max cDNA clone... 32 7.4
emb|AW459299|AW459299 sh23c01.y1 Gm-c1016 Glycine max cDNA clone... 32 7.4
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emb|AW757240|AW757240 sl30h11.y1 Gm-c1027 Glycine max cDNA clone... 32 7.4

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dehydrogenase /chip nova /gb_link
15 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi)
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(1812 letters)

20 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

25 Score E
Sequences producing significant alignments: (bits) Value

emb|AW930291|AW930291 EST340748 tomato fruit mature green, TAMU ... 415 e-115
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30 emb|AW666282|AW666282 sk34f11.y1 Gm-c1028 Glycine max cDNA clone... 393 e-108
emb|AW650696|AW650696 EST329150 tomato germinating seedlings, TA... 226 e-103
emb|AW691093|AW691093 NF041B09ST1F1000 Developing stem Medicago ... 355 e-102
emb|AW926942|AW926942 HVSMeg0009B01 Hordeum vulgare pre-anthesis... 339 e-102
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35 emb|AW696933|AW696933 NF112E03ST1F1021 Developing stem Medicago ... 357 4e-98
emb|AW731385|AW731385 GA_Ea0030K22 Gossypium arboreum 7-10 dpa ... 344 2e-95
emb|AW688234|AW688234 NF005A05ST1F1000 Developing stem Medicago ... 348 6e-95
gb|BE036418|BE036418 MO24D12 MO Mesembryanthemum crystallinum cD... 279 1e-94
gb|BE052354|BE052354 GA_Ea0034P16f Gossypium arboreum 7-10 dpa ... 346 3e-94
40 emb|AW423801|AW423801 sh52b02.y1 Gm-c1017 Glycine max cDNA clone... 339 4e-92
emb|AI813214|AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta... 336 4e-92
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emb|AW737130|AW737130 EST338557 tomato flower buds, anthesis, Co... 318 1e-85
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55 emb|AW398821|AW398821 EST309321 L. pennellii trichome, Cornell U... 201 2e-50
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60 emb|AW736943|AW736943 NXNV_081_H10_F Nsf Xylem Normal wood Verti... 180 3e-44
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- emb|AW695961|AW695961 NF101A09ST1F1068 Developing stem Medicago ... 172 6e-42
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 5 emb|AW688606|AW688606 NF009E07ST1F1000 Developing stem Medicago ... 112 2e-39
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 10 emb|AL031180|SPUNK4 S.pombe chromosome I cosmid c2E11. 103 1e-36
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 15 emb|AL157811|SPAC186 S.pombe chromosome I cosmid c186. 98 1e-32
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 emb|Z37997|SC9877 S.cerevisiae chromosome IX cosmid 9877. 84 5e-30
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 25 emb|AF079881|AF079881 Entodinium caudatum D-3-phosphoglycerate d... 56 1e-24
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 gb|H74366|H74366 270 Deletion-treated Brassica napus cDNA clone ... 82 2e-14
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 40 emb|AW442114|AW442114 EST311510 tomato fruit red ripe, TAMU Lyco... 77 4e-13
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 45 emb|AI484846|AI484846 EST243107 tomato ovary, TAMU Lycopersicon ... 77 4e-13
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15 Database: plantfungal
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30	emb Z49369 SCYJL094C S.cerevisiae chromosome X reading frame ORF...	150	5e-35
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	emb AW334422 AW334422 S34F3 AGS-1 Pneumocystis carinii f. sp. ca...	52	2e-05
40	emb AQ842018 AQ842018 T134304 Soybean RFLP probe Glycine max gen...	47	1e-04
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 5 emb|AQ845769|AQ845769 LMAJFV1_lm25g04.x1 Leishmania major FV1 ra... 34 6.8
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 35 http://www.ncgr.org/cgi-bin/ff?ac002387
 (2371 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

- 40 Searching.....done

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| 45 emb Z50099 STTKETMR S.tuberosum mRNA for transketolase. | 1372 | 0.0 |
| gb L76554 SPITRAN Spinacia oleracea transketolase mRNA, chloropl... | 1350 | 0.0 |
| emb Y15781 CAY15781 Capsicum annuum mRNA for plastid transketola... | 1344 | 0.0 |
| emb A52295 A52295 Sequence 1 from Patent EP0723017. | 1283 | 0.0 |
| emb Z46648 CPTKT7 C.plantagineum tkt7 gene for transketolase. | 1063 | 0.0 |
| 50 emb Z46647 CPTKT10 C.plantagineum tkt10 gene for transketolase. | 1038 | 0.0 |
| emb Z46646 CPTKT3 C.plantagineum tkt3 gene for transketolase. | 1014 | 0.0 |
| emb AJ249787 CPA249787 Cyanophora paradoxa mRNA for putative tra... | 557 | 0.0 |
| emb AL033501 CAC41C10 C.albicans cosmid Ca41C10. | 253 | e-175 |
| emb AC007872 AC007872 The sequence of an Aspergillus parasiticus... | 167 | e-158 |
| 55 gb H55032 H55032 HHU58a Sorghum bicolor cv. TX430 Sorghum bicolo... | 233 | e-151 |
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30 gb|U51033|YSCP9513 Saccharomyces cerevisiae chromosome XVI cosmi... 225 2e-88
emb|Z49219|SC9499X S.cerevisiae chromosome XVI cosmid 9499. 225 2e-88
emb|X73224|SCTKL1 S.cerevisiae TKL1 gene for transketolase. 225 2e-88
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 15 emb|AI726103|AI726103 BNLGHi5028 Six-day Cotton fiber Gossypium ... 260 3e-68
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 20 emb|AF086822|AF086822 Candida boidinii dihydroxyacetone synthase... 163 7e-65
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- 25 Query= AL022347.46 at 13659 at /id_source genbank /description
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- Database: plantfungal
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 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 343 e-111
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 348 e-109
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 346 e-109
 45 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 347 e-109
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 333 e-108
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 342 e-107
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 328 e-106
 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 334 e-105
 50 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 329 e-104
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 205 e-104
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 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 330 e-103
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 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 113 7e-83
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 55 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 135 2e-50
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 (966 letters)
 30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
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 (159 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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- Searching.....done
- Score E
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- emb|A67429|A67429 Sequence 2 from Patent WO9743429. 127 7e-49
emb|A67428|A67428 Sequence 1 from Patent WO9743429. 127 7e-49
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 (2508 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters
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Searching.....done

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 15 emb|X81369|TAAWJL218 T.aestivum (subclone pAWJL218) AWJL218 gene. 83 1e-14
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 emb|AW443205|AW443205 EST308135 tomato mixed elicitor, BTI Lycop... 83 1e-14
 emb|AW696757|AW696757 NF110F02ST1F1025 Developing stem Medicago ... 83 1e-14
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 25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af077407|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|af077407|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af077407|/ncgi)
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 emb|AJ132224|LES132224 Lycopersicon esculentum mRNA for hexose t... 819 0.0
 emb|AJ010942|LES010942 Lycopersicon esculentum mRNA for hexose t... 815 0.0
 40 gb|L21753|SCFGLUTRAB Saccharum hybrid cultivar H65-7052 glucose ... 222 e-176
 gb|U38651|MTU38651 Medicago truncatula sugar transporter mRNA, co... 354 e-174
 gb|L08196|RCCSCP Ricinus communis (clone PST293) sugar carrier p... 371 e-173
 emb|Y09590|VVHEXTRAN V.vinifera mRNA for hexose transporter. 356 e-170
 emb|AF061106|AF061106 Petunia x hybrida putative monosaccharide ... 255 e-170
 45 gb|L08188|RCCHCP Ricinus communis (clone ST330) hexose carrier p... 203 e-163
 emb|Z83829|PAMST1 P.abies mRNA for monosaccharide transporter Ms... 211 e-154
 emb|Z93775|VFZ93775 V.faba mRNA for hexose transporter. 362 e-129
 emb|X66856|NTMST1 N.tabacum MST1 mRNA. 215 e-129
 gb|L08197|RCCSCPS Ricinus communis (clone PST9) sugar carrier pr... 210 e-114
 50 emb|AI775535|AI775535 EST256635 tomato resistant, Cornell Lycope... 401 e-111
 gb|L21752|SCFGLUTRAA Saccharum hybrid cultivar H65-7052 glucose ... 193 2e-99
 emb|AI775204|AI775204 EST256304 tomato resistant, Cornell Lycope... 352 7e-98
 emb|AI772312|AI772312 EST253412 tomato resistant, Cornell Lycope... 214 6e-82
 emb|AJ132225|LES132225 Lycopersicon esculentum mRNA for hexose t... 188 5e-79
 55 emb|AF173655|AF173655 Beta vulgaris clone GTRTUNI glucose transp... 156 1e-73
 emb|AJ001061|VVHEXOSET Vitis vinifera hexose transporter gene. 276 3e-73
 emb|AI778344|AI778344 EST259223 tomato susceptible, Cornell Lyco... 259 1e-70
 emb|AV407522|AV407522 AV407522 Lotus japonicus young plants (two... 253 2e-66
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 60 emb|AW684560|AW684560 NF018C12NR1F1000 Nodulated root Medicago t... 208 9e-61
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- emb|AW73777|AW73777 EST339204 tomato flower buds, anthesis, Co... 223 3e-57
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5 emb|AI774617|AI774617 EST255717 tomato resistant, Cornell Lycopen... 188 4e-52
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10 emb|AW349933|AW349933 GM210006A20H11R Gm-r1021 Glycine max cDNA ... 189 2e-49
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emb|AI731272|AI731272 BNLGHi9072 Six-day Cotton fiber Gossypium ... 172 3e-45
emb|AW092826|AW092826 EST286006 tomato mixed elicitor, BTI Lycop... 173 6e-45
25 emb|AI730904|AI730904 BNLGHi8171 Six-day Cotton fiber Gossypium ... 156 2e-43
emb|AW737195|AW737195 EST338622 tomato flower buds, anthesis, Co... 173 3e-42
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30 emb|AI930883|AI930883 sb43g12.y1 Gm-c1015 Glycine max cDNA clone... 117 4e-38
gb|L08189|RCCSCP B Ricinus communis (clone PDG15) sugar carrier p... 158 1e-37
gb|L08191|RCCSCP B Ricinus communis (clone PDG19) sugar carrier p... 157 2e-37
emb|AW774154|AW774154 EST333237 KV3 Medicago truncatula cDNA clo... 153 4e-37
gb|L08194|RCCSCP B Ricinus communis (clone PDGK4) sugar carrier p... 155 6e-37
35 gb|U22525|KLU22525 Kluyveromyces lactis high affinity glucose tr... 109 3e-36
emb|AW234900|AW234900 sf20e02.y1 Gm-c1028 Glycine max cDNA clone... 152 8e-36
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emb|AW040775|AW040775 EST283639 tomato mixed elicitor, BTI Lycop... 141 2e-35
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40 emb|Z74186|SCYDL138W S.cerevisiae chromosome IV reading frame OR... 81 2e-35
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45 emb|AI780094|AI780094 EST260973 tomato susceptible, Cornell Lyco... 139 7e-35
emb|AF149282|AF149282 Phaseolus vulgaris clone pBHEX2 hexose car... 148 1e-34
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55 emb|AW432874|AW432874 sh99b03.y1 Gm-c1016 Glycine max cDNA clone... 130 5e-31
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60 emb|AV407618|AV407618 AV407618 Lotus japonicus young plants (two... 78 2e-24
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- emb|AI728506|AI728506 BNLGH10921 Six-day Cotton fiber Gossypium... 98 1e-23
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[post/entrez/query?db=n&form=6&dopt=g&uid=gb|aac02748.1|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|aac02748.1|/ncgi)
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 25 (1612 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| | emb Y09423 NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... | 136 | 8e-98 |
| | emb X71654 SMCYPEG3 S.melongena CYP71A2 mRNA for hydroxylase. | 124 | 9e-95 |
| | dbj D14990 POTCPEG4 Eggplant mRNA for cytochrome P-450EG4, compl... | 124 | 9e-95 |
| 40 | emb Y10489 GMC450CP1 G.max mRNA for putative cytochrome P450, cl... | 90 | 1e-84 |
| | emb X70982 SMCYPEG3 S.melongena CYP71A3 mRNA for P450 hydroxylase. | 126 | 3e-74 |
| | emb Y09424 NRCYP71A6 N.racemosa mRNA for cytochrome P450, CYP71A... | 154 | 3e-65 |
| | dbj E13663 E13663 cDNA encoding cytochrome P450 which is induced... | 71 | 9e-63 |
| | dbj D83968 SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... | 71 | 9e-63 |
| 45 | emb AF022157 AF022157 Glycine max cytochrome P450 monooxygenase ... | 126 | 3e-61 |
| | emb AW053855 AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... | 103 | 1e-53 |
| | emb Y09920 HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... | 94 | 1e-50 |
| | emb Y10098 HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... | 94 | 1e-50 |
| | emb AF022459 AF022459 Glycine max cytochrome P450 monooxygenase ... | 105 | 4e-50 |
| 50 | emb AJ238612 CRO238612 Catharanthus roseus mRNA for cytochrome P... | 89 | 2e-49 |
| | emb AF029858 AF029858 Sorghum bicolor cytochrome P450 CYP71E1 (C... | 139 | 3e-49 |
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| 55 | emb Y10490 GMC450CP3 G.max mRNA for putative cytochrome P450, cl... | 104 | 6e-46 |
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| | emb AF122821 AF122821 Capsicum annuum cytochrome P450 (PepCYP) m... | 118 | 4e-45 |
| | emb Z33875 CYMPCP450 M.piperita gene for cytochrome P-450 oxidase. | 88 | 7e-45 |
| | emb AI897763 AI897763 EST267206 tomato ovary, TAMU Lycopersicon ... | 84 | 1e-44 |
| 60 | emb AW830233 AW830233 sm24f03.y1 Gm-c1028 Glycine max cDNA clone... | 139 | 5e-44 |
| | gb U48435 SCU48435 Solanum chacoense putative cytochrome P450 ge... | 95 | 2e-43 |

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5 emb|AW034502|AW034502 EST278118 tomato callus, TAMU Lycopersicon... 107 2e-42
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15 dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 82 2e-39
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25 emb|AW132351|AW132351 se03a02.y1 Gm-c1013 Glycine max cDNA clone... 159 5e-38
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55 emb|AJ010324|PAJ10324 Populus trichocarpa cv trichobel mRNA for ... 95 2e-33
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60 emb|AB032833|AB032833 Cicer arietinum CYP76D1 mRNA for cytochrom... 77 4e-33
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5 emb|AI777331|AI777331 EST263739 tomato seed, TAMU Lycopersicon e... 86 1e-32
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10 emb|AW255299|AW255299 ML307 peppermint glandular trichome Menth... 88 2e-32
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661,018 sequences; 426,114,510 total letters
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Sequences producing significant alignments: (bits) Value

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35 emb|AB013598|AB013598 Verbena hybrida HGT8 mRNA for UDP-glucose:... 104 2e-34
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40 emb|AW398421|AW398421 EST298268 L. pennellii trichome, Cornell U... 84 6e-32
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45 emb|AB013597|AB013597 Perilla frutescens PF3R6 mRNA for UDP-gluc... 93 1e-30
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50 emb|X85138|LETW11 L.esculentum twil mRNA. 81 1e-28
emb|AB033758|AB033758 Citrus unshiu LGTase mRNA for limonoid UDP... 89 2e-28
emb|X72729|LEERT1B L.esculentum (ERT 1b) ripening-related mRNA. 87 9e-28
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55 emb|AQ580287|AQ580287 T135903b shotgun sub-library of BAC clone ... 93 1e-27
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emb|AW036493|AW036493 EST282992 tomato seed, TAMU Lycopersicon e... 92 5e-27
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60 emb|AQ368131|AQ368131 tox0001H06r CUGI Tomato BAC Library Lycop... 84 7e-27
emb|AF199453|AF199453 Sorghum bicolor UDP-glucose glucosyltransf... 76 9e-27

- emb|AI488782|AI488782 EST247121 tomato ovary, TAMU Lycopersicon ... 80 1e-26
emb|AI729108|AI729108 BNLGH12670 Six-day Cotton fiber Gossypium... 82 1e-26
gb|BE126076|BE126076 DG1_65_E03.g1_A002 Dark Grown 1 (DG1) Sorgh... 106 1e-26
dbj|D85186|D85186 Gentiana triflora mRNA for UDP-glucose:flavono... 86 3e-26
5 emb|X77369|SMGT S.melongena GT mRNA for glycosyltransferase. 97 5e-26
dbj|E12713|E12713 Solanum melongena cDNA encoding flavonoid-3-gl... 97 5e-26
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10 emb|AF101972|AF101972 Phaseolus lunatus zeatin O-glucosyltransfe... 87 2e-25
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emb|X15694|HVB RNZ1H Barley bronze 1 homologue for UDPglucose fla... 80 5e-25
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15 emb|AF116858|AF116858 Phaseolus vulgaris zeatin O-xylosyltransfe... 84 8e-25
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20 emb|AW221893|AW221893 EST298704 tomato fruit red ripe, TAMU Lyco... 84 2e-24
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25 emb|AW034671|AW034671 EST278402 tomato callus, TAMU Lycopersicon... 81 5e-24
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35 emb|X77463|MECGT6 M.esculenta Crantz CGT6 mRNA for UTP-glucose g... 74 2e-22
emb|AI487582|AI487582 EST245904 tomato ovary, TAMU Lycopersicon ... 82 2e-22
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40 emb|AW394450|AW394450 sh05d10.y1 Gm-c1016 Glycine max cDNA clone... 75 8e-22
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50 emb|AW650188|AW650188 EST328642 tomato germinating seedlings, TA... 89 9e-21
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- emb|AW781424|AW781424 sl78a07.y1 Gm-c1037 Glycine max cDNA clone... 95 9e-19
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- 15 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi
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- 20 Database: plantfungal
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 35 emb|A24084|A24084 pEUCAD1 cinnamyl alcohol dehydrogenase cDNA. 319 e-141
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 45 gb|U63534|FXU63534 Fragaria x ananassa cinnamyl alcohol dehydrog... 251 9e-89
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 emb|X67817|PCELI3 P.crispum mRNA for Eli3. 240 3e-77
 50 emb|X92855|LEMTD L.esculentum exon 1 of MTD gene. 130 6e-77
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 60 emb|AW350274|AW350274 GM210007B20B7R Gm-r1021 Glycine max cDNA 3... 262 1e-69
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- emb|AW031628|AW031628 EST275082 tomato callus, TAMU Lycopersicon... 182 7e-69
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 10 emb|AW568106|AW568106 si68e05.y1 Gm-r1030 Glycine max cDNA clone... 136 3e-59
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 15 emb|AI488134|AI488134 EST246456 tomato ovary, TAMU Lycopersicon ... 210 2e-53
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 25 emb|AW775567|AW775567 EST334632 DSIL Medicago truncatula cDNA cl... 105 7e-45
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 35 emb|AV412798|AV412798 AV412798 Lotus japonicus young plants (two... 137 6e-40
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 emb|AW775594|AW775594 EST334659 DSIL Medicago truncatula cDNA cl... 98 8e-40
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 40 emb|AW776649|AW776649 EST335714 DSIL Medicago truncatula cDNA cl... 94 1e-38
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 45 emb|AW648829|AW648829 EST327283 tomato germinating seedlings, TA... 89 3e-37
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AW733452 AW733452 sk73g05.y1 Gm-c1016 Glycine max cDNA clone...	77	4e-14
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	emb AW092074 AW092074 EST285350 tomato mixed elicitor, BTI Lycop...	57	4e-08
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 gb|BE023592|BE023592 sm82e07.y1 Gm-c1015 Glycine max cDNA clone ... 30 7.1
 20 emb|AZ220034|AZ220034 Sheared DNA-63D11.TR Sheared DNA Trypanoso... 30 7.1
 emb|AI110319|AI110319 TENU3289 T. cruzi epimastigote normalized ... 30 7.1
 emb|AW870077|AW870077 NXNV_123_G11_F Nsf Xylem Normal wood Verti... 30 7.1
 emb|AI057841|AI057841 TENU1932 T. cruzi epimastigote normalized ... 30 7.1
 emb|X83851|NTPAR1B N.tabacum mRNA for PAR-1b. 30 7.1
 25 gb|M18538|POPP3A Populus balsamifera subsp. trichocarpa X Popu... 30 7.1
 emb|AW203632|AW203632 sf36d11.y1 Gm-c1028 Glycine max cDNA clone... 30 7.1
 emb|AQ640232|AQ640232 927P1-18B11.TV 927P1 Trypanosoma brucei ge... 30 7.1
 emb|AI779122|AI779122 EST260001 tomato susceptible, Cornell Lyco... 27 8.3
 emb|AW096641|AW096641 EST289821 tomato mixed elicitor, BTI Lycop... 27 8.9
 30 gb|N98085|N98085 2245C3 czapPFDd2.1, Debopam Chakrabarti Plasmod... 29 9.7
 emb|AW929160|AW929160 EST337948 tomato flower buds 8 mm to pre-a... 29 9.7
 emb|AW037807|AW037807 EST279436 tomato mixed elicitor, BTI Lycop... 29 9.7
 emb|AW729409|AW729409 GA_Ea0024O24 Gossypium arboreum 7-10 dpa ... 29 9.7
 emb|AF193903|AF193903 Cafeteria roenbergensis mitochondrial DNA,... 29 9.7
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 emb|cab45069.1| (al078637) putative protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 40 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi)
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi)
 (990 letters)

- 45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

- 50 Score E
 Sequences producing significant alignments: (bits) Value

- emb|AW092074|AW092074 EST285350 tomato mixed elicitor, BTI Lycop... 145 1e-69
 emb|AI778762|AI778762 EST259641 tomato susceptible, Cornell Lyco... 149 1e-49
 55 gb|BE035944|BE035944 MO22E07 MO Mesembryanthemum crystallinum cD... 120 9e-49
 emb|AW618184|AW618184 EST314234 L. pennellii trichome, Cornell U... 138 2e-46
 emb|AI778761|AI778761 EST259640 tomato susceptible, Cornell Lyco... 133 6e-45
 emb|AW618179|AW618179 EST314229 L. pennellii trichome, Cornell U... 114 3e-39
 gb|S59422|S59422 Populus x canadensis major storage protein mRNA... 99 6e-32
 60 gb|M77504|POPBSP Populus deltoides bark storage protein mRNA, co... 99 3e-30
 emb|AW395908|AW395908 sh07c05.y1 Gm-c1016 Glycine max cDNA clone... 125 5e-28

	emb AW733452 AW733452 sk73g05.y1 Gm-c1016 Glycine max cDNA clone...	122	3e-27
	gb BE058639 BE058639 sn18g09.y1 Gm-c1016 Glycine max cDNA clone ...	122	4e-27
	emb AW394463 AW394463 sh32h06.y1 Gm-c1017 Glycine max cDNA clone...	111	4e-26
	emb AW563817 AW563817 LG1_261_C02.g1_A002 Light Grown 1 (LG1) So...	104	4e-25
5	emb AI822191 AI822191 L0-668T3 Ice plant Lambda Uni-Zap XR expre...	114	1e-24
	gb BE036341 BE036341 MO23E06 MO Mesembryanthemum crystallinum cD...	112	3e-24
	gb BE035204 BE035204 MO02A04 MO Mesembryanthemum crystallinum cD...	112	3e-24
	gb BE037538 BE037538 MP19G11 MP Mesembryanthemum crystallinum cD...	112	3e-24
	gb BE035225 BE035225 MO02E03 MO Mesembryanthemum crystallinum cD...	112	3e-24
10	gb BE059090 BE059090 sn25b08.y1 Gm-c1016 Glycine max cDNA clone ...	75	2e-23
	emb AW395168 AW395168 sh40g07.y1 Gm-c1017 Glycine max cDNA clone...	68	3e-21
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	emb AW625587 AW625587 EST319494 tomato radicle, 5 d post-imbibit...	92	3e-19
15	emb AW929488 AW929488 EST338276 tomato flower buds 8 mm to pre-a...	92	3e-19
	emb AI778197 AI778197 EST259076 tomato susceptible, Cornell Lyco...	92	3e-19
	emb AW648720 AW648720 EST327090 tomato germinating seedlings, TA...	92	3e-19
	emb AW625287 AW625287 EST319290 tomato radicle, 5 d post-imbibit...	92	3e-19
	emb AW648718 AW648718 EST327088 tomato germinating seedlings, TA...	92	3e-19
20	emb AW928879 AW928879 EST337667 tomato flower buds 8 mm to pre-a...	92	3e-19
	gb L20233 POPVEGSTRA P.trichocarpa x P.deltoides vegetative stor...	94	2e-18
	emb AW733620 AW733620 sk75h08.y1 Gm-c1016 Glycine max cDNA clone...	86	3e-18
	emb AW677327 AW677327 DG1_5_D03.g1_A002 Dark Grown 1 (DG1) Sorgh...	93	4e-18
	emb AI163910 AI163910 A051P26U Hybrid aspen plasmid library Popu...	56	1e-17
25	emb AW156195 AW156195 se20g08.y1 Gm-c1015 Glycine max cDNA clone...	90	2e-17
	emb AW775932 AW775932 EST334997 DSIL Medicago truncatula cDNA cl...	84	2e-17
	emb AW692820 AW692820 NF056A09ST1F1000 Developing stem Medicago ...	84	2e-17
	emb AW685340 AW685340 NF027C09NR1F1000 Nodulated root Medicago t...	83	4e-17
	emb AW684469 AW684469 NF017C09NR1F1000 Nodulated root Medicago t...	75	1e-16
30	gb BE037208 BE037208 MP18A03 MP Mesembryanthemum crystallinum cD...	84	2e-15
	gb BE023782 BE023782 sm92d02.y1 Gm-c1015 Glycine max cDNA clone ...	72	4e-14
	gb BE036234 BE036234 MO21C12 MO Mesembryanthemum crystallinum cD...	78	1e-13
	emb AW286123 AW286123 LG1_261_F11.b1_A002 Light Grown 1 (LG1) So...	64	5e-13
	emb AW626069 AW626069 EST319976 tomato radicle, 5 d post-imbibit...	69	1e-12
35	gb BE095283 BE095283 00344 leafy spurge Lambda HybriZAP 2.1 two-...	62	1e-12
	emb AW677160 AW677160 DG1_5_D03.b1_A002 Dark Grown 1 (DG1) Sorgh...	62	2e-12
	emb AW677332 AW677332 DG1_5_F03.g1_A002 Dark Grown 1 (DG1) Sorgh...	70	2e-11
	gb BE022753 BE022753 sm88a02.y1 Gm-c1015 Glycine max cDNA clone ...	61	5e-11
	emb AW424028 AW424028 sh59f09.y1 Gm-c1015 Glycine max cDNA clone...	62	8e-11
40	emb X70064 PDBSPA P.deltoides gene for poplar bark storage protein.	63	3e-09
	emb AW119934 AW119934 sd54g12.y1 Gm-c1016 Glycine max cDNA clone...	54	4e-09
	emb AW677125 AW677125 DG1_5_F03.b1_A002 Dark Grown 1 (DG1) Sorgh...	43	5e-07
	gb BE058421 BE058421 sn15h03.y1 Gm-c1016 Glycine max cDNA clone ...	56	6e-07
	emb AW119941 AW119941 sd54h12.y1 Gm-c1016 Glycine max cDNA clone...	46	1e-06
45	gb BE037054 BE037054 MP13H01 MP Mesembryanthemum crystallinum cD...	55	1e-06
	gb BE036004 BE036004 MO17H11 MO Mesembryanthemum crystallinum cD...	51	1e-06
	gb BE035382 BE035382 MO03G01 MO Mesembryanthemum crystallinum cD...	54	2e-06
	emb AW127599 AW127599 M110330 DSLC Medicago truncatula cDNA clon...	44	3e-06
	gb BE095282 BE095282 00343 leafy spurge Lambda HybriZAP 2.1 two-...	52	5e-06
50	emb AW287592 AW287592 LG1_244_A09.b1_A002 Light Grown 1 (LG1) So...	40	6e-06
	emb AA557101 AA557101 943 Loblolly pine N Pinus taeda cDNA clone...	47	2e-04
	gb BE037091 BE037091 MP14F10 MP Mesembryanthemum crystallinum cD...	47	2e-04
	gb M25340 POPCHIC Populus sp. chitinase mRNA fragment, clone 4.	46	6e-04
	gb BE036753 BE036753 MP04H07 MP Mesembryanthemum crystallinum cD...	46	6e-04
55	gb BE037437 BE037437 MP21A08 MP Mesembryanthemum crystallinum cD...	34	8e-04
	gb BE037490 BE037490 MP21G12 MP Mesembryanthemum crystallinum cD...	45	9e-04
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	gb BE034872 BE034872 ML05E09 ML Mesembryanthemum crystallinum cD...	38	0.10

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 gb|BE036480|BE036480 MP03G10 MP Mesembryanthemum crystallinum cD... 36 0.51
 emb|Z00044|CHNTXX Nicotiana tabacum chloroplast genome DNA. 35 0.70
 5 emb|AL160939|L1356CX Leishmania major Friedlin cosmid L1356.3 t3... 34 1.8
 gb|BE036897|BE036897 MP08B09 MP Mesembryanthemum crystallinum cD... 34 1.8
 emb|AI730722|AI730722 BNLGHi7729 Six-day Cotton fiber Gossypium ... 34 1.8
 emb|AB030726|AB030726 Nicotiana tabacum mRNA for DNA (cytosine-5... 34 2.5
 emb|AW397331|AW397331 sg77e08.y1 Gm-c1007 Glycine max cDNA clone... 34 2.5
 10 emb|AI210350|AI210350 i0c03a1.r1 Aspergillus nidulans 24hr asexu... 34 2.5
 emb|AA786346|AA786346 l3g09a1.fl Aspergillus nidulans 24hr asexu... 34 2.5
 emb|AW397063|AW397063 sg66e08.y1 Gm-c1007 Glycine max cDNA clone... 34 2.5
 emb|AI327733|AI327733 i0c03a1.fl Aspergillus nidulans 24hr asexu... 34 2.5
 emb|AW672119|AW672119 LG1_357_F07.b1_A002 Light Grown 1 (LG1) So... 33 3.4
 15 emb|AJ270207|ECA270207 Entodinium caudatum partial mRNA fro puta... 33 3.4
 emb|AW672133|AW672133 LG1_357_D07.b1_A002 Light Grown 1 (LG1) So... 33 3.4
 emb|AQ847463|AQ847463 LMAJFV1_lm34c05.y1 Leishmania major FV1 ra... 33 4.7
 emb|AZ212142|AZ212142 Sheared DNA-70G10.TF Sheared DNA Trypanoso... 32 6.4
 emb|AI163630|AI163630 A045p06u Hybrid aspen plasmid library Popu... 32 6.4
 20 emb|AL354532|LMFL1177 Leishmania major Friedlin chromosome 21 co... 30 6.9
 emb|AJ243516|NCR243516 Neurospora crassa partial nca-3 gene for ... 32 8.8
 emb|AL116648|CNS01DCG Botrytis cinerea strain T4 cDNA library un... 27 9.3
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 emb|caa50677.1| (x71794) peroxidase [arabidopsis thaliana]
 25 /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
 (1236 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

30

Searching.....done

	Score	E	(bits)	Value
35	Sequences producing significant alignments:			
	gb M60729 HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge...	744	0.0	
	emb A00741 A00741 A.rusticana synthetic gene (reverse complement...	692	0.0	
	emb A00740 A00740 A.rusticana synthetic gene for peroxidase.	692	0.0	
	dbj E01651 E01651 cDNA encoding horseradish peroxidase.	692	0.0	
40	gb M37157 HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge...	371	e-133	
	emb X97349 PTXP2PER P.trichocarpa mRNA for anionic peroxidase P...	473	e-132	
	emb X97350 PTXP3PER P.trichocarpa mRNA for anionic peroxidase P...	469	e-131	
	dbj D83224 POPP01 Populus nigra mRNA for peroxidase, complete cds.	468	e-131	
	gb M37156 HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge...	363	e-130	
45	emb X97348 PTXP1PER P.trichocarpa mRNA for anionic peroxidase P...	463	e-129	
	dbj D30652 POPPA Populus kitakamiensis mRNA for peroxidase, part...	441	e-123	
	emb X97351 PTXP4PER P.trichocarpa mRNA for anionic peroxidase P...	383	e-120	
	dbj D30653 POPPB Populus kitakamiensis mRNA for peroxidase, part...	356	e-112	
	emb AF149277 AF149277 Phaseolus vulgaris peroxidase 1 precursor ...	227	e-107	
50	gb L36157 ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple...	229	e-107	
	emb AF007211 AF007211 Glycine max peroxidase precursor (GMIPER1)...	229	e-106	
	gb L07554 LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA...	381	e-105	
	emb X90692 MSRNAPE1A M.sativa mRNA for peroxidase 1A.	211	e-105	
	dbj D90115 HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i...	296	e-103	
55	emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod ...	138	2e-97	
	emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor ...	142	4e-97	
	emb X90693 MSRNAPE1B M.sativa mRNA for peroxidase 1B.	231	1e-95	
	emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C.	226	7e-94	
	gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA.	210	2e-89	
60	emb AI959837 AI959837 sc94h07.y1 Gm-c1019 Glycine max cDNA clone...	228	6e-89	
	emb AF244924 AF244924 Spinacia oleracea peroxidase prx15 precurs...	208	9e-88	

- emb|AW559660|AW559660 EST314772 DSIR *Medicago truncatula* cDNA cl... 236 1e-87
emb|AW774581|AW774581 EST333732 KV3 *Medicago truncatula* cDNA clo... 236 7e-87
emb|AF155124|AF155124 *Gossypium hirsutum* bacterial-induced perox... 215 2e-86
emb|AW981426|AW981426 EST392579 DSIL *Medicago truncatula* cDNA cl... 236 2e-85
5 emb|AB042103|AB042103 *Asparagus officinalis* AspPOX1 mRNA for per... 209 2e-85
emb|AF244923|AF244923 *Spinacia oleracea* peroxidase prx14 precurs... 205 9e-85
emb|AJ250121|PAB250121 *Picea abies* mRNA for SPI2 protein (spi2 g... 253 1e-83
emb|AW775762|AW775762 EST334827 DSIL *Medicago truncatula* cDNA cl... 236 6e-83
emb|Y10466|SOPR XR5 *S.oleracea* mRNA for peroxidase, clone PC18. 218 3e-82
10 emb|AW775425|AW775425 EST334490 DSIL *Medicago truncatula* cDNA cl... 208 1e-81
emb|AW685437|AW685437 NF029D09NR1F1000 Nodulated root *Medicago* t... 230 9e-80
emb|AB024439|AB024439 *Scutellaria baicalensis* mRNA for peroxidase... 209 2e-79
emb|AF244922|AF244922 *Spinacia oleracea* peroxidase prx13 precurs... 212 3e-79
emb|X57564|ARNEUPERO *A.rusticana* mRNA for neutral peroxidase. 115 6e-78
15 emb|AW776273|AW776273 EST335338 DSIL *Medicago truncatula* cDNA cl... 222 1e-77
emb|AW267813|AW267813 EST305941 DSIR *Medicago truncatula* cDNA cl... 200 1e-76
emb|X91232|MARNAPRX *M.annua* mRNA for peroxidase. 196 5e-76
emb|AF049881|AF049881 *Linum usitatissimum* peroxidase FLXPER4 (PE... 207 7e-76
emb|AW256487|AW256487 EST304624 KV2 *Medicago truncatula* cDNA clo... 200 9e-76
20 emb|AW775890|AW775890 EST334955 DSIL *Medicago truncatula* cDNA cl... 200 3e-74
emb|AW257195|AW257195 EST305332 KV2 *Medicago truncatula* cDNA clo... 214 5e-74
gb|M91373|CUSPREPER *Cucumis sativus* peroxidase mRNA, complete cds. 86 2e-73
gb|U41657|GMU41657 *Glycine max* seed coat peroxidase isozyme (SPO... 159 3e-73
emb|AB027752|AB027752 *Nicotiana tabacum* mRNA for peroxidase, com... 197 5e-73
25 gb|L36110|SSNPEROXIA *Stylosanthes humilis* peroxidase mRNA. 199 5e-73
gb|M37636|ARCPNC1 *Arachis hypogaea* cationic peroxidase (PNC1) mR... 204 7e-73
emb|AW685235|AW685235 NF027H10NR1F1000 Nodulated root *Medicago* t... 236 9e-73
emb|AW278775|AW278775 sf97d02.y1 Gm-c1019 *Glycine max* cDNA clone... 155 1e-72
emb|X71593|LECEVI1A *L.esculentum* CEVI-1 mRNA. 99 2e-72
30 gb|J02979|TOBPXDLF *Nicotiana tabacum* lignin-forming peroxidase m... 100 2e-72
emb|AW559945|AW559945 EST314993 DSIR *Medicago truncatula* cDNA cl... 233 2e-72
emb|AW980744|AW980744 EST391897 GVN *Medicago truncatula* cDNA clo... 235 5e-70
emb|Y10467|SOPR XR6 *S.oleracea* mRNA for peroxidase, clone PC23. 105 1e-69
dbj|D83225|POPP02 *Populus nigra* peroxidase gene, complete cds. 196 2e-69
35 gb|M74103|TOBANPER *Nicotiana sylvestris* anionic peroxidase mRNA,... 205 6e-69
emb|AF043234|AF043234 *Striga asiatica* ferriprotein porphyrin-con... 211 1e-68
gb|BE034991|BE034991 MM01A12 MM Mesembryanthemum crystallinum cD... 202 6e-68
emb|AW574244|AW574244 EST316835 GVN *Medicago truncatula* cDNA clo... 202 1e-67
emb|Y10465|SOPR XR4 *S.oleracea* mRNA for peroxidase, clone PC44. 98 3e-67
40 emb|AW686084|AW686084 NF038B07NR1F1000 Nodulated root *Medicago* t... 236 5e-67
emb|AW561032|AW561032 EST316080 DSIR *Medicago truncatula* cDNA cl... 203 7e-67
emb|X56011|TAPERO Wheat mRNA for peroxidase. 111 2e-66
emb|AW185769|AW185769 se59d08.y1 Gm-c1019 *Glycine max* cDNA clone... 219 4e-65
emb|Y17192|CPY17192 *Cucurbita pepo* mRNA for peroxidase. 96 2e-64
45 gb|BE033422|BE033422 ME01E09 ME Mesembryanthemum crystallinum cD... 184 4e-64
emb|AB024438|AB024438 *Scutellaria baicalensis* mRNA for peroxidase... 205 7e-64
gb|M91374|CUSPREPERA *Cucumis sativus* peroxidase mRNA, complete cds. 76 2e-63
gb|L24120|LINFLXP *Linum usitatissimum* peroxidase precursor (FLXP... 167 2e-63
gb|M91372|CUSPREPERB *Cucumis sativus* peroxidase mRNA, complete cds. 134 2e-63
50 emb|AF043235|AF043235 *Striga asiatica* ferriprotein porphyrin-con... 199 3e-63
emb|AW288002|AW288002 N100846e rootphos(-) *Medicago truncatula* c... 182 7e-63
emb|AW126121|AW126121 N100318e rootphos(-) *Medicago truncatula* c... 216 1e-62
gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 133 5e-62
emb|AW687443|AW687443 NF009F07RT1F1062 Developing root *Medicago* ... 235 1e-61
55 emb|AW687957|AW687957 NF001D11ST1F1000 Developing stem *Medicago* ... 236 3e-61
emb|AB024437|AB024437 *Scutellaria baicalensis* mRNA for peroxidase... 163 3e-61
emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 133 5e-61
emb|AI496388|AI496388 sb04a11.y1 Gm-c1004 *Glycine max* cDNA clone... 224 6e-61
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60 dbj|D38050|POPP1 Aspen prx3a gene for peroxidase, complete cds. 121 9e-61
emb|AW704659|AW704659 sk54h10.y1 Gm-c1019 *Glycine max* cDNA clone... 149 9e-61

- emb|Y10464|SOPR XR3 *S.oleracea* mRNA for peroxidase, clone PC42. 80 3e-60
 emb|AW705730|AW705730 sk51b02.y1 *Gm-c1019* Glycine max cDNA clone... 149 8e-60
 gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 100 9e-60
 gb|U12314|CCU12314 *Cenchrus ciliaris* clone PX7 peroxidase mRNA, ... 105 9e-60
 5 emb|AI938533|AI938533 sb46h09.y1 *Gm-c1015* Glycine max cDNA clone... 145 1e-59
 emb|AW705617|AW705617 sk50d03.y1 *Gm-c1019* Glycine max cDNA clone... 149 2e-59
 emb|AI781859|AI781859 EST262738 tomato susceptible, Cornell Lyco... 102 2e-59
 emb|AF149278|AF149278 *Phaseolus vulgaris* peroxidase 3 precursor ... 90 3e-59
 gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 102 4e-59
 10 emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59
 emb|AF244921|AF244921 *Spinacia oleracea* peroxidase prx12 precurs... 156 8e-59
 gb|M32742|CUSCUPER *C.sativus* peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58
 emb|AW705946|AW705946 sk52h07.y1 *Gm-c1019* Glycine max cDNA clone... 224 6e-58

15

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 [arabidopsis thaliana] /blast_score 0 /ec_number /family translocase
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 20 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi)
[http://www.ncbi.nlm.nih.gov/htbin-](http://www.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi)
 (1530 letters)

25

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

30

Score E
 Sequences producing significant alignments: (bits) Value

- emb|AF006489|AF006489 *Gossypium hirsutum* adenine nucleotide tran... 325 0.0
 emb|X62123|STANTG *S.tuberosum* ant gene for ADP/ATP translocator. 328 0.0
 35 gb|U89839|LEU89839 *Lycopersicon esculentum* ADP/ATP translocator ... 327 0.0
 emb|X57557|STANT1 *S.tuberosum* PANT1 mRNA for adenine nucleotide ... 635 0.0
 emb|AJ003197|LAJ3197 *Lupinus albus* mRNA for adenine nucleotide ... 331 e-175
 emb|X80023|TTADPATP *T.turgidum* mRNA for ADP/ATP carrier. 322 e-172
 emb|X65194|CRANT *C.reinhardtii* mRNA CRANT for mitochondrial ADP/... 348 e-149
 40 emb|AL023634|SPBC530 *S.pombe* chromosome II cosmid c530. 265 e-139
 emb|Z49974|SPANCI1GN *S.pombe* ANC1 gene for adenine nucleotide car... 265 e-139
 emb|AF085429|AF085429 *Candida parapsilosis* ADP/ATP carrier prote... 311 e-134
 dbj|D89102|D89102 *Schizosaccharomyces pombe* mRNA, partial cds, c... 265 e-133
 gb|L33797|YSKAAAC *Kluyveromyces lactis* ADP/ATP translocase (AAC) ... 259 e-132
 45 emb|AF237675|AF237675 *Yarrowia lipolytica* ADP/ATP carrier protei... 247 e-132
 emb|AJ277099|CUT277099 *Candida utilis* anc gene for mitochondrial... 253 e-131
 emb|AJ277098|CUT277098 *Candida utilis* anc gene for mitochondrial... 253 e-131
 gb|M34075|YSCAAC3 *S.cerevisiae* ADP/ATP-translocator protein (AAC... 252 e-129
 emb|X77291|SCIILDNA *S.cerevisiae* YBL0421, YBL0438, YBL0418, YBL0... 252 e-129
 50 emb|Z35791|SCYBL030C *S.cerevisiae* chromosome II reading frame OR... 252 e-129
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 gb|J04021|YSCAAC2 *S.cerevisiae* ADP/ATP carrier protein (AAC2) ge... 252 e-129
 emb|X00363|NCADPATP *Neurospora crassa* mRNA for mitochondrial ADP... 280 e-126
 emb|Z49703|SC9796 *S.cerevisiae* chromosome XIII cosmid 9796. 248 e-125
 55 gb|M12514|YSCPET9 *S.cerevisiae* ADP/ATP translocator protein (AAC... 248 e-125
 emb|Z35954|SCYBR085W *S.cerevisiae* chromosome II reading frame OR... 247 e-125
 gb|M34076|YSCAAC2A *S.cerevisiae* ADP/ATP-translocator protein (AA... 247 e-125
 emb|AW774326|AW774326 EST333477 *Medicago truncatula* cDNA clo... 288 e-124
 emb|AL111975|CNS019QN *Botrytis cinerea* strain T4 cDNA library un... 254 e-122
 60 emb|AW647699|AW647699 EST307178 tomato germinating seedlings, TA... 299 e-120

- emb|AW349848|AW349848 GM210006A11G9R Gm-r1021 Glycine max cDNA 3... 326 e-118
- emb|AW624842|AW624842 EST313671 tomato radicle, 5 d post-imbibit... 229 e-116
- emb|X95863|TTANT1 T.turgidum ant gene (1549bp). 195 e-114
- 5 emb|AW041186|AW041186 EST284050 tomato mixed elicitor, BTI Lycop... 239 e-114
- emb|X95864|TTANT2 T.turgidum ant gene (1494bp). 191 e-112
- emb|AW706324|AW706324 sj54h05.y1 Gm-c1033 Glycine max cDNA clone... 245 e-110
- emb|AL157416|LMFL6066 Leishmania major Friedlin chromosome 19 co... 233 e-108
- 10 emb|AW160172|AW160172 EST290029 L. pennellii trichome, Cornell U... 328 e-108
- emb|AW928728|AW928728 EST337516 tomato flower buds 8 mm to pre-a... 247 e-107
- emb|AW218544|AW218544 EST303727 tomato radicle, 5 d post-imbibit... 325 e-105
- emb|AW830381|AW830381 sm26a12.y1 Gm-c1028 Glycine max cDNA clone... 268 e-105
- emb|AW201674|AW201674 sf05h11.y1 Gm-c1027 Glycine max cDNA clone... 309 e-104
- emb|AI812944|AI812944 22G12 Pine Lambda Zap Xylem library Pinus ... 251 e-103
- 15 emb|AI777865|AI777865 EST258744 tomato susceptible, Cornell Lyco... 284 e-102
- emb|AW234033|AW234033 sf33d01.y1 Gm-c1028 Glycine max cDNA clone... 237 e-101
- emb|AW831587|AW831587 sm28b02.y1 Gm-c1028 Glycine max cDNA clone... 300 e-101
- emb|AW668198|AW668198 GA_Ea0013C13 Gossypium arboreum 7-10 dpa ... 331 e-100
- 20 emb|AF049130|AF049130 Trypanosoma brucei brucei ADP/ATP carrier ... 238 1e-98
- emb|AI898886|AI898886 EST268329 tomato ovary, TAMU Lycopersicon... 213 2e-98
- gb|U32987|TBU32987 Trypanosoma brucei rhodesiense ADP/ATP carrie... 238 3e-98
- emb|AW223982|AW223982 EST300793 tomato fruit red ripe, TAMU Lyco... 327 1e-96
- emb|AW624951|AW624951 EST313780 tomato radicle, 5 d post-imbibit... 327 1e-96
- emb|AW348348|AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3... 328 2e-96
- 25 emb|AW441243|AW441243 EST310639 tomato fruit red ripe, TAMU Lyco... 324 1e-95
- emb|AW223973|AW223973 EST300784 tomato fruit red ripe, TAMU Lyco... 321 7e-95
- emb|AW931569|AW931569 EST357412 tomato fruit mature green, TAMU ... 328 2e-94
- emb|AW218871|AW218871 EST301353 tomato root during/after fruit s... 327 8e-94
- 30 emb|AL116444|CNS01D6S Botrytis cinerea strain T4 cDNA library un... 267 4e-93
- emb|AW831561|AW831561 sm34f06.y1 Gm-c1028 Glycine max cDNA clone... 312 2e-92
- emb|AI484151|AI484151 EST248958 tomato resistant, Cornell Lycope... 264 3e-91
- emb|AW925414|AW925414 HVSMEg0001L02 Hordeum vulgare pre-anthesis... 299 6e-91
- emb|AI731594|AI731594 BNLGHi10182 Six-day Cotton fiber Gossypium... 335 7e-91
- 35 emb|AW730597|AW730597 GA_Ea0027H02 Gossypium arboreum 7-10 dpa ... 333 1e-90
- emb|AW647665|AW647665 EST307143 tomato germinating seedlings, TA... 317 1e-90
- emb|AW395111|AW395111 sh40a06.y1 Gm-c1017 Glycine max cDNA clone... 303 6e-90
- emb|AI725588|AI725588 BNLGHi12376 Six-day Cotton fiber Gossypium... 288 1e-89
- emb|AW934656|AW934656 EST353548 tomato flower buds 0-3 mm, Corne... 328 2e-89
- 40 emb|AW757478|AW757478 874001D11.y1 C. reinhardtii CC-1690, Lambd... 202 3e-89
- emb|AW725897|AW725897 GA_Ea0020B06 Gossypium arboreum 7-10 dpa ... 328 8e-89
- emb|AW647757|AW647757 EST326211 tomato germinating seedlings, TA... 301 1e-88
- emb|AW509174|AW509174 sh92b04.y1 Gm-c1016 Glycine max cDNA clone... 297 4e-88
- emb|AW666654|AW666654 GA_Ea0005E11 Gossypium arboreum 7-10 dpa ... 279 7e-88
- 45 emb|AL114553|CNS01BQ9 Botrytis cinerea strain T4 cDNA library un... 231 3e-87
- gb|BE021489|BE021489 sm59b05.y1 Gm-c1028 Glycine max cDNA clone ... 322 5e-87
- emb|AW507801|AW507801 si45c02.y1 Gm-r1030 Glycine max cDNA clone... 259 2e-86
- emb|AW733916|AW733916 sk85a11.y1 Gm-c1035 Glycine max cDNA clone... 306 2e-86
- emb|AW096468|AW096468 EST289648 tomato mixed elicitor, BTI Lycop... 292 6e-86
- 50 emb|AW156741|AW156741 se30b08.y1 Gm-c1015 Glycine max cDNA clone... 184 1e-85
- emb|AI729625|AI729625 BNLGHi13824 Six-day Cotton fiber Gossypium... 276 4e-85
- emb|AW034214|AW034214 EST277785 tomato callus, TAMU Lycopersicon... 304 5e-85
- emb|AJ273864|AJ273864 AJ273864 Metarhizium anisopliae ARSEF 2575... 184 1e-84
- emb|AI775647|AI775647 EST256747 tomato resistant, Cornell Lycope... 297 1e-84
- 55 emb|AI822682|AI822682 L0-1204T3 Ice plant Lambda Uni-Zap XR expr... 314 2e-84
- emb|AW625107|AW625107 EST313924 tomato radicle, 5 d post-imbibit... 314 2e-84
- emb|AI726147|AI726147 BNLGHi5085 Six-day Cotton fiber Gossypium ... 263 6e-83
- emb|AW755396|AW755396 si03d11.y1 Gm-c1036 Glycine max cDNA clone... 306 3e-82
- emb|AI728088|AI728088 BNLGHi9938 Six-day Cotton fiber Gossypium ... 259 5e-82
- 60 emb|AW979992|AW979992 EST310378 tomato root deficiency, Cornell ... 285 8e-82
- emb|AW333018|AW333018 S16C3 AGS-1 Pneumocystis carinii f. sp. ca... 278 1e-81

- emb|AI780394|AI780394 EST261273 tomato susceptible, Cornell Lyco... 284 2e-81
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 5 emb|AW760027|AW760027 sl57b04.y1 Gm-c1027 Glycine max cDNA clone... 301 1e-80
 emb|AW667101|AW667101 GA_Ea0007F21 Gossypium arboreum 7-10 dpa ... 300 2e-80
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 10 emb|AW650428|AW650428 EST328882 tomato germinating seedlings, TA... 278 4e-79
 emb|AI775628|AI775628 EST256728 tomato resistant, Cornell Lycopersicon... 295 7e-79
 gb|BE024093|BE024093 sm96f04.y1 Gm-c1015 Glycine max cDNA clone ... 293 2e-78
 emb|AJ273749|AJ273749 AJ273749 Metarhizium anisopliae ARSEF 2575... 256 1e-77
 emb|AW737446|AW737446 EST338789 tomato flower buds, anthesis, Co... 290 2e-77
- 15 Query= Y14251.4_i_at 16053_i_at /id_source genbank /description
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 20 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14251|/ncgi)
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- 25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
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- 30 Score E
 Sequences producing significant alignments: (bits) Value
- emb|X78203|HMGST H.muticus mRNA for glutathione S-transferase. 271 4e-72
 emb|AW727692|AW727692 GA_Ea0015I24 Gossypium arboreum 7-10 dpa ... 146 9e-71
 35 emb|AF002692|AF002692 Solanum commersonii glutathione S-transfer... 264 3e-70
 dbj|D10524|TOBPARB Nicotiana tabacum mRNA for glutathione S-tran... 262 2e-69
 emb|AW731360|AW731360 GA_Ea0030G14 Gossypium arboreum 7-10 dpa ... 142 3e-69
 dbj|D29680|TOBAP12B Tobacco api2 mRNA (which expression is induc... 261 4e-69
 emb|AW220064|AW220064 EST302547 tomato root during/after fruit s... 260 5e-69
 40 emb|Z71749|NPGSTMR N.plumbaginifolia mRNA for glutathione S-tran... 260 8e-69
 emb|AI774583|AI774583 EST255683 tomato resistant, Cornell Lycopersicon... 258 3e-68
 emb|AW728413|AW728413 GA_Ea0016J18 Gossypium arboreum 7-10 dpa ... 142 7e-68
 emb|AI725552|AI725552 BNLGH12077 Six-day Cotton fiber Gossypium... 142 4e-67
 emb|AI728937|AI728937 BNLGH12090 Six-day Cotton fiber Gossypium... 142 4e-67
 45 gb|BE033971|BE033971 MG02G09 MG Mesembryanthemum crystallinum cD... 228 2e-65
 emb|AW735791|AW735791 EST336559 tomato flower buds 0-3 mm, Corne... 248 2e-65
 emb|AF242309|AF242309 Euphorbia esula glutathione S-transferase ... 130 3e-62
 emb|AW726844|AW726844 GA_Ea0022O11 Gossypium arboreum 7-10 dpa ... 140 5e-61
 emb|AI726215|AI726215 BNLGH15300 Six-day Cotton fiber Gossypium ... 142 5e-61
 50 emb|AW218151|AW218151 EST303332 tomato radicle, 5 d post-imbibit... 232 1e-60
 emb|AW728876|AW728876 GA_Ea0028P14 Gossypium arboreum 7-10 dpa ... 147 2e-60
 gb|M84968|SIPGTSTF Silene cucubalus glutathione-S-transferase mR... 115 5e-59
 emb|AF133894|AF133894 Persea americana glutathione S-transferase... 220 8e-57
 emb|AI352770|AI352770 MB58-4B PZ204.BNlib Brassica napus cDNA cl... 174 7e-55
 55 emb|AW040790|AW040790 EST283654 tomato mixed elicitor, BTI Lycop... 210 6e-54
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 emb|AW862639|AW862639 00097 leafy spurge Lambda HybriZAP 2.1 two... 128 2e-48
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 60 emb|AW684286|AW684286 NF015A06NR1F1000 Nodulated root Medicago t... 186 1e-46
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5 emb|AV414359|AV414359 AV414359 Lotus japonicus young plants (two... 182 2e-45
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10 emb|AV417287|AV417287 AV417287 Lotus japonicus young plants (two... 173 9e-43
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15 dbj|D49526|TOBPBARBA Tobacco chimeric parB promoter/beta-glucuron... 163 1e-39
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20 emb|Y07721|PHGLSTRAN P.hybrida mRNA for glutathione S-transferase. 151 5e-36
gb|BE053268|BE053268 GA_Ea0035A09f Gossypium arboreum 7-10 dpa ... 137 7e-36
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25 emb|AW926756|AW926756 HVSMEg0008B23 Hordeum vulgare pre-anthesis... 92 3e-35
emb|AJ279691|BPE279691 Betula pendula partial mRNA for glutathio... 144 8e-34
emb|AV427165|AV427165 AV427165 Lotus japonicus young plants (two... 142 3e-33
emb|AJ010451|AMY010451 Alopecurus myosuroides mRNA for glutathio... 97 4e-33
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30 emb|AW164336|AW164336 se71b09.y1 Gm-cl023 Glycine max cDNA clone... 139 1e-32
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35 emb|AW561921|AW561921 IPPGHZ0010 Cotton fiber and embryo Lambda ... 137 7e-32
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40 emb|AI823144|AI823144 L30-1027T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-31
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emb|AI773198|AI773198 EST254298 tomato resistant, Cornell Lycop... 133 1e-30
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45 emb|AW279568|AW279568 sf95d06.y1 Gm-cl019 Glycine max cDNA clone... 131 4e-30
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60 emb|AW689646|AW689646 NF022G04ST1F1000 Developing stem Medicago ... 66 3e-25
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 5 emb|AI352728|AI352728 MB47-17 PZ204.BNlib Brassica napus cDNA cl... 110 1e-23
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 10 emb|AI444064|AI444064 sa31g12.y1 Gm-c1004 Glycine max cDNA clone... 109 2e-23
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20 Database: plantfungal
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30	emb AJ007574 RCO7574 Ricinus communis mRNA for amino acid carrier.	410	0.0
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	emb Y09826 STAAP2 S.tuberosum mRNA for amino acid transporter AA...	354	0.0
	emb AF080544 AF080544 Nepenthes alata amino acid transporter (AA...	596	0.0
35	emb Y09825 STAAP1 S.tuberosum mRNA for amino acid transporter AA...	288	e-158
	emb Z68759 RCAACMR R.communis mRNA for amino acid carrier.	334	e-155
	emb AF080542 AF080542 Nepenthes alata amino acid transporter (AA...	239	e-145
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40	emb Y11121 RCAACARR Ricinus communis mRNA for amino acid carrier...	264	e-123
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	emb AW399595 AW399595 EST310095 L. pennellii trichome, Cornell U...	192	8e-58
55	emb AW737124 AW737124 EST338551 tomato flower buds, anthesis, Co...	217	2e-55
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	emb AW432416 AW432416 sh73f10.y1 Gm-c1015 Glycine max cDNA clone...	89	8e-51
	emb AW255060 AW255060 ML1355 peppermint glandular trichome Menth...	111	1e-50
	emb AW685782 AW685782 NF035B03NR1F1000 Nodulated root Medicago t...	201	1e-50
60	gb BE125804 BE125804 DG1_57_F07.b1_A002 Dark Grown 1 (DG1) Sorgh...	178	3e-50
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- emb|AW349599|AW349599 GM210005A21G12R Gm-r1021 Glycine max cDNA ... 140 5e-49
- emb|AI487167|AI487167 EST245489 tomato ovary, TAMU Lycopersicon ... 122 2e-48
- emb|AW737784|AW737784 EST339211 tomato flower buds, anthesis, Co... 192 6e-48
- 5 emb|AW309945|AW309945 sf27a03.x1 Gm-cl028 Glycine max cDNA clone... 149 5e-47
- emb|AW738557|AW738557 EST339984 tomato flower buds, anthesis, Co... 188 8e-47
- emb|AQ842052|AQ842052 T134338 Soybean RFLP probe Glycine max gen... 148 2e-44
- emb|AF074703|AF074703 Glycine max pA381 marker, sequence tagged ... 149 1e-43
- emb|AW649763|AW649763 EST328217 tomato germinating seedlings, TA... 127 3e-43
- 10 gb|BE022301|BE022301 sm73b09.y1 Gm-cl028 Glycine max cDNA clone ... 176 4e-43
- emb|AW597381|AW597381 si92b03.y1 Gm-cl031 Glycine max cDNA clone... 175 1e-42
- emb|AW310916|AW310916 sg29h08.x1 Gm-cl024 Glycine max cDNA clone... 172 5e-42
- emb|AW306512|AW306512 se51h04.y1 Gm-cl017 Glycine max cDNA clone... 140 1e-41
- emb|AW395873|AW395873 sh01d01.y1 Gm-cl026 Glycine max cDNA clone... 112 4e-41
- 15 emb|AW201454|AW201454 sf03c12.y1 Gm-cl027 Glycine max cDNA clone... 127 9e-41
- emb|AW684816|AW684816 NF021D09NR1F1000 Nodulated root Medicago t... 164 2e-39
- emb|AZ051221|AZ051221 Gm_UMB001_166_P11R UMN Soybean BAC Library... 159 7e-38
- emb|AI779305|AI779305 EST260184 tomato susceptible, Cornell Lyco... 155 1e-36
- emb|AI779304|AI779304 EST260183 tomato susceptible, Cornell Lyco... 155 1e-36
- 20 emb|AW830977|AW830977 sm31a10.y1 Gm-cl028 Glycine max cDNA clone... 149 4e-35
- emb|AW096758|AW096758 EST289938 tomato mixed elicitor, BTI Lycop... 147 3e-34
- emb|AJ004829|STAJ4829 Solanum tuberosum fdh3 pseudogene. 110 3e-33
- emb|AQ841805|AQ841805 T134055 Soybean RFLP probe Glycine max gen... 140 2e-32
- emb|AW736648|AW736648 EST333140 KV3 Medicago truncatula cDNA clo... 138 1e-31
- 25 emb|AV418629|AV418629 AV418629 Lotus japonicus young plants (two... 130 3e-29
- emb|AW442349|AW442349 EST311745 tomato fruit red ripe, TAMU Lyco... 130 3e-29
- emb|AW738564|AW738564 EST339991 tomato flower buds, anthesis, Co... 104 7e-29
- emb|AW561095|AW561095 EST316143 DSIR Medicago truncatula cDNA cl... 126 6e-28
- emb|AW234791|AW234791 sf19c06.y1 Gm-cl028 Glycine max cDNA clone... 124 2e-27
- 30 gb|U31932|NSU31932 Nicotiana sylvestris amino acid permease 1 (N... 61 3e-27
- emb|AI441371|AI441371 sa64f02.y1 Gm-cl004 Glycine max cDNA clone... 72 2e-26
- emb|AW438003|AW438003 ST83D04 Pine TriplEx shoot tip library Pin... 111 2e-23
- emb|AW056573|AW056573 ST52G03 Pine TriplEx shoot tip library Pin... 109 8e-23
- emb|AW923686|AW923686 DG1_57_F07.g1_A002 Dark Grown 1 (DG1) Sorg... 107 3e-22
- 35 emb|AW924285|AW924285 WS1_52_F10.b1_A002 Water-stressed 1 (WS1) ... 106 5e-22
- emb|AJ238635|CPR238635 Chlorella protothecoides partial mRNA for... 75 4e-20
- emb|AW102174|AW102174 sd84c08.y1 Gm-cl009 Glycine max cDNA clone... 100 6e-20
- emb|AW102244|AW102244 sd85c02.y1 Gm-cl009 Glycine max cDNA clone... 92 1e-17
- emb|AW620352|AW620352 sj04b02.y1 Gm-cl032 Glycine max cDNA clone... 92 1e-17
- 40 emb|AW288077|AW288077 N100921e rootphos(-) Medicago truncatula c... 84 2e-15
- emb|AW396191|AW396191 sh02e09.y1 Gm-cl026 Glycine max cDNA clone... 57 2e-14
- emb|AI773761|AI773761 EST254861 tomato resistant, Cornell Lycop... 65 2e-12
- gb|BE020684|BE020684 sm45f08.y1 Gm-cl028 Glycine max cDNA clone ... 74 3e-12
- emb|AF014810|AF014810 Lycopersicon esculentum proline transporte... 54 9e-12
- 45 emb|AI728355|AI728355 BNLGHi10544 Six-day Cotton fiber Gossypium... 70 4e-11
- emb|AW780460|AW780460 sl71b05.y1 Gm-cl027 Glycine max cDNA clone... 70 6e-11
- emb|AF014808|AF014808 Lycopersicon esculentum proline transporte... 55 5e-09
- emb|AF014809|AF014809 Lycopersicon esculentum proline transporte... 52 2e-08
- emb|AW832495|AW832495 sm11e04.y1 Gm-cl027 Glycine max cDNA clone... 60 2e-08
- 50 emb|AW563318|AW563318 LG1_228_A07.g1_A002 Light Grown 1 (LG1) So... 48 2e-07
- gb|U64823|NSU64823 Nicotiana sylvestris amino acid permease (nsa... 37 2e-06
- emb|AI489487|AI489487 EST247826 tomato ovary, TAMU Lycopersicon ... 52 1e-05
- emb|AV417239|AV417239 AV417239 Lotus japonicus young plants (two... 52 1e-05
- emb|AI772468|AI772468 EST253568 tomato resistant, Cornell Lycop... 52 1e-05
- 55 gb|BE023644|BE023644 sm83e05.y1 Gm-cl015 Glycine max cDNA clone ... 51 2e-05
- emb|AW102341|AW102341 sd86d12.y1 Gm-cl009 Glycine max cDNA clone... 49 9e-05
- emb|AW560837|AW560837 EST315885 DSIR Medicago truncatula cDNA cl... 47 3e-04
- emb|AW720608|AW720608 LjNEST20d11rc Lotus japonicus nodule libra... 47 4e-04
- emb|AW720138|AW720138 LjNEST15d10r Lotus japonicus nodule librar... 47 4e-04
- 60 emb|AV409658|AV409658 AV409658 Lotus japonicus young plants (two... 47 4e-04
- emb|AW691465|AW691465 NF045C04ST1F1000 Developing stem Medicago ... 44 8e-04

- emb|AW428965|AW428965 EST306505 tomato flower buds 0-3 mm, Corne... 35 0.001
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 emb|Z49501|SCYJR001W S.cerevisiae chromosome X reading frame ORF... 44 0.003
 5 emb|X87611|SCXCOSM83 S.cerevisiae chromosome X DNA (cosmid 83). 44 0.003
 emb|AW677443|AW677443 DG1_7_D10.b1_A002 Dark Grown 1 (DG1) Sorgh... 44 0.004
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- Query= AL049500.57_s_at 16914_s_at /id_source genbank /description
 10 emb|cab39936.1| (al049500) osmotin precursor [arabidopsis thaliana]
 /blast_score 1.00e-143 /ec_number /family /chip nova /gb_link /ncgi
 (735 letters)
- 15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
- Searching.....done
- 20 Score E
 Sequences producing significant alignments: (bits) Value
- emb|AW685448|AW685448 NF029F08NR1F1000 Nodulated root Medicago t... 409 e-114
 emb|AJ010501|CAR010501 Cicer arietinum L. mRNA for thaumatin-lik... 409 e-114
 25 emb|AW573922|AW573922 EST316513 GVN Medicago truncatula cDNA clo... 409 e-113
 emb|AW685184|AW685184 NF026H08NR1F1000 Nodulated root Medicago t... 338 e-105
 emb|AW348587|AW348587 GM210002B22C8R Gm-r1021 Glycine max cDNA 3... 365 e-101
 emb|AW685583|AW685583 NF029C04NR1F1000 Nodulated root Medicago t... 320 e-100
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 30 emb|X12739|NTPRRMAJ N. tabacum mRNA for pathogenesis-related pro... 201 4e-99
 emb|AF003007|AF003007 Vitis vinifera thaumatin-like protein VVTL... 214 7e-98
 emb|X15223|NTE2TLP Tobacco E2 gene for a thaumatin-like protein. 195 2e-97
 emb|X03913|NTTHAUR Tobacco mRNA for TMV induced protein homologo... 195 2e-97
 emb|AW684755|AW684755 NF021G01NR1F1000 Nodulated root Medicago t... 348 3e-95
 35 emb|AV428977|AV428977 AV428977 Lotus japonicus young plants (two... 343 7e-94
 emb|Y10992|VVOSM1 V. vinifera mRNA for osmotin-like protein. 224 3e-90
 emb|AF199508|AF199508 Fragaria x ananassa osmotin-like protein (... 220 1e-89
 emb|X72928|SC13OLP S. commersonii (pOSML13) gene for osmotin-like... 200 1e-88
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 40 emb|X70787|LEPRPA L. esculentum pr p23 mRNA for pathogenesis-rela... 200 1e-88
 emb|AW039873|AW039873 EST282346 tomato mixed elicitor, BTI Lycop... 200 1e-88
 emb|X66416|LETPM1M L. esculentum tpm 1 mRNA. 199 1e-88
 emb|AW218786|AW218786 EST301266 tomato root during/after fruit s... 197 9e-88
 dbj|D76437|TOBNP50 Nicotiana sylvestris DNA for neutral PR-5 (os... 193 8e-87
 45 emb|X95308|NTOSPR N. tabacum osmotin gene. 195 8e-87
 gb|S40046|S40046 abscisic acid-activated [Nicotiana tabacum L.=t... 195 1e-86
 emb|X65701|NTAP24G N. tabacum ap24 gene. 195 1e-86
 emb|X65700|NTAP24 N. tabacum mRNA ap24. 195 1e-86
 gb|S44889|S44889 osmotin= pathogenesis-related protein homolog [N... 195 1e-86
 50 emb|A16782|A16782 osmotin-like protein gene without 20 C- termin... 195 1e-86
 emb|A16780|A16780 osmotin-like protein gene seq ID No: 5. 195 1e-86
 emb|A83550|A83550 Sequence 1 from Patent WO9849331. 195 1e-86
 gb|M64081|TOBOLP Nicotiana tabacum osmotin-like protein (OLP1) m... 193 1e-86
 dbj|E03321|E03321 DNA encoding osmotin-like protein. 193 1e-86
 55 emb|X72927|SC81OLP S. commersonii (pOSML81) gene for osmotin-like... 193 7e-86
 emb|AW218785|AW218785 EST301265 tomato root during/after fruit s... 200 7e-86
 emb|AF093743|AF093743 Lycopersicon esculentum pathogenesis-relat... 193 1e-85
 gb|M21346|TOMNP24 Tomato NP24 protein mRNA, 3' end. 193 1e-85
 emb|AW035171|AW035171 EST280433 tomato callus, TAMU Lycopersicon... 193 1e-85
 60 emb|AW223970|AW223970 EST300781 tomato fruit red ripe, TAMU Lyco... 193 1e-85
 emb|AW223507|AW223507 EST300318 tomato fruit red ripe, TAMU Lyco... 193 1e-85

- emb|AW222204|AW222204 EST299015 tomato fruit red ripe, TAMU Lyco... 193 1e-85
emb|AW217005|AW217005 EST295719 tomato callus, TAMU Lycopersicon... 193 1e-85
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5 emb|AW684839|AW684839 NF022B04NR1F1000 Nodulated root Medicago t... 316 1e-85
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emb|X67244|CSOSLP S.commersonii mRNA for osmotin-like protein. 193 2e-85
emb|AW216590|AW216590 EST295304 tomato callus, TAMU Lycopersicon... 193 3e-85
emb|X72926|SCA81OLP S.commersonii (pA81) mRNA for osmotin-like p... 189 6e-85
10 emb|AF001528|AF001528 Musa acuminata ripening-associated protein... 307 8e-85
emb|AW622107|AW622107 EST312905 tomato root during/after fruit s... 192 9e-85
emb|AW218972|AW218972 EST301454 tomato root during/after fruit s... 191 1e-84
emb|AW033829|AW033829 EST277400 tomato callus, TAMU Lycopersicon... 193 2e-84
emb|AW221921|AW221921 EST298732 tomato fruit red ripe, TAMU Lyco... 187 4e-84
emb|AF109653|AF109653 AF109653 Capsicum annuum root susceptible ... 192 9e-84
15 emb|AW621924|AW621924 EST312722 tomato root during/after fruit s... 192 2e-83
emb|AW650675|AW650675 EST329129 tomato germinating seedlings, TA... 193 1e-82
emb|AW034088|AW034088 EST277583 tomato callus, TAMU Lycopersicon... 193 1e-81
emb|AW219330|AW219330 EST301812 tomato root during/after fruit s... 193 1e-81
emb|AW034433|AW034433 EST278004 tomato callus, TAMU Lycopersicon... 175 2e-80
20 emb|AI895910|AI895910 EST265353 tomato callus, TAMU Lycopersicon... 177 3e-80
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emb|AI896330|AI896330 EST265773 tomato callus, TAMU Lycopersicon... 193 4e-80
emb|AJ277064|LES277064 Lycopersicon esculentum PR-5 gene for pat... 192 3e-79
gb|M29279|TOBOSM N.tabacum osmotin mRNA, complete cds. 242 4e-79
25 emb|AW029746|AW029746 EST273001 tomato callus, TAMU Lycopersicon... 168 2e-78
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emb|AW650717|AW650717 EST329171 tomato germinating seedlings, TA... 165 2e-77
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emb|X61679|NTOSMOTIN N.tabacum mRNA for osmotin. 193 8e-77
30 emb|AW686653|AW686653 NF043G01NR1F1000 Nodulated root Medicago t... 265 1e-76
emb|AW220061|AW220061 EST302544 tomato root during/after fruit s... 193 1e-76
emb|AW830631|AW830631 sm04e12.y1 Gm-c1027 Glycine max cDNA clone... 230 2e-76
emb|AW099440|AW099440 sd40e08.y1 Gm-c1016 Glycine max cDNA clone... 227 2e-76
emb|AW458142|AW458142 sh78g09.y1 Gm-c1016 Glycine max cDNA clone... 185 2e-75
35 emb|AJ131731|PME131731 Pseudotsuga menziesii mRNA for Thaumatin-... 237 3e-74
gb|BE033983|BE033983 MG02H11 MG Mesembryanthemum crystallinum cD... 155 2e-73
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emb|A15671|A15671 proprothaumatin. 116 4e-72
40 gb|J01209|TDATHAU2 T.daniellii preprothaumatin-2 mRNA, complete ... 116 4e-72
emb|A15673|A15673 proprothaumatin and the coding strand of its ... 116 4e-72
emb|A15677|A15677 proprothaumatin and the coding stand of its s... 116 4e-72
emb|AF110151|AF110151 AF110151 Capsicum annuum root 1st-branched... 192 4e-72
emb|A15675|A15675 proprothaumatin and the coding strand of its ... 116 2e-71
45 emb|A15660|A15660 Mature thaumatin. 116 2e-71
emb|A46806|A46806 Sequence 3 from Patent EP0684312. 115 5e-71
emb|AF121776|AF121776 Juniperus ashei allergen Jun a 3 mRNA, com... 144 1e-70
emb|AF016327|AF016327 Hordeum vulgare Barperml (perml) mRNA, par... 221 3e-70
50 emb|AW031249|AW031249 EST274624 tomato callus, TAMU Lycopersicon... 200 3e-70
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emb|AV423642|AV423642 AV423642 Lotus japonicus young plants (two... 263 1e-69
emb|AI055586|AI055586 coau0004G15 Cotton Boll Abscission Zone cD... 262 2e-69
emb|AW032915|AW032915 EST276474 tomato callus, TAMU Lycopersicon... 200 2e-69
55 emb|A46810|A46810 Sequence 7 from Patent EP0684312. 108 1e-68
emb|AW441774|AW441774 EST311170 tomato fruit red ripe, TAMU Lyco... 193 1e-68
emb|AW223623|AW223623 EST300434 tomato fruit red ripe, TAMU Lyco... 193 1e-68
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emb|AW224329|AW224329 EST301140 tomato fruit red ripe, TAMU Lyco... 193 1e-68
60 emb|AI895353|AI895353 EST264796 tomato callus, TAMU Lycopersicon... 193 1e-68
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 (357 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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	(bits)		Value
15	Sequences producing significant alignments:		
	emb X89759 BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen...	194	2e-49
	gb U59379 BNU59379 Brassica napus thioredoxin-h-like-1 (THL-1) m...	194	2e-49
	emb AB010434 AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ...	192	9e-49
	emb AW255457 AW255457 ML480 peppermint glandular trichome Menth...	190	3e-48
20	emb AW569018 AW569018 si74e02.yl Gm-c1031 Glycine max cDNA clone...	185	1e-46
	emb AI988470 AI988470 sd02f07.yl Gm-c1020 Glycine max cDNA clone...	185	1e-46
	emb Z70677 RCTHIORXN R.communis mRNA for thioredoxin.	183	5e-46
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	gb BE053835 BE053835 GA_Ea0009P21f Gossypium arboreum 7-10 dpa ...	182	9e-46
25	emb AW677726 AW677726 WS1_10_F03.g1_A002 Water-stressed 1 (WS1) ...	181	2e-45
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30	emb AW349345 AW349345 GM210007A20B10R Gm-r1021 Glycine max cDNA ...	179	6e-45
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	emb AI461219 AI461219 sa76f11.yl Gm-c1004 Glycine max cDNA clone...	179	6e-45
	emb AJ009762 TAE9762 Triticum aestivum mRNA for thioredoxin H.	179	9e-45
35	emb AW164730 AW164730 se77a02.yl Gm-c1023 Glycine max cDNA clone...	179	9e-45
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	dbj D87984 D87984 Fagopyrum esculentum mRNA for thioredoxin, com...	177	4e-44
40	emb AW983331 AW983331 HVSMEg0010D20f Hordeum vulgare pre-anthesi...	177	4e-44
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	gb BE053246 BE053246 GA_Ea0021K08f Gossypium arboreum 7-10 dpa ...	176	8e-44
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50	emb AJ001903 TDAJ1903 Triticum durum mRNA for thioredoxin H.	175	1e-43
	emb A48520 A48520 Sequence 8 from Patent WO9603505.	175	1e-43
	emb A48514 A48514 Sequence 2 from Patent WO9603505.	175	1e-43
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55	emb AW983305 AW983305 HVSMEg0010C12f Hordeum vulgare pre-anthesi...	174	3e-43
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	emb AW982237 AW982237 HVSMEg0002G18f Hordeum vulgare pre-anthesi...	174	3e-43
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60	gb C95504 C95504 C95504 Citrus unshiu Miyagawa-wase maturation s...	172	7e-43
	emb AW277335 AW277335 sf80b02.yl Gm-c1019 Glycine max cDNA clone...	171	1e-42

- emb|AI441505|AI441505 sa87c03.y1 Gm-c1004 Glycine max cDNA clone... 171 1e-42
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5 emb|AW096472|AW096472 EST289652 tomato mixed elicitor, BTI Lycop... 171 3e-42
emb|AI775760|AI775760 EST256860 tomato resistant, Cornell Lycop... 171 3e-42
emb|AI773303|AI773303 EST254403 tomato resistant, Cornell Lycop... 171 3e-42
emb|AI776110|AI776110 EST257198 tomato resistant, Cornell Lycop... 171 3e-42
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10 emb|AW040011|AW040011 EST282502 tomato mixed elicitor, BTI Lycop... 171 3e-42
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emb|AW621673|AW621673 EST312471 tomato root during/after fruit s... 171 3e-42
emb|AI780240|AI780240 EST261119 tomato susceptible, Cornell Lyco... 171 3e-42
emb|AW041395|AW041395 EST284259 tomato mixed elicitor, BTI Lycop... 171 3e-42
emb|AW038141|AW038141 EST279798 tomato mixed elicitor, BTI Lycop... 171 3e-42
15 emb|AW038924|AW038924 EST280880 tomato mixed elicitor, BTI Lycop... 171 3e-42
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25 emb|AW038564|AW038564 EST280247 tomato mixed elicitor, BTI Lycop... 168 1e-41
gb|BE057793|BE057793 sn07c11.y1 Gm-c1016 Glycine max cDNA clone ... 168 1e-41
emb|AW217307|AW217307 EST296026 tomato flower buds 0-3 mm, Corne... 165 2e-40
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30 emb|AW064893|AW064893 ST37B02 Pine TriplEx shoot tip library Pin... 162 8e-40
emb|AW065132|AW065132 ST40A08 Pine TriplEx shoot tip library Pin... 162 1e-39
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 (1896 letters)

5

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E
 Sequences producing significant alignments: (bits) Value

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Database: plantfungal

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50	emb Z73261 SCYLR089C S.cerevisiae chromosome XII reading frame O...	51	2e-14
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	dbj D01033 CUCACCA Cucurbita maxima mRNA for 1-aminocyclopropane...	50	2e-06
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Database: plantfungal
 60 661,018 sequences; 426,114,510 total letters

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10 gb M37637 ARCPNC2 A.hypogaea cationic peroxidase mRNA, complete ...	271	2e-72	
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emb AI777064 AI777064 EST252031 tomato callus, TAMU Lycopersicon...	261	3e-69	
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15 emb AB027753 AB027753 Nicotiana tabacum mRNA for peroxidase, com...	255	1e-67	
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 20 emb|Y10470|SOPR XR9 S.oleracea mRNA for peroxidase, clone PC56. 151 1e-39
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 (2766 letters)

55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

60 Searching.....done

Score E

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	gb U42444 U42444 <i>Lycopersicon pimpinellifolium</i> leucine rich repe... 198 1e-70	
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	gb U42445 U42445 <i>Lycopersicon pimpinellifolium</i> leucine rich repe... 198 1e-70	
	emb A57133 A57133 Sequence 4 from Patent WO9531564. 198 1e-70	
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	gb U77888 INU77888 <i>Ipomoea nil</i> receptor-like protein kinase (inr... 174 2e-66	
	emb AF053995 AF053995 <i>Lycopersicon esculentum</i> Hcr2-0B (Hcr2-0B) ... 195 1e-65	
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	emb A67428 A67428 Sequence 1 from Patent WO9743429. 198 2e-65	
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	emb AW035394 AW035394 EST281132 tomato callus, TAMU Lycopersicon... 136 1e-30	
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	emb AW932515 AW932515 EST358358 tomato fruit mature green, TAMU ... 78 1e-30	
60	emb AI166936 AI166936 xylem.est.719 Poplar xylem Lambda ZAPII li... 85 1e-30	
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 (921 letters)

50 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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55 Score E
 Sequences producing significant alignments: (bits) Value

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- emb|A26447|A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f... 259 e-117
emb|A26451|A26451 Soya beta-1,3-glucanase plasmid pBR59 NdeI-Hin... 259 e-117
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20 emb|AF004838|AF004838 *Musa acuminata* beta-1,3-glucanase mRNA, pa... 205 8e-95
gb|M60403|TOBGLB13B *Nicotiana tabacum* glucan beta-1,3-glucosidas... 238 2e-94
emb|AF034117|AF034117 Glycine max beta-1,3-glucanase 12 (SGlu12)... 180 3e-94
gb|M59442|TOBGLUCA *N. tabacum* basic-1,3-glucanase gene, complete cds. 236 7e-94
emb|A16121|A16121 Intracellular Beta-1, 3 glucanase gene (SEQ ID... 236 7e-94
25 gb|M59443|TOBGLUCB *N. tabacum* acidic beta-1,3-glucanase gene, com... 150 2e-92
emb|A16120|A16120 Extracellular Beta-1, 3 glucanase gene (SEQ ID... 150 2e-92
gb|M60460|TOBPR2A Tobacco PR2 protein mRNA, complete cds. 149 4e-91
emb|AJ277900|VVI277900 *Vitis vinifera* mRNA for beta 1-3 glucanas... 221 8e-91
gb|U01902|U01902 *Solanum tuberosum* *Datura* endo-1,3-beta-D-glucan... 238 3e-90
30 gb|U49454|PPU49454 *Prunus persica* beta-1,3-glucanase (Gns1) gene... 211 2e-89
emb|AF227953|AF227953 *Capsicum annuum* basic beta-1,3-glucanase (... 224 4e-89
emb|AF034106|AF034106 Glycine max beta-1,3-glucanase 1 (SGlu1) g... 221 2e-88
emb|AF141654|AF141654 *Nicotiana tabacum* beta-1,3-glucanase (GGL4... 139 3e-88
gb|M60463|TOBGL153A Tobacco GL153 protein mRNA, complete cds. 139 3e-88
35 gb|M20620|TOBGLUBC *N. tabacum* beta-1,3-glucanase mRNA, clone pGL43. 238 4e-88
emb|AF034113|AF034113 Glycine max beta-1,3-glucanase 8 (SGlu8) g... 222 1e-87
emb|X54431|NTSP41B Tobacco sp41b mRNA for (1-3)-beta-glucanase. 136 6e-87
emb|AF141653|AF141653 *Nicotiana tabacum* beta-1,3-glucanase (GGL1... 136 1e-86
gb|M60464|TOBB13G Tobacco beta-1,3-glucanase mRNA, complete cds. 136 1e-86
40 emb|AJ000081|CSAJ81 *Citrus sinensis* mRNA for beta-1,3-glucanase. 113 2e-86
emb|X81560|NTSP41AGN *N. tabacum* Sp41a gene. 136 4e-86
emb|X54430|NTSP41A Tobacco sp41a mRNA for (1-3)-beta-glucanase. 135 8e-86
dbj|E03985|E03985 DNA encoding beta-1,3-endoglucanase. 167 3e-84
dbj|E02108|E02108 cDNA sequence coding for beta-1,3-endoglucanase. 167 3e-84
45 gb|M37753|SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple... 167 3e-84
emb|AJ009932|STAJ9932 *Solanum tuberosum* mRNA for beta-1,3-glucan... 144 4e-84
emb|AW034632|AW034632 EST278316 tomato callus, TAMU *Lycopersicon*... 188 1e-82
gb|U41323|GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c... 169 3e-82
emb|AW033770|AW033770 EST277341 tomato callus, TAMU *Lycopersicon*... 186 5e-82
50 gb|M80604|TOMB13GLUA *Lycopersicon esculentum* beta-1,3-glucanase ... 142 5e-82
emb|X74905|LEQA *L. esculentum* TomQ'a mRNA for beta(1,3)glucanase. 128 4e-79
emb|AI896001|AI896001 EST265444 tomato callus, TAMU *Lycopersicon*... 175 9e-79
emb|AW034584|AW034584 EST278268 tomato callus, TAMU *Lycopersicon*... 226 9e-79
emb|X54456|NTEC32139 *N. tabacum* mRNA for acidic beta-1,3 glucana... 127 2e-78
55 emb|AJ012751|CAR012751 *Cicer arietinum* mRNA for glucan endo-beta... 126 2e-78
emb|AW034478|AW034478 EST278049 tomato callus, TAMU *Lycopersicon*... 227 8e-78
emb|AW031078|AW031078 EST274385 tomato callus, TAMU *Lycopersicon*... 169 4e-77
emb|AW035235|AW035235 EST280497 tomato callus, TAMU *Lycopersicon*... 179 5e-77
gb|M60462|TOBPRNA Tobacco PRN protein mRNA, 3' end. 117 5e-76
60 emb|AW775271|AW775271 EST334336 *DSIL* *Medicago truncatula* cDNA cl... 163 6e-76
emb|AW776932|AW776932 EST335997 *DSIL* *Medicago truncatula* cDNA cl... 156 7e-76

- emb|AW216637|AW216637 EST295351 tomato callus, TAMU Lycopersicon... 164 2e-75
 emb|AW032447|AW032447 EST276006 tomato callus, TAMU Lycopersicon... 227 2e-74
 emb|AW156463|AW156463 se26e04.y1 Gm-c1015 Glycine max cDNA clone... 256 3e-74
 5 emb|Z68154|GHBGLUCS *G.hirsutum* mRNA for 1,3-beta-glucanase. 152 1e-73
 gb|M63634|TOBGCBREG *Nicotiana plumbaginifolia* beta(1,3)-glucanas... 250 9e-73
 emb|AW032644|AW032644 EST276203 tomato callus, TAMU Lycopersicon... 189 1e-71
 emb|AF230109|AF230109 *Populus alba* x *Populus tremula* beta-1,3 gl... 173 3e-71
 gb|M20618|TOBGLUBA *N.tabacum* beta-1,3-glucanase mRNA, clones pGL... 238 3e-71
 10 emb|AI894445|AI894445 EST263900 tomato callus, TAMU Lycopersicon... 231 3e-71
 emb|AF034107|AF034107 Glycine max beta-1,3-glucanase 2 (SGlu2) g... 142 7e-71
 emb|AW031387|AW031387 EST274841 tomato callus, TAMU Lycopersicon... 237 7e-71
 emb|AW035366|AW035366 EST280928 tomato callus, TAMU Lycopersicon... 237 7e-71
 emb|AI896035|AI896035 EST265478 tomato callus, TAMU Lycopersicon... 237 7e-71
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 15 emb|AW030447|AW030447 EST273702 tomato callus, TAMU Lycopersicon... 236 3e-70
 emb|AF034116|AF034116 Glycine max beta-1,3-glucanase 11 (SGlu11)... 124 9e-70
 emb|AW030277|AW030277 EST273532 tomato callus, TAMU Lycopersicon... 144 2e-69
 emb|AF034110|AF034110 Glycine max beta-1,3-glucanase 5 (SGlu5) g... 122 3e-69
 emb|AW035160|AW035160 EST280422 tomato callus, TAMU Lycopersicon... 142 6e-69
 20 emb|AW032444|AW032444 EST276003 tomato callus, TAMU Lycopersicon... 142 6e-69
 emb|X74906|LEQB *L.esculentum* TomQ'b mRNA for beta(1,3)glucanase. 101 1e-68
 emb|AJ011769|CIN011769 *Cichorium intybus* X *Cichorium endivia* sub... 97 1e-68
 emb|AW030283|AW030283 EST273538 tomato callus, TAMU Lycopersicon... 140 2e-68
 gb|M13237|BLYGLUCB Barley beta glucanase mRNA. 158 7e-68
 25 emb|Z15131|ASBGLUCAN *A.sativa* mRNA for beta glucanase. 158 9e-68
 emb|AI896042|AI896042 EST265485 tomato callus, TAMU Lycopersicon... 237 1e-67
 gb|M62740|BLYGLB2 *Hordeum vulgare* 1,3-1,4-beta-D glucan 4-glucan... 158 2e-67
 emb|AW031259|AW031259 EST274634 tomato callus, TAMU Lycopersicon... 136 3e-67
 emb|AW035840|AW035840 EST281994 tomato callus, TAMU Lycopersicon... 136 3e-67
 30 emb|AW032451|AW032451 EST276010 tomato callus, TAMU Lycopersicon... 136 3e-67
 emb|AW031353|AW031353 EST274807 tomato callus, TAMU Lycopersicon... 136 3e-67
 emb|AI895981|AI895981 EST265424 tomato callus, TAMU Lycopersicon... 136 3e-67
 gb|U73709|VVU73709 *Vitis vinifera* beta-1,3-glucanase mRNA, parti... 244 3e-67
 emb|Z22874|TABETGLUB *T.aestivum* (1,3;1,4) beta glucanase mRNA, c... 160 3e-67
 35 emb|AF034114|AF034114 Glycine max beta-1,3-glucanase 9 (SGlu9) p... 119 7e-67

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 40 thaliana] /blast_score 1.00e-158 /ec_number /family /chip nova
 /gb_link /ncgi
 (939 letters)

Database: plantfungal

45 661,018 sequences; 426,114,510 total letters

Searching.....done

50 Score E
 Sequences producing significant alignments: (bits) Value

- emb|AW730233|AW730233 GA_Ea0014B16 *Gossypium arboreum* 7-10 dpa ... 352 5e-98
 emb|AW649960|AW649960 EST328414 tomato germinating seedlings, TA... 308 4e-83
 emb|AW621664|AW621664 EST312462 tomato root during/after fruit s... 290 1e-77
 55 emb|AW031327|AW031327 EST274781 tomato callus, TAMU Lycopersicon... 282 3e-75
 gb|U38804|PPU38804 *Porphyra purpurea* chloroplast, complete genome. 271 4e-72
 emb|AW775853|AW775853 EST334918 DSIL *Medicago truncatula* cDNA cl... 264 9e-70
 emb|Z21642|CHASTRNAA *Antithamnion* sp. Chloroplast trnK, trnE, trpA... 255 4e-67
 gb|BE124387|BE124387 EST393422 GVN *Medicago truncatula* cDNA clon... 227 9e-59
 60 gb|BE121873|BE121873 894015F07.y1 *C. reinhardtii* CC-1690, normal... 227 1e-58
 emb|AF022186|AF022186 *Cyanidium caldarium* strain RK1 chloroplast... 220 1e-56

- emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53
 emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49
 dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49
 5 emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49
 emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47
 dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46
 emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46
 dbj|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45
 gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43
 10 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42
 emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42
 emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38
 emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38
 emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32
 15 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycopersicon... 138 5e-32
 emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 74 3e-30
 emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26
 emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21
 emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19
 20 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17
 emb|AF084886|AF084886 Neurospora crassa 314-448A mutant tryptoph... 68 9e-11
 emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptoph... 53 4e-10
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 25 emb|AF084884|AF084884 Neurospora crassa 314-722A mutant tryptoph... 64 1e-09
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 30 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08
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 emb|AW693052|AW693052 NF059C08ST1F1065 Developing stem Medicago ... 51 1e-05
 emb|AV390244|AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla... 49 4e-05
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 35 emb|AL354022|P761R Leishmania major Friedlin PAC P761 right end... 44 0.002
 gb|M91656|CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1... 43 0.005
 emb|AQ903789|AQ903789 GSSTc04230 Trypanosome cruzi random genomi... 35 0.24
 emb|AW727215|AW727215 GA_Ea0023N23 Gossypium arboreum 7-10 dpa ... 36 0.52
 gb|M91654|CCITRP03 Coprinus cinereus tryptophan synthetase (TRP1... 36 0.52
 40 emb|AW728975|AW728975 GA_Ea0018P19 Gossypium arboreum 7-10 dpa ... 35 0.64
 emb|AL139794|LMFP1105 Leishmania major Friedlin chromosome 4 PAC... 35 0.87
 emb|AW926438|AW926438 HVSMEg0007D14 Hordeum vulgare pre-anthesis... 34 1.2
 emb|AA965348|AA965348 e9d04a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
 gb|U12630|ENU12630 Emericella nidulans R153 core histone H3 (H3)... 34 1.3
 45 emb|AI007494|AI007494 e9c09a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
 emb|AA787433|AA787433 n3d04a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
 emb|X55548|ANH3GENE A.nidulans gene for core histone for H3. 34 1.3
 emb|AQ396426|AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P... 34 1.6
 emb|AF262997|AF262997 Ricinus communis NADP-dependent malic prot... 34 1.6
 50 gb|M19025|CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c... 34 1.6
 emb|AF084888|AF084888 Neurospora crassa 656-2A mutant tryptophan... 31 1.7
 emb|AF084887|AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta... 31 1.7
 emb|AW694774|AW694774 NF080A05ST1F1036 Developing stem Medicago ... 34 1.8
 emb|Y18012|TVE18012 Trametes versicolor mRNA for laccase. 33 2.3
 55 emb|AQ500614|AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc... 33 2.5
 emb|AW187498|AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium ... 33 3.1
 emb|AW187530|AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium ... 33 3.1
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 emb|AW186883|AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium ... 33 3.1
 60 emb|AW187537|AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ... 33 3.1
 emb|AW187474|AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium ... 33 3.1

	emb AA167859 AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor...	33 3.5
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	emb AF129874 AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp...	33 4.3
5	emb AL112679 CNS01AA7 Botrytis cinerea strain T4 cDNA library un...	33 4.7
	gb BE028433 BE028433 EtESTea78d07.y1 Eimeria M5-6 Merozoite stag...	32 5.9
	emb AI166784 AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li...	32 5.9
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10	gb BE027723 BE027723 EtESTea86c08.y1 Eimeria M5-6 Merozoite stag...	32 5.9
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	gb BE027843 BE027843 EtESTea88c05.y1 Eimeria M5-6 Merozoite stag...	32 5.9
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	dbj D85261 D85261 Plasmodium vivax clone TD439B DNA for merozoit...	32 5.9
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15	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom...	32 6.5
	emb Z71509 SCYNL233W S.cerevisiae chromosome XIV reading frame O...	32 6.5
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35 http://www3.ncbi.nlm.nih.gov/htbin-
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http://www.ncgr.org/cgi-bin/ff?z97339
(441 letters)

40 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	emb AW687017 AW687017 NF005A10RT1F1072 Developing root Medicago ...	123 6e-28
50	emb AW687794 AW687794 NF013E08RT1F1066 Developing root Medicago ...	89 3e-23
	emb AW310121 AW310121 sF31d07.x1 Gm-c1028 Glycine max cDNA clone...	68 3e-19
	emb AW704640 AW704640 sk54f05.y1 Gm-c1019 Glycine max cDNA clone...	68 3e-19
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	emb AW687188 AW687188 NF006H09RT1F1079 Developing root Medicago ...	82 3e-15
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60	emb AW233878 AW233878 sF31d07.y1 Gm-c1028 Glycine max cDNA clone...	69 3e-13
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5 emb|AW687565|AW687565 NF011A04RT1F1024 Developing root Medicago ... 48 2e-11
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10 emb|AW394608|AW394608 sh33e11.y1 Gm-c1017 Glycine max cDNA clone... 46 2e-07
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emb|AI794716|AI794716 sb68b06.y1 Gm-c1019 Glycine max cDNA clone... 48 5e-06
gb|BE024111|BE024111 sm96h03.y1 Gm-c1015 Glycine max cDNA clone ... 48 9e-06
emb|Z99969|MAZ99969 Musa acuminata mRNA for putative beta-1,3-gl... 41 6e-05
15 emb|AV412437|AV412437 AV412437 Lotus japonicus young plants (two... 47 9e-05
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emb|AW775954|AW775954 EST335019 DSIL Medicago truncatula cDNA cl... 42 7e-04
20 gb|BE122569|BE122569 Ljirp29-344-g6 Ljirp Lambda HybriZap t... 43 0.001
emb|AW299135|AW299135 EST305809 KV2 Medicago truncatula cDNA clo... 43 0.002
emb|AW423359|AW423359 sh06g04.y1 Gm-c1016 Glycine max cDNA clone... 41 0.004
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25 emb|AW747074|AW747074 WS1_65_A07.g1_A002 Water-stressed 1 (WS1) ... 39 0.026
emb|AW649685|AW649685 EST328139 tomato germinating seedlings, TA... 38 0.036
emb|AW299176|AW299176 EST305986 KV2 Medicago truncatula cDNA clo... 38 0.036
emb|AW220014|AW220014 EST302497 tomato root during/after fruit s... 38 0.050
gb|C96140|C96140 C96140 Marchantia polymorpha immature sex organ... 38 0.050
30 emb|AW625648|AW625648 EST319555 tomato radicle, 5 d post-imbibit... 38 0.050
emb|AW926780|AW926780 HVSMEg0008D23 Hordeum vulgare pre-anthesis... 37 0.094
gb|L05906|PMCMSGF Pneumocystis carinii (clone GP3) major surface... 36 0.18
emb|AW333354|AW333354 S20F5 AGS-1 Pneumocystis carinii f. sp. ca... 36 0.18
emb|Z98595|SPAC11E3 S.pombe chromosome I cosmid c11E3. 35 0.24
35 emb|AW725520|AW725520 GA_Ea0018G22 Gossypium arboreum 7-10 dpa ... 35 0.46
gb|BE052896|BE052896 GA_Ea0025I06f Gossypium arboreum 7-10 dpa ... 35 0.46
emb|AW309936|AW309936 sf26g12.x1 Gm-c1028 Glycine max cDNA clone... 35 0.46
emb|AW310120|AW310120 sf31d06.x1 Gm-c1028 Glycine max cDNA clone... 35 0.46
emb|AW233798|AW233798 sf26g12.y1 Gm-c1028 Glycine max cDNA clone... 35 0.46
40 gb|BE053040|BE053040 GA_Ea0015D14f Gossypium arboreum 7-10 dpa ... 35 0.46
emb|AW310598|AW310598 sg21h03.x1 Gm-c1024 Glycine max cDNA clone... 35 0.46
emb|AI731906|AI731906 BNLGHi1249 Six-day Cotton fiber Gossypium... 35 0.46
gb|BE054609|BE054609 GA_Ea0006A14f Gossypium arboreum 7-10 dpa ... 35 0.46
emb|AW278505|AW278505 sf45c08.y1 Gm-c1009 Glycine max cDNA clone... 35 0.46
45 emb|AC013353|AC013353 Trypanosoma brucei chromosome VI clone RPC... 34 0.63
emb|AI728996|AI728996 BNLGHi12315 Six-day Cotton fiber Gossypium... 34 0.63
emb|AW691828|AW691828 NF044F04ST1F1000 Developing stem Medicago ... 34 0.63
emb|AI729057|AI729057 BNLGHi12476 Six-day Cotton fiber Gossypium... 34 0.63
emb|AI731500|AI731500 BNLGHi9982 Six-day Cotton fiber Gossypium ... 34 0.63
50 emb|AQ660279|AQ660279 Sheared DNA-3L23.TF Sheared DNA Trypanosom... 34 0.63
emb|AI729672|AI729672 BNLGHi13930 Six-day Cotton fiber Gossypium... 34 0.63
emb|AI725456|AI725456 BNLGHi12219 Six-day Cotton fiber Gossypium... 34 0.63
emb|AQ656131|AQ656131 Sheared DNA-27G20.TF Sheared DNA Trypanoso... 34 0.63
emb|AI731231|AI731231 BNLGHi8954 Six-day Cotton fiber Gossypium ... 34 0.87
55 emb|AL035477|PFMAL4P4 Plasmodium falciparum chromosome 4 strain ... 34 0.87
gb|BE033791|BE033791 MF06E10 MF Mesembryanthemum crystallinum cD... 34 0.87
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emb|AI731464|AI731464 BNLGHi9855 Six-day Cotton fiber Gossypium ... 34 0.87
emb|AI727451|AI727451 BNLGHi8020 Six-day Cotton fiber Gossypium ... 34 0.87
60 emb|AW620830|AW620830 sj47b03.y1 Gm-c1033 Glycine max cDNA clone... 28 1.1
dbj|D63449|YSCATF1A Yeast ATF1 gene for alcohol acetyltransferas... 33 1.2

- dbj|E08050|E08050 cDNA encoding beer yeast alcohol acetyltransfe... 33 1.2
 dbj|E06817|E06817 DNA encoding alcohol acetyltransferase 1. 33 1.2
 dbj|D26554|YSCATF1 Yeast ATF1 gene for alcohol acetyltransferase... 33 1.2
 dbj|E08049|E08049 cDNA encoding sake yeast alcohol acetyltransfe... 33 1.2
 5 dbj|E06816|E06816 DNA encoding alcohol acetyltransferase 1. 33 1.2
 emb|Z75285|SCYOR377W *S.cerevisiae* chromosome XV reading frame OR... 33 1.2
 emb|AW725476|AW725476 GA_Ea0018C14 *Gossypium arboreum* 7-10 dpa ... 33 1.6
 emb|AI812453|AI812453 11C3 Pine Lambda Zap Xylem library *Pinus t...* 33 1.6
 emb|AW459992|AW459992 si07c04.y1 Gm-c1029 Glycine max cDNA clone... 33 1.6
 10 emb|X01777|HVB3HORD Barley mRNA fragment for B3-hordein. 33 1.6
 emb|AQ449927|AQ449927 500006A04.x1 CpIOWAM13mp18gDNA1 *Cryptospor...* 33 1.6
 emb|AE001274|AE001274 *Leishmania* major chromosome 1, complete se... 32 2.2
 emb|AL031261|SPBC3H7 *S.pombe* chromosome II cosmid c3H7. 32 2.2
 emb|AI812374|AI812374 1F12 Pine Lambda Zap Xylem library *Pinus t...* 32 2.2
 15 emb|AI728744|AI728744 BNLGHi11492 Six-day Cotton fiber *Gossypium...* 32 2.2
 gb|BE036189|BE036189 MO20F12 MO *Mesembryanthemum crystallinum* cD... 32 3.1
 emb|AW925749|AW925749 HVSMEg0005G16 *Hordeum vulgare* pre-anthesis... 32 3.1
 emb|AQ411951|AQ411951 CpG0926A CpIOWAgDNA1 *Cryptosporidium parvu...* 32 3.1
 emb|AQ935548|AQ935548 CpG2528A CpIOWAgDNA1 *Cryptosporidium parvu...* 32 3.1
 20 emb|AQ411952|AQ411952 CpG0926B CpIOWAgDNA1 *Cryptosporidium parvu...* 32 3.1
 gb|B67221|B67221 CpG0036A CpIOWAgDNA1 *Cryptosporidium parvum* gen... 32 3.1
 emb|AW030301|AW030301 EST273556 tomato callus, TAMU *Lycopersicon...* 31 4.2
 emb|AL160371|LMFLCHR15 *Leishmania* major Friedlin assembled chrom... 31 4.2
 emb|AL122012|LMFL8342 *Leishmania* major Friedlin chromosome 23 co... 31 4.2
 25 emb|X60772|GMOLEOA *G.max* mRNA for 24 kDa oleosin isoform (partia... 31 4.2

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 emb|caa07352.1| (aj006960) peroxidase [*arabidopsis thaliana*]
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(592 letters)

Database: plantfungal

35 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E

40 Sequences producing significant alignments: (bits) Value

- emb|X90695|MSRNAPE02 *M.sativa* mRNA for peroxidase 2. 339 1e-92
 emb|AJ011939|TRE011939 *Trifolium repens* mRNA for peroxidase. 335 2e-91
 emb|Y10469|SOPR XR8 *S.oleracea* mRNA for peroxidase, clone PC55. 332 2e-90
 45 emb|AI487510|AI487510 EST245832 tomato ovary, TAMU *Lycopersicon* ... 327 5e-89
 emb|AI486784|AI486784 EST245106 tomato ovary, TAMU *Lycopersicon* ... 327 5e-89
 emb|AI895842|AI895842 EST265285 tomato callus, TAMU *Lycopersicon*... 325 1e-88
 emb|AW032442|AW032442 EST276001 tomato callus, TAMU *Lycopersicon*... 325 2e-88
 gb|L36158|ALFPXDD *Medicago sativa* peroxidase (pxdD) mRNA, 3' end. 320 6e-87
 50 emb|AW216351|AW216351 EST295095 tomato callus, TAMU *Lycopersicon*... 319 1e-86
 emb|AW691003|AW691003 NF040C11ST1F1000 Developing stem *Medicago* ... 319 2e-86
 emb|AW625601|AW625601 EST319508 tomato radicle, 5 d post-imbibit... 318 3e-86
 gb|BE124281|BE124281 EST394406 DSIL *Medicago truncatula* cDNA clo... 314 4e-85
 emb|AI894487|AI894487 EST263930 tomato callus, TAMU *Lycopersicon*... 307 4e-83
 55 emb|AW666274|AW666274 sk34e11.y1 Gm-c1028 Glycine max cDNA clone... 304 4e-82
 emb|AI897419|AI897419 EST266862 tomato ovary, TAMU *Lycopersicon* ... 295 2e-79
 emb|AW329042|AW329042 N200241e rootphos(-) *Medicago truncatula* c... 292 2e-78
 emb|AW666298|AW666298 sk34h04.y1 Gm-c1028 Glycine max cDNA clone... 292 2e-78
 emb|AW030788|AW030788 EST274043 tomato callus, TAMU *Lycopersicon*... 292 2e-78
 60 emb|AW031625|AW031625 EST275079 tomato callus, TAMU *Lycopersicon*... 291 3e-78
 emb|AW278809|AW278809 sf98g02.y1 Gm-c1019 Glycine max cDNA clone... 200 3e-78

	emb AW221693 AW221693 EST298504 tomato fruit red ripe, TAMU Lyco...	290 7e-78
	emb AW216725 AW216725 EST295439 tomato callus, TAMU Lycopersicon...	287 4e-77
	emb AW035689 AW035689 EST281843 tomato callus, TAMU Lycopersicon...	286 1e-76
	emb AW221724 AW221724 EST298535 tomato fruit red ripe, TAMU Lyco...	285 2e-76
5	emb AW030405 AW030405 EST273660 tomato callus, TAMU Lycopersicon...	285 2e-76
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	emb AW032463 AW032463 EST276022 tomato callus, TAMU Lycopersicon...	282 2e-75
10	emb AW596100 AW596100 si97h09.y1 Gm-c1032 Glycine max cDNA clone...	281 2e-75
	emb AW035606 AW035606 EST281344 tomato callus, TAMU Lycopersicon...	281 4e-75
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	emb AW686501 AW686501 NF038G03NR1F1000 Nodulated root Medicago t...	279 2e-74
	emb AW031359 AW031359 EST274813 tomato callus, TAMU Lycopersicon...	278 2e-74
	emb AW650288 AW650288 EST328742 tomato germinating seedlings, TA...	277 4e-74
15	emb AW705765 AW705765 sk51f01.y1 Gm-c1019 Glycine max cDNA clone...	184 6e-74
	emb AI895322 AI895322 EST264765 tomato callus, TAMU Lycopersicon...	268 2e-71
	emb AW649016 AW649016 EST327470 tomato germinating seedlings, TA...	265 2e-70
	emb AW703879 AW703879 sk25c06.y1 Gm-c1028 Glycine max cDNA clone...	264 5e-70
	emb AW306953 AW306953 sf50h05.y1 Gm-c1009 Glycine max cDNA clone...	263 1e-69
20	emb AW306251 AW306251 se48c03.y1 Gm-c1017 Glycine max cDNA clone...	261 4e-69
	emb AW704671 AW704671 sk39a11.y1 Gm-c1028 Glycine max cDNA clone...	259 1e-68
	emb AI895156 AI895156 EST264599 tomato callus, TAMU Lycopersicon...	257 6e-68
	emb AW686857 AW686857 NF003C01RT1F1000 Developing root Medicago ...	241 8e-68
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25	emb AW029767 AW029767 EST273022 tomato callus, TAMU Lycopersicon...	253 8e-67
	emb AW687854 AW687854 NF014B12RT1F1096 Developing root Medicago ...	214 1e-66
	emb AW704702 AW704702 sk39d10.y1 Gm-c1028 Glycine max cDNA clone...	248 3e-65
	emb AI899344 AI899344 EST268787 tomato ovary, TAMU Lycopersicon ...	248 3e-65
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30	emb AI895840 AI895840 EST265283 tomato callus, TAMU Lycopersicon...	248 4e-65
	emb AI894658 AI894658 EST264101 tomato callus, TAMU Lycopersicon...	246 1e-64
	emb AW030796 AW030796 EST274051 tomato callus, TAMU Lycopersicon...	243 6e-64
	emb AI896743 AI896743 EST266186 tomato callus, TAMU Lycopersicon...	242 2e-63
	emb AW687617 AW687617 NF011E10RT1F1082 Developing root Medicago ...	241 4e-63
35	emb AW029904 AW029904 EST273159 tomato callus, TAMU Lycopersicon...	239 1e-62
	emb AW676864 AW676864 DG1_1_D12.b1_A002 Dark Grown 1 (DG1) Sorgh...	237 4e-62
	emb AI896941 AI896941 EST266384 tomato callus, TAMU Lycopersicon...	236 1e-61
	emb AW622528 AW622528 EST313328 tomato root during/after fruit s...	232 1e-60
40	emb AW208032 AW208032 M111060e DSIR Medicago truncatula cDNA clo...	232 1e-60
	emb AW830948 AW830948 sm30f07.y1 Gm-c1028 Glycine max cDNA clone...	232 2e-60
	emb AI055677 AI055677 coau0004L19 Cotton Boll Abscission Zone cD...	205 4e-58
	emb AW034420 AW034420 EST277991 tomato callus, TAMU Lycopersicon...	149 6e-56
	emb AW032120 AW032120 EST275574 tomato callus, TAMU Lycopersicon...	217 6e-56
	emb AW039340 AW039340 EST281597 tomato mixed elicitor, BTI Lycop...	217 6e-56
45	emb AI896467 AI896467 EST265898 tomato callus, TAMU Lycopersicon...	216 9e-56
	emb AV422712 AV422712 AV422712 Lotus japonicus young plants (two...	216 1e-55
	emb AW651552 AW651552 EST330018 tomato germinating seedlings, TA...	131 1e-54
	emb AW706479 AW706479 sj57a08.y1 Gm-c1033 Glycine max cDNA clone...	204 2e-54
	emb AW234624 AW234624 sf17d08.y1 Gm-c1028 Glycine max cDNA clone...	212 2e-54
50	emb AW832025 AW832025 sm30b11.y1 Gm-c1028 Glycine max cDNA clone...	210 1e-53
	emb AV416661 AV416661 AV416661 Lotus japonicus young plants (two...	209 1e-53
	gb BE053882 BE053882 GA_Ea0034G19f Gossypium arboreum 7-10 dpa ...	123 2e-53
	emb AW033980 AW033980 EST277642 tomato callus, TAMU Lycopersicon...	208 3e-53
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55	emb AW428756 AW428756 Ljimp23-845-c9 Ljimp Lambda HybriZap ...	207 5e-53
	emb AV409794 AV409794 AV409794 Lotus japonicus young plants (two...	205 2e-52
	emb AI895300 AI895300 EST264743 tomato callus, TAMU Lycopersicon...	204 3e-52
	emb AV417685 AV417685 AV417685 Lotus japonicus young plants (two...	204 5e-52
	emb AW033463 AW033463 EST277034 tomato callus, TAMU Lycopersicon...	202 2e-51
60	emb AW030999 AW030999 EST274306 tomato callus, TAMU Lycopersicon...	201 3e-51
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 5 emb|AI896550|AI896550 EST265993 tomato callus, TAMU Lycopersicon... 193 7e-49
 emb|AW559285|AW559285 EST306328 DSIR Medicago truncatula cDNA cl... 95 3e-48
 emb|AW684576|AW684576 NF018E05NR1F1000 Nodulated root Medicago t... 93 1e-46
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 emb|AW216534|AW216534 EST295248 tomato callus, TAMU Lycopersicon... 186 2e-46
 10 emb|AW620815|AW620815 sj09h04.y1 Gm-c1032 Glycine max cDNA clone... 109 7e-46
 emb|AI728054|AI728054 BNLGH19697 Six-day Cotton fiber Gossypium ... 107 1e-45
 emb|AI730473|AI730473 BNLGH17273 Six-day Cotton fiber Gossypium ... 105 2e-44
 emb|AI729618|AI729618 BNLGH13779 Six-day Cotton fiber Gossypium... 105 3e-44
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 15 emb|AW622012|AW622012 EST312810 tomato root during/after fruit s... 106 1e-43
 emb|AW621198|AW621198 EST311996 tomato root during/after fruit s... 106 1e-43
 emb|AW031587|AW031587 EST275041 tomato callus, TAMU Lycopersicon... 176 1e-43
 gb|U51193|GMU51193 Glycine max peroxidase (sEPb1) mRNA, partial ... 95 2e-43
 gb|L13654|TOMTPX1A Lycopersicon esculentum peroxidase (TPX1) mRN... 105 2e-43
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 http://www.ncgr.org/cgi-bin/ff?x95573
 (940 letters)

Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

Searching.....done

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| 35 | Sequences producing significant alignments: | | | |
| | emb AF119050 AF119050 Datisca glomerata zinc-finger protein I (z... | 73 | 1e-43 | |
| | gb U68763 GMU68763 Glycine max putative transcription factor SCO... | 72 | 2e-39 | |
| | dbj D26083 PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... | 69 | 4e-38 | |
| 40 | emb Y18788 MSY18788 Medicago sativa mRNA for putative TFIIIA (or... | 125 | 7e-38 | |
| | dbj D26086 PETZFP4 Petunia zinc-finger protein gene. | 62 | 3e-36 | |
| | emb AW560934 AW560934 EST315982 DSIR Medicago truncatula cDNA cl... | 133 | 3e-35 | |
| | emb AW729218 AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ... | 70 | 8e-35 | |
| | dbj D26084 PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... | 70 | 2e-34 | |
| 45 | gb BE095284 BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two... | 70 | 2e-34 | |
| | emb AW781249 AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... | 67 | 4e-32 | |
| | emb AI988290 AI988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone... | 69 | 1e-31 | |
| | emb AI487287 AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... | 62 | 3e-30 | |
| | emb AW775559 AW775559 EST334624 DSIL Medicago truncatula cDNA cl... | 66 | 6e-30 | |
| 50 | gb BE123920 BE123920 EST394045 DSIL Medicago truncatula cDNA clo... | 66 | 6e-30 | |
| | dbj D26085 PETZFDB3 Petunia zinc-finger DNA binding protein gene. | 59 | 8e-29 | |
| | emb AW102472 AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone... | 70 | 1e-28 | |
| | emb AI988657 AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone... | 70 | 2e-28 | |
| | emb AF053077 AF053077 Nicotiana tabacum osmotic stress-induced z... | 66 | 5e-27 | |
| 55 | emb AW706944 AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone... | 64 | 8e-27 | |
| | emb AI778714 AI778714 EST259593 tomato susceptible, Cornell Lyco... | 62 | 2e-26 | |
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| | emb AW164639 AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone... | 62 | 3e-26 | |
| | emb Y16131 Y16131 Y16131 young root nodules Medicago sativa subs... | 119 | 3e-26 | |
| 60 | emb AW153229 AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone... | 62 | 4e-26 | |
| | emb AW616587 AW616587 EST322998 L. hirsutum trichome, Cornell Un... | 63 | 6e-26 | |

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	emb AW278572 AW278572 sf46c03.y1 Gm-c1009 Glycine max cDNA clone...	62 5e-25
	emb AW034622 AW034622 EST278306 tomato callus, TAMU Lycopersicon...	62 9e-25
	emb AV426673 AV426673 AV426673 Lotus japonicus young plants (two...	76 1e-24
5	emb AI488218 AI488218 EST246540 tomato ovary, TAMU Lycopersicon...	62 2e-24
	emb AW037956 AW037956 EST279600 tomato mixed elicitor, BTI Lycop...	62 2e-24
	emb AI966679 AI966679 sc55a11.y1 Gm-c1015 Glycine max cDNA clone...	68 1e-23
	emb AW720367 AW720367 LjNEST21g11r Lotus japonicus nodule librar...	69 5e-23
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10	gb U76555 BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA...	63 4e-22
	gb U76554 BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR...	63 4e-22
	emb AW625323 AW625323 EST319146 tomato radicle, 5 d post-imbibit...	62 4e-22
	emb AW219736 AW219736 EST302218 tomato root during/after fruit s...	62 2e-21
	emb AW185023 AW185023 se85f12.y1 Gm-c1023 Glycine max cDNA clone...	58 5e-21
15	emb AW277333 AW277333 sf80a11.y1 Gm-c1019 Glycine max cDNA clone...	69 6e-21
	emb AI900061 AI900061 sb98d02.y1 Gm-c1012 Glycine max cDNA clone...	69 6e-21
	emb AW219517 AW219517 EST301915 tomato root during/after fruit s...	62 8e-21
	emb AW032112 AW032112 EST275566 tomato callus, TAMU Lycopersicon...	62 1e-20
	emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon ...	62 4e-20
20	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds.	62 7e-20
	dbj D16416 WHTWZF1B Wheat mRNA for WZF1, complete cds.	62 7e-20
	emb AV422972 AV422972 AV422972 Lotus japonicus young plants (two...	76 3e-19
	emb AV423707 AV423707 AV423707 Lotus japonicus young plants (two...	76 3e-19
	emb AV424707 AV424707 AV424707 Lotus japonicus young plants (two...	76 3e-19
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	emb AV411580 AV411580 AV411580 Lotus japonicus young plants (two...	76 3e-19
	emb AV412443 AV412443 AV412443 Lotus japonicus young plants (two...	76 3e-19
30	emb AV412455 AV412455 AV412455 Lotus japonicus young plants (two...	76 3e-19
	emb AW033574 AW033574 EST277145 tomato callus, TAMU Lycopersicon...	61 9e-19
	emb AI896031 AI896031 EST265474 tomato callus, TAMU Lycopersicon...	61 1e-18
	emb AW030858 AW030858 EST274148 tomato callus, TAMU Lycopersicon...	61 1e-18
	emb AW033257 AW033257 EST276828 tomato callus, TAMU Lycopersicon...	61 1e-18
35	emb AI771191 AI771191 EST252387 tomato ovary, TAMU Lycopersicon ...	61 1e-18
	emb AV424248 AV424248 AV424248 Lotus japonicus young plants (two...	73 1e-18
	emb AW032357 AW032357 EST275811 tomato callus, TAMU Lycopersicon...	61 1e-18
	emb AW706014 AW706014 sk64g01.y1 Gm-c1016 Glycine max cDNA clone...	66 3e-18
	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA...	62 4e-18
40	emb AW622660 AW622660 EST313460 tomato root during/after fruit s...	62 5e-18
	emb AV411226 AV411226 AV411226 Lotus japonicus young plants (two...	71 6e-18
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45	emb AV423254 AV423254 AV423254 Lotus japonicus young plants (two...	76 3e-17
	emb AW755973 AW755973 sl11h06.y1 Gm-c1036 Glycine max cDNA clone...	70 4e-17
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50	emb AV413163 AV413163 AV413163 Lotus japonicus young plants (two...	68 7e-17
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon...	54 3e-16
	emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t...	70 3e-16
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 15 emb|AW738399|AW738399 EST339826 tomato flower buds, anthesis, Co... 62 5e-14

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(940 letters)

Database: plantfungal
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Searching.....done

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Sequences producing significant alignments: (bits) Value

emb|AF119050|AF119050 Datisca glomerata zinc-finger protein 1 (z... 73 1e-43
 gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 72 2e-39
 dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 69 4e-38
 emb|Y18788|MSY18788 Medicago sativa mRNA for putative TFIIIA (or... 125 7e-38
 35 dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 62 3e-36
 emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 133 3e-35
 emb|AW729218|AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ... 70 8e-35
 dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 70 2e-34
 gb|BE095284|BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two-... 70 2e-34
 40 emb|AW781249|AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... 67 4e-32
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 gb|BE123920|BE123920 EST394045 DSIL Medicago truncatula cDNA clo... 66 6e-30
 45 dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene. 59 8e-29
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 50 emb|AI778714|AI778714 EST259593 tomato susceptible, Cornell Lyco... 62 2e-26
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5	gb U76555 BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA...	63 4e-22
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	emb AW219736 AW219736 EST302218 tomato root during/after fruit s...	62 2e-21
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15 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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emb AW034892 AW034892 EST279121 tomato callus, TAMU Lycopersicon...	244	3e-64		
gb BE124622 BE124622 EST393657 GVN Medicago truncatula cDNA clon...	243	5e-64		
30 emb AW747419 AW747419 WS1_68_E10.b1_A002 Water-stressed 1 (WS1) ...	242	1e-63		
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emb AI960575 AI960575 sc86c01.y1 Gm-c1018 Glycine max cDNA clone...	240	4e-63		
35 emb AW706639 AW706639 sj62h07.y1 Gm-c1033 Glycine max cDNA clone...	240	4e-63		
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emb AW186193 AW186193 se64g04.y1 Gm-c1019 Glycine max cDNA clone...	240	5e-63		
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emb|AW933878|AW933878 EST359721 tomato fruit mature green, TAMU ... 89 7e-25
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5 emb|X59720|SCCHRIII S.cerevisiae chromosome III complete DNA seq... 80 8e-25
emb|AW617209|AW617209 EST323620 L. hirsutum trichome, Cornell Un... 89 1e-24
emb|AW775277|AW775277 EST334342 DSIL Medicago truncatula cDNA cl... 85 3e-24
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emb|AI939238|AI939238 sc68h11.yl Gm-cl016 Glycine max cDNA clone... 82 5e-20
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20 emb|AW220746|AW220746 EST297215 tomato fruit mature green, TAMU ... 89 2e-17
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30 emb|AZ215418|AZ215418 Sheared DNA-79B7.TF Sheared DNA Trypanosom... 54 2e-09
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emb|AW282515|AW282515 LG1_312_G03.g1_A002 Light Grown 1 (LG1) So... 31 5.5
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments:

(bits) Value

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	emb AF082028 AF082028 Hemerocallis hybrid cultivar senescence-as...	194	3e-67
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	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber Gossypium...	183	4e-58
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30	emb AW329224 AW329224 N200436e rootphos(-) Medicago truncatula c...	220	2e-56
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35	emb AW684707 AW684707 NF020A02NR1F1000 Nodulated root Medicago t...	189	7e-53
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	emb AW688601 AW688601 NF009D12ST1F1000 Developing stem Medicago ...	185	2e-51
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40	emb AW299084 AW299084 EST305758 KV2 Medicago truncatula cDNA clo...	182	8e-51
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- dbj|E13663|E13663 cDNA encoding cytochrome P450 which is induced... 103 8e-43
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 5 emb|Y10492|GMC450CP5 *G.max* mRNA for putative cytochrome P450, cl... 105 2e-42
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 45 emb|AF195804|AF195804 *Lens culinaris* isoflavone synthase 1 (ifs1... 96 6e-40
 emb|AF195816|AF195816 *Beta vulgaris* isoflavone synthase 1 (ifs1)... 99 6e-40
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 55 [post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004411|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004411|/ncgi)
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Database: plantfungal

- 60 661,018 sequences; 426,114,510 total letters

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emb AW729170 AW729170 GA_Ea0024E17 <i>Gossypium arboreum</i> 7-10 dpa ...	126	3e-59	
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emb AW625848 AW625848 EST319755 tomato radicle, 5 d post-imbibit...	125	2e-54	
emb AW096560 AW096560 EST289740 tomato mixed elicitor, BTI <i>Lycop...</i>	117	5e-52	
emb AI494929 AI494929 sa92g06.y1 <i>Gm-c1004</i> Glycine max cDNA clone...	203	1e-51	
emb AB018559 AB018559 <i>Citrullus lanatus</i> mRNA for wts2L, complete...	74	1e-50	
emb AF053638 AF053638 <i>Pisum sativum</i> short-chain alcohol dehydrog...	103	3e-50	
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emb AF097651 AF097651 <i>Pisum sativum</i> short-chain alcohol dehydrog...	103	8e-50	
emb AF053639 AF053639 <i>Pisum sativum</i> short-chain alcohol dehydrog...	103	2e-49	
emb AW092874 AW092874 EST286054 tomato mixed elicitor, BTI <i>Lycop...</i>	112	3e-49	
emb AJ223178 NTAJ3178 <i>Nicotiana tabacum</i> SCANT gene.	93	7e-49	
emb AJ223177 NTAJ3177 <i>Nicotiana tabacum</i> mRNA for short chain alc...	93	7e-49	
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emb AW093147 AW093147 EST286327 tomato mixed elicitor, BTI <i>Lycop...</i>	118	8e-47	
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gb U53829 SLU53829 <i>Silene latifolia</i> ssp. alba STA1-18 (STA1-18) ...	140	2e-46	
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emb AF072447 AF072447 <i>Ipomoea trifida</i> short-chain alcohol dehydr...	97	5e-45	
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emb AI778245 AI778245 EST259124 tomato susceptible, Cornell <i>Lyco...</i>	117	3e-41	
emb AW776982 AW776982 EST336047 DSIL <i>Medicago truncatula</i> cDNA cl...	105	5e-41	
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emb AW032711 AW032711 EST276270 tomato callus, TAMU <i>Lycopersicon</i> ...	98	9e-35	
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emb AW031891 AW031891 EST275345 tomato callus, TAMU <i>Lycopersicon</i> ...	60	2e-24	
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emb AW093827 AW093827 EST287007 tomato mixed elicitor, BTI <i>Lycop...</i>	60	1e-23	
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 5 emb|AW686040|AW686040 NF037F07NR1F1000 Nodulated root Medicago t... 104 1e-21
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 emb|AW928544|AW928544 EST337332 tomato flower buds 8 mm to pre-a... 85 5e-16
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55 Database: plantfungal
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 (1216 letters)

50 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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55 Score E
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- emb|AW775409|AW775409 EST334474 DSIL *Medicago truncatula* cDNA cl... 304 9e-94
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(1716 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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60 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago ...	88	2e-16		
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 5 emb|AW981624|AW981624 PC14G07 Pine TriplEx pollen cone library P... 58 2e-07
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 (2403 letters)

- 40 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 55 emb|AJ006379|LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142
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 emb|AJ006786|LES6786 Lycopersicon esculentum p69d gene. 141 e-136
 emb|AJ005171|LEAJ5171 Lycopersicon esculentum p69c gene, complete... 142 e-136
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- emb|X95270|LESUBENDO *L. esculentum* mRNA for subtilisin-like endop... 138 e-126
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35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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- 40 Score E
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- emb|AJ006378|LES6378 Lycopersicon esculentum sbt1 gene. 240 e-157
 emb|X98929|LESBT1 L.esculentum mRNA for serine protease, SBT1. 240 e-157
 45 emb|Y18932|LES18932 Lycopersicon esculentum p69F gene. 142 e-152
 emb|Y17278|LES17278 Lycopersicon esculentum p69d gene, complete ... 141 e-146
 emb|AJ005173|LEAJ5173 Lycopersicon esculentum p69f gene, complet... 141 e-146
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 emb|Y18931|LES18931 Lycopersicon esculentum p69E gene. 144 e-144
 50 emb|AJ006379|LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142
 emb|X98930|LESBT2 L.esculentum mRNA for serine protease, SBT2. 163 e-142
 emb|AJ006786|LES6786 Lycopersicon esculentum p69d gene. 141 e-136
 emb|AJ005171|LEAJ5171 Lycopersicon esculentum p69c gene, complete... 142 e-136
 emb|Y17276|LES17276 Lycopersicon esculentum p69b gene, complete ... 138 e-130
 55 emb|Y10149|LESUBTILI L.esculentum mRNA for subtilisin-like protein. 138 e-130
 emb|Y17275|LES17275 Lycopersicon esculentum p69a gene, complete ... 138 e-126
 emb|X95270|LESUBENDO L.esculentum mRNA for subtilisin-like endop... 138 e-126
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20 emb|AW695319|AW695319 NF093H12ST1F1103 Developing stem Medicago ... 105 2e-57
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25 emb|AW668484|AW668484 GA_Ea0014C06 Gossypium arboreum 7-10 dpa ... 188 4e-56
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35 emb|AW221342|AW221342 EST297811 tomato fruit mature green, TAMU ... 154 7e-52
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 30 (2002 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| | gb U43542 NTU43542 Nicotiana tabacum diphenol oxidase mRNA, comp... | 379 | e-104 |
| | gb U73103 LTU73103 Liriodendron tulipifera high-pl laccase (LAC2... | 363 | e-103 |
| | gb U12757 APU12757 Acer pseudoplatanus laccase mRNA, complete cds. | 368 | e-100 |
| 50 | gb U73104 LTU73104 Liriodendron tulipifera high-pl laccase (LAC2... | 353 | 3e-99 |
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emb|AW694631|AW694631 NF078E04ST1F1034 Developing stem Medicago ... 190 3e-48
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emb|AW736716|AW736716 EST333208 KV3 Medicago truncatula cDNA clo... 187 2e-46
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45 emb|AA556518|AA556518 373 Loblolly pine C Pinus taeda cDNA clone... 164 1e-45
emb|AW985001|AW985001 NXNV_118_H12_F Nsf Xylem Normal wood Verti... 122 2e-45
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50 emb|AW985217|AW985217 NXNV_132_E12_F Nsf Xylem Normal wood Verti... 178 1e-43
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55 emb|AW887962|AW887962 NXNV_127_D08_F Nsf Xylem Normal wood Verti... 176 7e-43
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- emb|AW693471|AW693471 NF065C09ST1F1000 Developing stem Medicago ... 169 8e-41
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 emb|AW032099|AW032099 EST275553 tomato callus, TAMU Lycopersicon... 163 3e-40
 5 emb|AW691027|AW691027 NF036H01ST1F1000 Developing stem Medicago ... 115 5e-40
 emb|AW290667|AW290667 NXNV044G05F Nsf Xylem Normal wood Vertical... 166 8e-40
 gb|BE123599|BE123599 NXNV_146_A10_F Nsf Xylem Normal wood Vertic... 163 5e-39
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 10 emb|AW695246|AW695246 NF092G11ST1F1087 Developing stem Medicago ... 92 5e-37
 gb|BE020582|BE020582 sm51a03.y1 Gm-c1028 Glycine max cDNA clone ... 133 7e-37
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 emb|AW597115|AW597115 sj71g06.y1 Gm-c1034 Glycine max cDNA clone... 150 4e-35
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 15 emb|AW626664|AW626664 NXNV068B04 Nsf Xylem Normal wood Vertical ... 146 6e-34
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 http://www.ncgr.org/cgi-bin/ff7y11788
 (965 letters)

Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

Searching.....done

- | | Score | E | (bits) | Value |
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| 35 | Sequences producing significant alignments: | | | |
| | gb M37637 ARCPNC2 A.hypogaea cationic peroxidase mRNA, complete ... | 230 | e-105 | |
| | emb X94943 LECEVI16G L.esculentum mRNA for peroxidase. | 212 | e-100 | |
| | emb AB027753 AB027753 Nicotiana tabacum mRNA for peroxidase, com... | 191 | 1e-94 | |
| 40 | emb AF149279 AF149279 Phaseolus vulgaris peroxidase 4 precursor ... | 220 | 2e-94 | |
| | gb L36112 SSNPEROXIC Stylosanthes humilis peroxidase mRNA. | 157 | 2e-86 | |
| | emb AW033820 AW033820 EST277391 tomato callus, TAMU Lycopersicon... | 170 | 2e-79 | |
| | emb Y10468 SOPRXXR7 S.oleracea mRNA for peroxidase, clone PC36. | 196 | 6e-78 | |
| | emb AW759829 AW759829 sl54f01.y1 Gm-c1027 Glycine max cDNA clone... | 213 | 1e-77 | |
| 45 | emb AW216873 AW216873 EST295587 tomato callus, TAMU Lycopersicon... | 212 | 3e-73 | |
| | emb AW224632 AW224632 EST303075 tomato root, plants pre-anthesis... | 193 | 2e-66 | |
| | emb AF145349 AF145349 Glycine max peroxidase (Prx3) mRNA, partia... | 131 | 4e-66 | |
| | emb AW219312 AW219312 EST301794 tomato root during/after fruit s... | 193 | 2e-65 | |
| | emb AW219112 AW219112 EST301594 tomato root during/after fruit s... | 193 | 2e-65 | |
| 50 | emb AW032353 AW032353 EST275807 tomato callus, TAMU Lycopersicon... | 137 | 1e-61 | |
| | emb AW031362 AW031362 EST274816 tomato callus, TAMU Lycopersicon... | 180 | 9e-60 | |
| | emb AW035239 AW035239 EST280501 tomato callus, TAMU Lycopersicon... | 212 | 1e-58 | |
| | emb AW035958 AW035958 EST282817 tomato callus, TAMU Lycopersicon... | 212 | 1e-58 | |
| | emb AW035446 AW035446 EST281184 tomato callus, TAMU Lycopersicon... | 212 | 1e-58 | |
| 55 | emb AW029850 AW029850 EST273105 tomato callus, TAMU Lycopersicon... | 170 | 5e-58 | |
| | emb AW030052 AW030052 EST273307 tomato callus, TAMU Lycopersicon... | 165 | 7e-58 | |
| | emb AW569733 AW569733 si79g02.y1 Gm-c1031 Glycine max cDNA clone... | 153 | 1e-57 | |
| | emb AW224631 AW224631 EST303074 tomato root, plants pre-anthesis... | 193 | 3e-57 | |
| 60 | emb AW348753 AW348753 GM210003A22D6R Gm-r1021 Glycine max cDNA 3... | 144 | 6e-57 | |
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- emb|AV414872|AV414872 *Lotus japonicus* young plants (two... 182 2e-55
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 emb|AV414074|AV414074 *Lotus japonicus* young plants (two... 215 4e-55
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 5 emb|AW216562|AW216562 EST295276 tomato callus, TAMU Lycopersicon... 210 2e-53
 emb|X57564|ARNEUPERO *A. rusticana* mRNA for neutral peroxidase. 118 2e-53
 emb|AI777064|AI777064 EST252031 tomato callus, TAMU Lycopersicon... 206 2e-52
 emb|AF155124|AF155124 *Gossypium hirsutum* bacterial-induced perox... 93 6e-52
 10 emb|AW219314|AW219314 EST301796 tomato root during/after fruit s... 193 4e-51
 emb|AB042103|AB042103 *Asparagus officinalis* AspPOX1 mRNA for per... 84 5e-51
 emb|AW219926|AW219926 EST302409 tomato root during/after fruit s... 193 8e-51
 emb|AW224630|AW224630 EST303073 tomato root, plants pre-anthesis... 193 8e-51
 emb|AF149280|AF149280 *Phaseolus vulgaris* peroxidase 5 precursor ... 81 8e-51
 gb|L13654|TOMTPX1A *Lycopersicon esculentum* peroxidase (TPX1) mRN... 104 3e-50
 15 emb|AJ242742|IBA242742 *Ipomoea batatas* mRNA for peroxidase (pod ... 82 5e-50
 emb|Y10470|SOPRXX9 *S. oleracea* mRNA for peroxidase, clone PC56. 132 3e-49
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 20 emb|X56011|TAPERO Wheat mRNA for peroxidase. 102 2e-48
 emb|X97351|PTPXP4PER *P. trichocarpa* mRNA for anionic peroxidase P... 90 8e-48
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 gb|M37636|ARCPNC1 *Arachis hypogaea* cationic peroxidase (PNC1) mR... 89 1e-47
 emb|AB024437|AB024437 *Scutellaria baicalensis* mRNA for peroxidase... 122 1e-47
 25 gb|M74103|TOBANPER *Nicotiana sylvestris* anionic peroxidase mRNA,... 100 2e-47
 gb|M60729|HRAHRPCC *A. rusticana* peroxidase isoenzyme C (HPR C) ge... 78 3e-47
 emb|AW621675|AW621675 EST312473 tomato root during/after fruit s... 189 3e-47
 emb|Y17192|CPY17192 *Cucurbita pepo* mRNA for peroxidase. 109 5e-47
 emb|AI895427|AI895427 EST264870 tomato callus, TAMU Lycopersicon... 121 7e-47
 30 emb|AW035207|AW035207 EST280469 tomato callus, TAMU Lycopersicon... 188 8e-47
 gb|L13653|TOMTPX2A *Lycopersicon esculentum* peroxidase (TPX2) mRN... 101 1e-46
 emb|Y10463|SOPRXX2 *S. oleracea* mRNA for peroxidase, clone PB22. 140 4e-46
 emb|AW224633|AW224633 EST303076 tomato root, plants pre-anthesis... 185 4e-46
 gb|L36157|ALFPXDC *Medicago sativa* peroxidase (pxdC) mRNA, comple... 73 9e-46
 35 gb|M91372|CUSPREPERB *Cucumis sativus* peroxidase mRNA, complete cds. 89 2e-45
 emb|X91232|MARNAPRX *M. annua* mRNA for peroxidase. 90 2e-45
 emb|AF244924|AF244924 *Spinacia oleracea* peroxidase prx15 precurs... 92 2e-45
 emb|Z22920|SPPEROXDS *S. polyrrhiza* mRNA for peroxidase. 96 2e-45
 emb|X90694|MSRNAPE1C *M. sativa* mRNA for peroxidase 1C. 75 3e-45
 40 gb|M91374|CUSPREPERA *Cucumis sativus* peroxidase mRNA, complete cds. 109 4e-45
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 emb|Y16776|SOY16776 *Spinacia oleracea* mRNA for peroxidase, prx10... 95 5e-45
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 dbj|D42064|TOBCPI38KA Tobacco mRNA for cationic peroxidase isozy... 77 1e-44
 45 emb|AI772237|AI772237 EST253337 tomato resistant, Cornell Lycope... 180 2e-44
 emb|AF149278|AF149278 *Phaseolus vulgaris* peroxidase 3 precursor ... 84 2e-44
 emb|AW035660|AW035660 EST281492 tomato callus, TAMU Lycopersicon... 178 5e-44
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 emb|X97350|PTPXP3PER *P. trichocarpa* mRNA for anionic peroxidase P... 83 2e-43
 50 gb|L36111|SSNPEROXIB *Stylosanthes humilis* peroxidase mRNA. 77 3e-43
 emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 90 3e-43
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 gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 89 4e-43
 emb|AF043234|AF043234 *Striga asiatica* ferriprotein porphyrin-con... 83 7e-43
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 gb|L24120|LINFLXP *Linum usitatissimum* peroxidase precursor (FLXP... 88 2e-42
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 emb|AW705312|AW705312 sk59d04.y1 Gm-c1019 Glycine max cDNA clone... 128 2e-42
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 gb|L77080|SSNCAPEA *Stylosanthes humilis* cationic peroxidase gene... 122 1e-41

- emb|AI778513|AI778513 EST259392 tomato susceptible, Cornell Lyco... 170 1e-41
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 dbj|E01651|E01651 cDNA encoding horseradish peroxidase. 76 2e-41
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 10 emb|Y10469|SOPR XR8 S.oleracea mRNA for peroxidase, clone PC55. 111 4e-41
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 emb|Y10465|SOPR XR4 S.oleracea mRNA for peroxidase, clone PC44. 86 6e-41
 gb|U12315|CCU12315 Cenchrus ciliaris clone PX18 peroxidase mRNA,... 106 9e-41
 dbj|D11337|VIRPRX Vigna angularis mRNA for peroxidase basic isoz... 77 1e-40
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 (1025 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

30 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

- emb|AJ130885|FSY130885 Fagus sylvatica mRNA for xyloglucan endot... 424 e-134
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- gb|BE036915|BE036915 MP09A12 MP Mesembryanthemum crystallinum cD... 368 e-101
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 10 emb|AW218862|AW218862 EST301344 tomato root during/after fruit s... 354 5e-97
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 emb|X82685|LETXETB1 L.esculentum tXET-B1 mRNA for xyloglucan end... 354 7e-97
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 15 emb|AI773291|AI773291 EST254391 tomato resistant, Cornell Lycope... 293 1e-95
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 25 emb|AI485855|AI485855 EST244176 tomato ovary, TAMU Lycopersicon ... 343 1e-93
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 dbj|E06969|E06969 DNA encoding xyloglucan endotransferase. 310 4e-93
 dbj|E06964|E06964 Anti-sense RNA of xyloglucan endotransferase g... 310 4e-93
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 emb|AI898758|AI898758 EST268201 tomato ovary, TAMU Lycopersicon ... 286 7e-93
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 35 dbj|D16458|VIREXT5 V.angularis mRNA for endo-xyloglucan transfer... 314 1e-90
 gb|L43094|TRUXET1G Tropaeolum majus xyloglucan endotransglycosyl... 324 1e-90
 dbj|E06968|E06968 DNA encoding xyloglucan endotransferase. 314 1e-90
 dbj|E06963|E06963 Anti-sense RNA of xyloglucan endotransferase g... 314 1e-90
 dbj|E06958|E06958 Anti-sense DNA of xyloglucan endotransferase g... 314 1e-90
 40 emb|AJ004917|CAAJ4917 Cicer arietinum mRNA for endoxyloglucan tr... 310 1e-89
 emb|X91659|HVEXTGENE H.vulgare mRNA for endoxyloglucan transferase. 318 1e-89
 dbj|D16457|WHEXT4 Wheat mRNA for endo-xyloglucan transferase, c... 319 2e-89
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 45 dbj|E06962|E06962 Anti-sense DNA of xyloglucan endotransferase g... 319 6e-89
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 emb|AW184781|AW184781 se82c12.y1 Gm-c1023 Glycine max cDNA clone... 274 8e-88
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emb|AI729066|AI729066 BNLGHi12528 Six-day Cotton fiber Gossypium... 315 4e-85
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5 dbj|E06966|E06966 Anti-sense RNA of xyloglucan endotransferase g... 295 4e-85
dbj|E06961|E06961 Anti-sense DNA of xyloglucan endotransferase g... 295 4e-85
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20 Database: plantfungai
661,018 sequences; 426,114,510 total letters

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emb|AJ130885|FSY130885 Fagus sylvatica mRNA for xyloglucan endot... 424 e-134
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30 gb|L22162|SOYMER5HOM Glycine max brassinosteroid-regulated prote... 384 e-118
emb|AW220372|AW220372 EST302855 tomato root during/after fruit s... 416 e-115
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emb|AW032346|AW032346 EST275800 tomato callus, TAMU Lycopersicon... 415 e-115
emb|AW218856|AW218856 EST301338 tomato root during/after fruit s... 413 e-115
35 emb|AW031139|AW031139 EST274446 tomato callus, TAMU Lycopersicon... 380 e-115
emb|AI725820|AI725820 BNLGHi13219 Six-day Cotton fiber Gossypium... 413 e-114
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emb|AW218734|AW218734 EST301214 tomato root during/after fruit s... 388 e-107
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5 emb|AI725839|AI725839 BNLGHi13291 Six-day Cotton fiber Gossypium... 354 7e-97
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20 emb|AW432541|AW432541 sb75f05.y1 Gm-cl015 Glycine max cDNA clone... 342 3e-93
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dbj|E06964|E06964 Anti-sense RNA of xyloglucan endotransferase g... 310 4e-93
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25 emb|AI898758|AI898758 EST268201 tomato ovary, TAMU Lycopersicon ... 286 7e-93
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30 gb|L43094|TRUXET1G Tropaeolum majus xyloglucan endotransglycosyl... 324 1e-90
dbj|E06968|E06968 DNA encoding xyloglucan endotransferase. 314 1e-90
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35 emb|X91659|HVEXTGENE H.vulgare mRNA for endoxyloglucan transferase. 318 1e-89
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40 emb|AW687253|AW687253 NF007F05RT1F1046 Developing root Medicago ... 292 1e-88
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45 emb|AW038999|AW038999 EST280972 tomato mixed elicitor, BTI Lycop... 303 3e-88
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55 emb|AI489200|AI489200 EST247539 tomato ovary, TAMU Lycopersicon ... 274 2e-85
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters
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25	emb AW685869 AW685869-NF031B09NR1F1000	Nodulated root Medicago t...	95 2e-22
	gb BE124445 BE124445-EST393480	GVN Medicago truncatula cDNA clon...	95 2e-22
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 (1579 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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25	emb AW672225 AW672225	LG1_358_C11.b1_A002 Light Grown 1 (LG1) So...	192 6e-48
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	emb AW694902 AW694902	NF081C08ST1F1065 Developing stem Medicago ...	88 1e-24
	emb AW754669 AW754669	PC04H09 Pine TriplEx pollen cone library P...	113 4e-24
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	emb Y09825 STAAP1	S.tuberosum mRNA for amino acid transporter AA...	48 7e-06
	emb AJ004959 CAA004959	Cicer arietinum mRNA for hypothetical pro...	52 9e-06
	emb AF080542 AF080542	Nepenthes alata amino acid transporter (AA...	47 2e-05
	emb AW164093 AW164093	Ljirmp19-543-g11 Ljirmp Lambda HybriZap...	50 5e-05
45	emb AW309945 AW309945	sf27a03.x1 Gm-c1028 Glycine max cDNA clone...	50 5e-05
	emb AF080544 AF080544	Nepenthes alata amino acid transporter (AA...	45 6e-05
	gb U64823 NSU64823	Nicotiana sylvestris amino acid permease (nsa...	50 6e-05
	emb AJ238635 CPR238635	Chlorella protothecoides partial mRNA for...	49 1e-04
	emb AI974813 AI974813	T113295e KV2 Medicago truncatula cDNA clon...	49 1e-04
50	emb AI773761 AI773761	EST254861 tomato resistant, Cornell Lycope...	48 2e-04
	emb AW736648 AW736648	EST333140 KV3 Medicago truncatula cDNA clo...	47 3e-04
	emb AW255060 AW255060	ML1355 peppermint glandular trichome Menth...	40 4e-04
	emb Y09591 VFAMACTRA	V.faba mRNA for amino acid transporter.	46 6e-04
	emb AI441371 AI441371	sa64f02.y1 Gm-c1004 Glycine max cDNA clone...	46 6e-04
55	emb AW396191 AW396191	sh02e09.y1 Gm-c1026 Glycine max cDNA clone...	46 6e-04
	emb AW395873 AW395873	sh01d01.y1 Gm-c1026 Glycine max cDNA clone...	37 0.003
	emb AI166826 AI166826	xylem.est.62 Poplar xylem Lambda ZAPII lib...	44 0.003
	emb AW830239 AW830239	sm24g01.y1 Gm-c1028 Glycine max cDNA clone...	44 0.004
	emb AF074703 AF074703	Glycine max pA381 marker, sequence tagged ...	43 0.005
60	emb AQ842052 AQ842052	T134338 Soybean RFLP probe Glycine max gen...	43 0.005
	gb BE022301 BE022301	sm73b09.y1 Gm-c1028 Glycine max cDNA clone ...	43 0.007

- emb|AW102174|AW102174 sd84c08.y1 Gm-c1009 Glycine max cDNA clone... 42 0.010
 emb|AI166882|AI166882 xylem.est.670 Poplar xylem Lambda ZAPII li... 41 0.019
 emb|Y09826|STAAP2 S.tuberosum mRNA for amino acid transporter AA... 36 0.020
 emb|AW307208|AW307208 sf54b08.y1 Gm-c1009 Glycine max cDNA clone... 41 0.026
 5 emb|AF080543|AF080543 Nepenthes alata amino acid transporter (AA... 40 0.049
 emb|AW096758|AW096758 EST289938 tomato mixed elicitor, BTI Lycop... 40 0.068
 emb|AI727855|AI727855 BNLGH9274 Six-day Cotton fiber Gossypium ... 29 0.17
 emb|AI487167|AI487167 EST245489 tomato ovary, TAMU Lycopersicon ... 38 0.18
 emb|AW649763|AW649763 EST328217 tomato germinating seedlings, TA... 38 0.18
 10 emb|AW310916|AW310916 sg29h08.x1 Gm-c1024 Glycine max cDNA clone... 38 0.24
 emb|AJ400848|SOL400848 Spinacia oleracea complete chloroplast ge... 37 0.46
 emb|AW203255|AW203255 sf27a03.y1 Gm-c1028 Glycine max cDNA clone... 36 0.63
 emb|AI778004|AI778004 EST258883 tomato susceptible, Cornell Lyco... 36 0.86
 emb|AW649841|AW649841 EST328295 tomato germinating seedlings, TA... 36 0.86
 15 emb|AF061435|AF061435 Vicia faba amino acid transporter b (AAPB)... 35 1.2
 emb|AQ492251|AQ492251 V109G12 mTn-3xHA/lacZ Insertion Library Sa... 35 1.2
 emb|AI779305|AI779305 EST260184 tomato susceptible, Cornell Lyco... 35 1.2
 emb|AI779304|AI779304 EST260183 tomato susceptible, Cornell Lyco... 35 1.2
 emb|AW982545|AW982545 HVSMEg0003I22f Hordeum vulgare pre-anthesi... 29 1.4
 20 emb|AQ874703|AQ874703 V113C6 mTn-3xHA/lacZ Insertion Library, st... 35 1.6
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 emb|AI856198|AI856198 sb39a11.x1 Gm-c1014 Glycine max cDNA clone... 35 1.6
 gb|L28920|YSCCHR1RAA Saccharomyces cerevisiae chromosome I right... 35 2.2
 emb|AQ874913|AQ874913 V118E8 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 25 emb|AF061434|AF061434 Vicia faba amino acid transporter a (AAPA)... 35 2.2
 emb|AQ876251|AQ876251 V153B8 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 emb|AQ874228|AQ874228 V105B1 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 emb|X74552|SCSWH1 S.cerevisiae SWH1 gene. 35 2.2
 emb|AQ876104|AQ876104 V133C7 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 30 emb|AQ876111|AQ876111 V133D2 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 emb|AQ875710|AQ875710 V128E8 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 emb|AW092708|AW092708 EST285888 tomato mixed elicitor, BTI Lycop... 34 3.1
 emb|AI938816|AI938816 sc60f01.y1 Gm-c1016 Glycine max cDNA clone... 34 4.2
 emb|AW704460|AW704460 sk53c11.y1 Gm-c1019 Glycine max cDNA clone... 34 4.2
 35 emb|AI965655|AI965655 sc75b03.y1 Gm-c1018 Glycine max cDNA clone... 34 4.2
 emb|AW010573|AW010573 ST08D02 Pine TriplEx shoot tip library Pin... 34 4.2
 emb|AJ277985|NTA277985 Nicotiana tabacum drepp1 gene, exons 1-4. 33 5.8
 emb|AL049559|SPCC1450 S.pombe chromosome III cosmid c1450. 33 8.0
 emb|Z72791|SCYGR006W S.cerevisiae chromosome VII reading frame O... 33 8.0
 40 emb|Z34930|TV18SRRN T.violaceum (var. violaceum) gene for 18S rRNA. 33 8.0
 gb|U42663|TGU42663 Tuber gibbosum 18S small subunit ribosomal RN... 33 8.0
 emb|AQ940191|AQ940191 Sheared DNA-42C20.TF Sheared DNA Trypanoso... 33 8.0
 emb|AA274279|AA274279 TgESTzz24b06.s1 TgME49 invivo Bradyzoite c... 33 8.0
 emb|AU006886|AU006886 AU006886 Schizosaccharomyces pombe late lo... 33 8.0
 45 emb|AW926892|AW926892 HVSMEg0008N19 Hordeum vulgare pre-anthesis... 33 8.0
 dbj|D64123|D64123 Fibulobasidium inconspicuum DNA for small subu... 33 8.0

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 50 gb|aab64325.1| (ac002335) putative trypsin inhibitor [arabidopsis
 thaliana] /blast_score 7.00e-40 /ec_number /family /chip nova
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 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002335| /ncgi
 http://www.ncgr.org/cgi-bin/ff?ac002335
 55 (449 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

60 Searching.....done

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	Sequences producing significant alignments:				
	emb Y16190 SAMTI2	Sinapsis alba mRNA for trypsin inhibitor 2.	161	2e-39	
5	emb X84208 SSAMTI2	Sinapsis alba mti-2 gene for trypsin inhibitor 2.	161	3e-39	
	emb AT002119 AT002119	AT002119 Flower bud cDNA Brassica rapa sub...	72	5e-14	
	gb L33539 L33539	BNAESTF178 Mustard flower buds Brassica rapa cD...	72	6e-14	
	emb AF025857 AF025857	Aegilops caudata RAPD marker generated by ...	36	0.18	
	emb AI065316 AI065316	TENU2203 T. cruzi epimastigote normalized ...	31	0.42	
10	emb AF066077 AF066077	Helianthus annuus RPL5A-related protein (R...	34	0.89	
	emb AL356173 NCB14D6	Neurospora crassa DNA linkage group II BAC ...	34	0.89	
	emb AF242188 AF242188	Plasmodium falciparum membrane protein Pfl...	34	0.89	
	gb M28889 PFAMEM12A	P.falciparum membrane protein Pfl2 gene, com...	34	0.89	
	emb AL160371 LMFLCHR15	Leishmania major Friedlin assembled chrom...	33	1.2	
15	gb U47092 U47092	DCU47092 Carrot somatic embryos Daucus carota c...	33	1.2	
	emb AL354533 LMFL6294	Leishmania major Friedlin chromosome 21 co...	33	1.2	
	emb AW278233 AW278233	sf41d09.y1 Gm-c1009 Glycine max cDNA clone...	33	1.2	
	emb AQ849793 AQ849793	LMAJFV1_lm49f04.x1 Leishmania major FV1 ra...	33	1.2	
	gb U91982 SHU91982	Stylosanthes hamata EREBP-3 homolog mRNA, com...	33	1.7	
20	emb AW727560 AW727560	GA_Ea0012P04 Gossypium arboreum 7-10 dpa ...	33	1.7	
	emb AQ848503 AQ848503	LMAJFV1_lm10a08.x1 Leishmania major FV1 ra...	33	1.7	
	emb AW668496 AW668496	GA_Ea0014C23 Gossypium arboreum 7-10 dpa ...	33	1.7	
	emb AL136236 SPAPJ696	S.pombe chromosome I PCR product p696.	32	2.3	
	emb AL133359 SPAP696	S.pombe chromosome I PCR product p696.	32	2.3	
25	emb AW728870 AW728870	GA_Ea0028O24 Gossypium arboreum 7-10 dpa ...	32	2.3	
	emb AW099428 AW099428	sd40c12.y1 Gm-c1016 Glycine max cDNA clone...	32	2.3	
	emb AV389315 AV389315	AV389315 Chlamydomonas reinhardtii C9 Chla...	32	2.3	
	emb AW707869 AW707869	832013D08.y1 C. reinhardtii CC-125 nutrien...	32	2.3	
	emb AC068564 AC068564	Filobasidiella neoformans var. neoformans,...	32	3.2	
30	emb Z38058 LMCLPB	L.major (MHOM/SU/5ASKH) DNA for 100 kDa heat s...	32	3.2	
	emb AW932211 AW932211	EST358054 tomato fruit mature green, TAMU ...	32	3.2	
	emb AL356172 NCB23L21	Neurospora crassa DNA linkage group II BAC...	32	3.2	
	emb AQ445563 AQ445563	GSSTc0014 Trypanosoma cruzi random genomic...	32	3.2	
	emb AF263283 AF263283	Filobasidiella neoformans var. neoformans ...	32	3.2	
35	emb X95256 HVXYLISOG	H.vulgare xylose isomerase gene.	32	3.2	
	emb AW217087 AW217087	EST295801 tomato callus, TAMU Lycopersicon...	32	3.2	
	emb X62675 TRMINEX5S	T.rangeli DNA for mini-exon and 5S rRNA.	29	3.5	
	emb AW745480 AW745480	WS1_35_H03.b1_A002 Water-stressed 1 (WS1) ...	31	4.4	
	emb AW705201 AW705201	sk43a03.y1 Gm-c1019 Glycine max cDNA clone...	31	4.4	
40	emb AI496396 AI496396	sb04b11.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	emb AW694532 AW694532	NF077E02ST1F1017 Developing stem Medicago ...	31	4.4	
	emb AW598155 AW598155	sj89b07.y1 Gm-c1034 Glycine max cDNA clone...	31	4.4	
	emb AW508121 AW508121	si51a09.y1 Gm-r1030 Glycine max cDNA clone...	31	4.4	
	emb AW317929 AW317929	sg59a02.y1 Gm-c1007 Glycine max cDNA clone...	31	4.4	
45	emb AW185756 AW185756	se59c04.y1 Gm-c1019 Glycine max cDNA clone...	31	4.4	
	emb AW119645 AW119645	sd50d05.y1 Gm-c1016 Glycine max cDNA clone...	31	4.4	
	emb AI522947 AI522947	sa92d09.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	gb L38627 GYNRGNA	Gymnodinium catenatum 24S ribosomal RNA (24S r...	31	4.4	
	emb AW926726 AW926726	HVSMEg0007P17 Hordeum vulgare pre-anthesis...	31	4.4	
50	emb AW307483 AW307483	sf57e09.y1 Gm-c1009 Glycine max cDNA clone...	31	4.4	
	emb AW307220 AW307220	sf54c09.y1 Gm-c1009 Glycine max cDNA clone...	31	4.4	
	emb AI437852 AI437852	sa40e07.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	emb AW733531 AW733531	sk74g09.y1 Gm-c1016 Glycine max cDNA clone...	31	4.4	
	emb AW186505 AW186505	se68f10.y1 Gm-c1019 Glycine max cDNA clone...	31	4.4	
55	emb AW099682 AW099682	sd29g03.y2 Gm-c1012 Glycine max cDNA clone...	31	4.4	
	emb AW761228 AW761228	sl64h04.y1 Gm-c1027 Glycine max cDNA clone...	31	4.4	
	emb AI900314 AI900314	sc03h10.y1 Gm-c1012 Glycine max cDNA clone...	31	4.4	
	emb AF031065 AF031065	Dipsacomyces acuminosporus 28S ribosomal R...	31	4.4	
	emb AW099689 AW099689	sd29h03.y2 Gm-c1012 Glycine max cDNA clone...	31	4.4	
60	emb AI494951 AI494951	sa93a10.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	emb AI988406 AI988406	sd01f04.y1 Gm-c1020 Glycine max cDNA clone...	31	4.4	

emb|AW782121|AW782121 sm01g01.y1 Gm-cl027 Glycine max cDNA clone... 31 4.4
emb|AW100084|AW100084 sd20b03.y2 Gm-cl012 Glycine max cDNA clone... 31 4.4
emb|AI939026|AI939026 sc64f02.y1 Gm-cl016 Glycine max cDNA clone... 31 4.4
5 emb|AI736322|AI736322 sb27a03.y1 Gm-cl009 Glycine max cDNA clone... 31 4.4
emb|AI965890|AI965890 sc79c09.y1 Gm-cl018 Glycine max cDNA clone... 31 4.4
emb|AI901200|AI901200 sc22a07.y1 Gm-cl013 Glycine max cDNA clone... 31 4.4
emb|AI736604|AI736604 sb31b04.y1 Gm-cl012 Glycine max cDNA clone... 31 4.4
emb|AW666300|AW666300 sk34h06.y1 Gm-cl028 Glycine max cDNA clone... 31 6.0
10 emb|AW831353|AW831353 sm32e10.y1 Gm-cl028 Glycine max cDNA clone... 31 6.0
gb|L37877|CPCRPL27P *Cryptococcus neoformans* ribosomal protein L2... 31 6.0
emb|Z75290|SCYOR382W *S.cerevisiae* chromosome XV reading frame OR... 31 6.0
emb|AQ850290|AQ850290 LMAJFV1_lm28c06.x1 *Leishmania major* FV1 ra... 31 6.0
gb|L26508|CPCAAA *Filobasidiella neoformans* CAP59 gene, complete ... 31 6.0
emb|AQ847349|AQ847349 LMAJFV1_lm30a04.x1 *Leishmania major* FV1 ra... 31 6.0
15 emb|AC008241|AC008241 *Leishmania major* clone L952b strain Friedl... 31 6.0
emb|AW667667|AW667667 GA_Ea0010C24 *Gossypium arboreum* 7-10 dpa ... 31 6.0
emb|AF031066|AF031066 *Martensiomycetes pterosporus* 28S ribosomal R... 31 6.0
emb|AQ398504|AQ398504 mgxb0019M20f CUGI Rice Blast BAC Library P... 31 6.0
emb|AZ215468|AZ215468 Sheared DNA-79C4.TF Sheared DNA Trypanosom... 25 7.1
20 dbj|D50617|YSCCHR VIN *Saccharomyces cerevisiae* chromosome VI comp... 30 8.3
dbj|D44598|YSCF4121F *Saccharomyces cerevisiae* chromosome VI phag... 30 8.3
dbj|D87895|D87895 *Aspergillus nidulans* chiA gene for chitinase, ... 30 8.3
emb|AQ162420|AQ162420 mgxb0012N11r CUGI Rice Blast BAC Library P... 30 8.3
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25 emb|AW101721|AW101721 sd69c10.y1 Gm-cl008 Glycine max cDNA clone... 30 8.3
emb|AW980894|AW980894 EST392047 GVN *Medicago truncatula* cDNA clo... 30 8.3
emb|AQ447068|AQ447068 mgxb0004O05f CUGI Rice Blast BAC Library P... 30 8.3
emb|AW727134|AW727134 GA_Ea0023J07 *Gossypium arboreum* 7-10 dpa ... 26 8.7
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35 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&cuid=gb|x99923|/ncgi)
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(1710 letters)

40 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

45 Score E
Sequences producing significant alignments: (bits) Value

emb|AF149917|AF149917 *Simmondsia chinensis* acyl CoA reductase mR... 158 e-144
emb|X99922|BNMS2PROT *B.napus* mRNA for male sterility protein 2. 137 2e-74
50 emb|A45743|A45743 Sequence 22 from Patent WO9520668. 137 2e-74
emb|AW615992|AW615992 EST325442 tomato flower buds 0-3 mm, Corne... 277 2e-73
emb|AI730540|AI730540 BNLGHi7015 Six-day Cotton fiber *Gossypium* ... 153 4e-59
emb|AW738637|AW738637 EST340064 tomato flower buds, anthesis, Co... 158 3e-51
emb|AW931162|AW931162 EST357005 tomato fruit mature green, TAMU ... 201 1e-50
55 emb|AW616784|AW616784 EST323195 *L. hirsutum* trichome, Cornell Un... 200 3e-50
emb|AW308800|AW308800 sf72b03.y1 Gm-cl013 Glycine max cDNA clone... 141 7e-50
emb|AW278653|AW278653 sf63e03.y1 Gm-cl013 Glycine max cDNA clone... 110 1e-46
emb|AI727421|AI727421 BNLGHi7945 Six-day Cotton fiber *Gossypium* ... 106 3e-46
emb|AI901240|AI901240 sc22e07.y1 Gm-cl013 Glycine max cDNA clone... 166 3e-40
60 emb|AW306151|AW306151 se46e08.y1 Gm-cl017 Glycine max cDNA clone... 145 2e-39
emb|AW688482|AW688482 NF008B06ST1F1000 Developing stem *Medicago* ... 127 6e-38

- emb|AW648210|AW648210 EST326664 tomato germinating seedlings, TA... 107 1e-37
- emb|AW279265|AW279265 sf68h11.y1 Gm-c1013 Glycine max cDNA clone... 123 3e-37
- emb|AW671408|AW671408 LG1_343_A01.b1_A002 Light Grown 1 (LG1) So... 156 4e-37
- emb|AW306626|AW306626 se53c07.y1 Gm-c1017 Glycine max cDNA clone... 145 5e-37
- 5 emb|AW624291|AW624291 EST322152 tomato flower buds 3-8 mm, Come... 121 1e-32
- emb|AW688474|AW688474 NF008A09ST1F1000 Developing stem Medicago ... 106 5e-31
- emb|AW781535|AW781535 sl81d04.y1 Gm-c1037 Glycine max cDNA clone... 109 7e-30
- emb|AW622996|AW622996 EST320941 tomato flower buds 3-8 mm, Come... 128 1e-28
- emb|AI055562|AI055562 coau0004F11 Cotton Boll Abscission Zone cD... 98 1e-27
- 10 emb|AW287082|AW287082 LG1_265_C07.b2_A002 Light Grown 1 (LG1) So... 119 7e-26
- emb|AW691252|AW691252 NF042F05ST1F1000 Developing stem Medicago ... 100 3e-25
- emb|AW649410|AW649410 EST327864 tomato germinating seedlings, TA... 115 1e-24
- emb|AW705269|AW705269 sk59a03.y1 Gm-c1019 Glycine max cDNA clone... 70 3e-18
- emb|AW217786|AW217786 EST296500 tomato flower buds 8 mm to pre-a... 92 6e-18
- 15 emb|AW217788|AW217788 EST296502 tomato flower buds 8 mm to pre-a... 91 8e-18
- emb|AW217787|AW217787 EST296501 tomato flower buds 8 mm to pre-a... 91 3e-17
- emb|AW928598|AW928598 EST337386 tomato flower buds 8 mm to pre-a... 86 1e-16
- emb|Z11889|MITTARRNG T.aestivum mitochondrion rrn26 gene for rRN... 88 2e-16
- emb|AW565061|AW565061 LG1_320_C11.b1_A002 Light Grown 1 (LG1) So... 78 2e-13
- 20 emb|AW980920|AW980920 EST392073 GVN Medicago truncatula cDNA clo... 50 3e-13
- emb|AV428628|AV428628 AV428628 Lotus japonicus young plants (two... 71 2e-11
- emb|AV419850|AV419850 AV419850 Lotus japonicus young plants (two... 68 2e-10
- emb|AF076792|AF076792 Irvingia gabonensis clone BM35, genomic su... 51 2e-08
- emb|AW056631|AW056631 ST53H08 Pine TriplEx shoot tip library Pin... 36 7e-05
- 25 emb|AW289724|AW289724 NXNV005H02F Nsf Xylem Normal wood Vertical... 48 2e-04
- gb|BE057395|BE057395 sn02f06.y1 Gm-c1015 Glycine max cDNA clone ... 44 2e-04
- emb|AZ050471|AZ050471 GSSTc11316 Trypanosoma cruzi random genomi... 48 2e-04
- emb|AW758790|AW758790 NXNV_089_G03_F Nsf Xylem Normal wood Verti... 47 5e-04
- emb|AA952454|AA952454 TENS1392 T. cruzi epimastigote normalized ... 46 0.001
- 30 emb|AQ361876|AQ361876 mgxb0005G07r CUGI Rice Blast BAC Library P... 42 0.015
- emb|AI069380|AI069380 mgac0006dC11f Magnaporthe grisea Appressor... 42 0.015
- emb|AW649203|AW649203 EST327657 tomato germinating seedlings, TA... 41 0.021
- emb|Y13967|PCLYS2 Penicillium chrysogenum lys2 gene. 41 0.021
- emb|AW929360|AW929360 EST338148 tomato flower buds 8 mm to pre-a... 40 0.074
- 35 emb|AW564691|AW564691 LG1_300_C05.b1_A002 Light Grown 1 (LG1) So... 37 0.50
- emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 37 0.50
- gb|BE033566|BE033566 MF03E04 MF Mesembryanthemum crystallinum cD... 36 0.69
- emb|AI488290|AI488290 EST246612 tomato ovary, TAMU Lycopersicon ... 36 0.94
- emb|AW932683|AW932683 EST358526 tomato fruit mature green, TAMU ... 36 0.94
- 40 emb|AW932440|AW932440 EST358283 tomato fruit mature green, TAMU ... 36 0.94
- emb|AQ874417|AQ874417 V108D3 mTn-3xHA/lacZ Insertion Library, st... 35 1.3
- emb|AF156928|AF156928 Candida albicans folypolyglutamate synthe... 28 1.4
- emb|AW720470|AW720470 LjNEST19f2r Lotus japonicus nodule library... 35 1.8
- emb|AW397976|AW397976 sg70f10.y1 Gm-c1007 Glycine max cDNA clone... 35 1.8
- 45 emb|AV409049|AV409049 AV409049 Lotus japonicus young plants (two... 35 1.8
- emb|AL353821|NC68B2 Neurospora crassa DNA linkage group V Cosmid... 35 2.4
- emb|AW775233|AW775233 EST331955 GVN Medicago truncatula cDNA clo... 35 2.4
- emb|AW694088|AW694088 NF072C08ST1F1065 Developing stem Medicago ... 35 2.4
- emb|AW693849|AW693849 NF069G11ST1F1087 Developing stem Medicago ... 35 2.4
- 50 emb|AW694067|AW694067 NF072D11ST1F1093 Developing stem Medicago ... 35 2.4
- emb|AW773778|AW773778 EST332764 KV3 Medicago truncatula cDNA clo... 35 2.4
- emb|AW774799|AW774799 EST333950 KV3 Medicago truncatula cDNA clo... 35 2.4
- emb|AW774591|AW774591 EST333742 KV3 Medicago truncatula cDNA clo... 35 2.4
- emb|AW689574|AW689574 NF021H08ST1F1000 Developing stem Medicago ... 35 2.4
- 55 emb|AW694736|AW694736 NF079D09ST1F1077 Developing stem Medicago ... 35 2.4
- emb|AI075585|AI075585 TENU3007 T. cruzi epimastigote normalized ... 35 2.4
- emb|AW691920|AW691920 NF050F11ST1F1000 Developing stem Medicago ... 35 2.4
- emb|AW690529|AW690529 NF035F03ST1F1000 Developing stem Medicago ... 35 2.4
- emb|AA660549|AA660549 00435 MtRHE Medicago truncatula cDNA 5' si... 35 2.4
- 60 emb|AQ841091|AQ841091 T132045b Medicago truncatula BAC library M... 35 2.4
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- emb|AW299108|AW299108 EST305782 KV2 Medicago truncatula cDNA clo... 35 2.4
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 10 gb|U58133|CAU58133 Candida albicans alpha-aminoadipate reductase... 26 6.1
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 15 emb|AW618444|AW618444 EST320430 L. pennellii trichome, Cornell U... 33 6.3
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 emb|AF180560|AF180560 Emericella nidulans sgdA gene, partial seq... 33 8.7
 dbj|D29761|YSACSI Candida maltosa gene for chitin synthase 2, p... 33 8.7
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 25 dbj|D50617|YSCCHRVIN Saccharomyces cerevisiae chromosome VI comp... 33 8.7

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35 Database: plantfungal
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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30	emb AW099977 AW099977 sd19c07.y2 Gm-c1012 Glycine max cDNA clone...	253	7e-69
	emb AW733661 AW733661 sk83d11.y1 Gm-c1016 Glycine max cDNA clone...	223	4e-65
	emb AW164658 AW164658 se75h05.y1 Gm-c1023 Glycine max cDNA clone...	162	1e-64
	emb AW689466 AW689466 NF019F01ST1F1000 Developing stem Medicago ...	159	1e-62
	emb AI441647 AI441647 sa65a03.y1 Gm-c1004 Glycine max cDNA clone...	212	9e-58
35	emb AI729737 AI729737 BNLGH14077 Six-day Cotton fiber Gossypium...	128	7e-55
	emb AI771313 AI771313 EST252329 tomato ovary, TAMU Lycopersicon ...	137	3e-46
	emb AW033056 AW033056 EST276615 tomato callus, TAMU Lycopersicon...	177	3e-43
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Database: plantfungal
 10 661,018 sequences; 426,114,510 total letters

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35	emb AW423428 AW423428 sh66f08.y1 Gm-c1015 Glycine max cDNA clone... 38	0.003	
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45	emb AA520781 AA520781 TgESTzz64a03.r1 TgME49 invivo Bradyzoite c... 35	0.37	
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	emb AW310598 AW310598 sg21h03.x1 Gm-c1024 Glycine max cDNA clone... 34	0.96	
	emb AW233878 AW233878 sf31d07.y1 Gm-c1028 Glycine max cDNA clone... 34	0.96	
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60	gb M62740 BLYGLB2 Hordeum vulgare 1,3-1,4-beta-D glucan 4-glucan... 34	0.96	
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 5 emb|AV393790|AV393790 AV393790 *Chlamydomonas reinhardtii* C9 Chla... 33 2.5
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 emb|AL157415|LMFL8325 *Leishmania major* Friedlin chromosome 5 cos... 32 3.4
 emb|AQ935443|AQ935443 CpG2473A CpIOWAgDNA1 *Cryptosporidium parvu...* 32 3.4
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 10 emb|AW687188|AW687188 NF006H09RT1F1079 Developing root Medicago ... 32 3.4
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 45 (1212 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

- 50 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

- 55 gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 388 e-129
 gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 385 e-128
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 gb|L13654|TOMTPX1A *Lycopersicon esculentum* peroxidase (TPX1) mRNA... 204 e-118
 emb|Y16776|SOY16776 *Spinacia oleracea* mRNA for peroxidase, prx10... 210 e-113
 60 emb|Z22920|SPPEROXDS *S. polyrrhiza* mRNA for peroxidase. 183 5e-90
 emb|AI495190|AI495190 sa89c07.y1 Gm-c1004 Glycine max cDNA clone... 325 6e-88

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	emb AW625780 AW625780 EST319687 tomato radicle, 5 d post-imbibit...	211	1e-84
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5	emb AW329363 AW329363 N200592e rootphos(-) Medicago truncatula c...	307	1e-82
	emb AW647641 AW647641 EST307119 tomato germinating seedlings, TA...	190	9e-82
	emb AW625441 AW625441 EST319348 tomato radicle, 5 d post-imbibit...	187	7e-80
	emb AW621198 AW621198 EST311996 tomato root during/after fruit s...	206	9e-80
10	emb AW704698 AW704698 sk39d06.y1 Gm-c1028 Glycine max cDNA clone...	297	1e-79
	emb AW219160 AW219160 EST301642 tomato root during/after fruit s...	190	2e-79
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25	emb AW649146 AW649146 EST327600 tomato germinating seedlings, TA...	178	3e-71
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	emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C.	164	3e-63
	emb AW621842 AW621842 EST312640 tomato root during/after fruit s...	151	4e-63
45	emb X94943 LECEVI16G L.esculentum mRNA for peroxidase.	104	4e-63
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	emb AW625242 AW625242 EST319245 tomato radicle, 5 d post-imbibit...	149	9e-63
	emb AF149279 AF149279 Phaseolus vulgaris peroxidase 4 precursor ...	100	2e-62
	emb AW621971 AW621971 EST312769 tomato root during/after fruit s...	147	6e-62
50	emb AW218589 AW218589 EST303772 tomato radicle, 5 d post-imbibit...	147	6e-62
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	emb AB027753 AB027753 Nicotiana tabacum mRNA for peroxidase, com...	105	1e-60
	emb Y16778 SPY16778 Spinacia oleracea mRNA for peroxidase, prx11...	109	3e-60
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	emb X90693 MSRNAPE1B M.sativa mRNA for peroxidase 1B.	153	6e-60

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 5 gb|L36111|SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 161 2e-58
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 15 emb|AB024438|AB024438 Scutellaria baicalensis mRNA for peroxidase... 141 6e-57
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 25 emb|AW625144|AW625144 EST319051 tomato radicle, 5 d post-imbibit... 123 8e-55
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 40 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|aac004561|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|aac004561|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|aac004561|/ncgi)
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[post/entrez/query?db=n&form=6&dopt=g&uid=gb|aac004561|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|aac004561|/ncgi)
 (675 letters)

45

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

50

Score E
 Sequences producing significant alignments: (bits) Value

55

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 emb|AW728749|AW728749 GA_Ea0028D12 Gossypium arboreum 7-10 dpa ... 112 5e-40
 emb|AW622625|AW622625 EST313425 tomato root during/after fruit s... 73 6e-40
 emb|AW267974|AW267974 EST306196 DSIR Medicago truncatula cDNA cl... 115 1e-39
 emb|AW224728|AW224728 EST303171 tomato root, plants pre-anthesis... 88 1e-37
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 60 emb|AW186185|AW186185 se64f07.y1 Gm-c1019 Glycine max cDNA clone... 112 3e-36
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	emb AW569900 AW569900 si83a10.y1 Gm-c1031 Glycine max cDNA clone...	89 2e-35
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	emb X56263 NTAUX103 N.tabacum auxin-induced mRNA (pCNT103).	79 2e-33
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	emb AW776620 AW776620 EST335685 DSIL Medicago truncatula cDNA cl...	79 2e-31
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	emb AW306150 AW306150 se46e07.y1 Gm-c1017 Glycine max cDNA clone...	85 7e-30
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50	emb AJ010448 AMY010448 Alopecurus myosuroides mRNA for glutathio...	63 2e-28
	emb AJ010449 AMY010449 Alopecurus myosuroides mRNA for glutathio...	64 2e-28
	emb AW687500 AW687500 NF010C06RT1F1049 Developing root Medicago ...	84 3e-28
	emb AB027501 AB027501 Daucus carota Dcarg-1 mRNA, complete cds.	62 4e-28
	emb AW684848 AW684848 NF022C03NR1F1000 Nodulated root Medicago t...	84 4e-28
55	emb AW684915 AW684915 NF023A04NR1F1000 Nodulated root Medicago t...	75 4e-28
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	emb AW677374 AW677374 DG1_6_A02.b1_A002 Dark Grown 1 (DG1) Sorgh...	66 8e-28
	emb AW040981 AW040981 EST283845 tomato mixed elicitor, BTI Lycop...	88 9e-28
60	emb AW759593 AW759593 sl45c12.y1 Gm-c1027 Glycine max cDNA clone...	87 2e-27
	gb BE124079 BE124079 EST394204 DSIL Medicago truncatula cDNA clo...	75 3e-27

- emb|X56268|NTAUX1 N.tabacum gene for an auxin-induced protein (p... 79 4e-27
 emb|AW687359|AW687359 NF008G06RT1F1051 Developing root Medicago ... 84 4e-27
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 5 emb|AI778504|AI778504 EST259383 tomato susceptible, Cornell Lyco... 72 1e-26
 emb|AW508224|AW508224 si51d09.y1 Gm-r1030 Glycine max cDNA clone... 86 1e-26
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 25 emb|AW127655|AW127655 M110397 DSLC Medicago truncatula cDNA clon... 84 1e-25
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 30 emb|AW443955|AW443955 EST308885 tomato mixed elicitor, BTI Lycop... 75 5e-25
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 40 http://www.ncgr.org/cgi-bin/ff?al050351
 (927 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

45 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

- 50 emb|AF071477|AF071477 Pyrus communis isoflavone reductase relate... 583 e-166
 emb|AF202184|AF202184 Glycine max isoflavone reductase homolog 2... 581 e-165
 emb|X92075|STISORED H S.tuberosum mRNA for isoflavone reductase h... 542 e-153
 emb|AF135127|AF135127 Betula pendula isoflavone reductase homolo... 534 e-151
 55 emb|AF242491|AF242491 Forsythia x intermedia clone 1 phenylcouma... 527 e-149
 emb|AF242492|AF242492 Forsythia x intermedia clone 2 phenylcouma... 512 e-144
 emb|AJ005806|PTR5806 Populus trichocarpa mRNA for phenylcoumaran... 497 e-140
 emb|AJ005805|PTR5805 Populus trichocarpa mRNA for phenylcoumaran... 497 e-140
 emb|AJ005804|PTR5804 Populus trichocarpa mRNA for phenylcoumaran... 497 e-140
 60 emb|AJ005803|PTR5803 Populus trichocarpa mRNA for phenylcoumaran... 495 e-139
 emb|AF201458|AF201458 Medicago sativa isoflavone reductase-like ... 294 e-136

	dbj D28505 TOBA622A Tobacco mRNA for A622, complete cds.	462 e-129
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	emb AF202183 AF202183 Glycine max isoflavone reductase homolog 1...	403 e-124
	emb AF242497 AF242497 Tsuga heterophylla clone 5 phenylcoumaran ...	416 e-123
5	emb AW164323 AW164323 se71a03.y1 Gm-c1023 Glycine max cDNA clone...	426 e-118
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10	emb AW560052 AW560052 EST315100 DSIR Medicago truncatula cDNA cl...	369 e-114
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	emb AW423683 AW423683 sh50d08.y1 Gm-c1017 Glycine max cDNA clone...	258 2e-96
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	emb AW278000 AW278000 sf89e04.y1 Gm-c1019 Glycine max cDNA clone...	286 2e-76
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45	emb AF242504 AF242504 Thuja plicata clone 2 pinoresinol-laricire...	160 7e-76
	emb AF242503 AF242503 Thuja plicata clone 1 pinoresinol-laricire...	120 7e-76
	emb AW623613 AW623613 EST321558 tomato flower buds 3-8 mm, Come...	199 3e-75
	emb AW164589 AW164589 se73h03.y1 Gm-c1023 Glycine max cDNA clone...	281 6e-75
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50	emb AI726822 AI726822 BNLGHi6647 Six-day Cotton fiber Gossypium ...	279 2e-74
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 35 [post/entrez/query?db=n&form=6&dopt=g&cuid=gb|ac005687|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&cuid=gb|ac005687|/ncgi)
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 (734 letters)

Database: plantfungal
 40 661,018 sequences; 426,114,510 total letters

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	emb AW221854 AW221854 EST298665 tomato fruit red ripe, TAMU Lyco...	102	3e-21
	emb AW441715 AW441715 EST311111 tomato fruit red ripe, TAMU Lyco...	102	3e-21
	emb AW219198 AW219198 EST301680 tomato root during/after fruit s...	102	3e-21
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	emb AI487067 AI487067 EST245389 tomato ovary, TAMU Lycopersicon ...	101	5e-21
	emb AW442735 AW442735 EST307665 tomato mixed elicitor, BTI Lycop...	101	5e-21
	emb AW218830 AW218830 EST301310 tomato root during/after fruit s...	101	5e-21
	emb AI483782 AI483782 EST249653 tomato ovary, TAMU Lycopersicon ...	101	5e-21
50	emb AW218836 AW218836 EST301316 tomato root during/after fruit s...	101	5e-21
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55	emb AW308962 AW308962 sf92d05.y1 Gm-cl019 Glycine max cDNA clone...	101	7e-21
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35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

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 50 emb|Z46949|SNPR6JT11 S.nigra mRNA for pathogenesis-related prote... 86 9e-17
 gb|BE024084|BE024084 sm96e02.y1 Gm-c1015 Glycine max cDNA clone ... 85 2e-16
 emb|AI938085|AI938085 sc41h07.x1 Gm-c1014 Glycine max cDNA clone... 84 3e-16
 emb|AI930853|AI930853 sb43c07.y1 Gm-c1015 Glycine max cDNA clone... 84 6e-16
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 55 emb|AI966712|AI966712 sc55h06.y1 Gm-c1015 Glycine max cDNA clone... 80 6e-15
 gb|BE023986|BE023986 sm95a07.y1 Gm-c1015 Glycine max cDNA clone ... 78 2e-14
 emb|AW433320|AW433320 sh55e08.y1 Gm-c1015 Glycine max cDNA clone... 78 2e-14
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5	emb AW432580 AW432580 sh76c09.y1 Gm-c1015 Glycine max cDNA clone...	75 3e-13
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	gb J05094 TOMP II <i>L.peruvianum</i> proteinase inhibitor I mRNA, compl...	50 2e-10
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25	dbj D26455 TOBTID44 <i>Nicotiana glauca</i> X <i>Nicotiana langsdorffii</i> mR...	51 5e-10
	emb Z12623 NTPII3PI <i>N.tabacum</i> pre-pro-PI-Ib gene encoding pre-pr...	50 8e-10
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	emb AW432477 AW432477 sh74f01.y1 Gm-c1015 Glycine max cDNA clone...	61 4e-09
	emb AW092750 AW092750 EST285930 tomato mixed elicitor, BTI Lycop...	45 4e-09
	gb M74102 TOBCPII <i>Nicotiana sylvestris</i> serine proteinase inhibit...	52 6e-09
35	emb AW622766 AW622766 EST306752 tomato flower buds 3-8 mm, Corne...	46 1e-08
	emb AI563053 AI563053 EST00177 watermelon lambda zap library Cit...	58 3e-08
	emb AI563140 AI563140 EST00264 watermelon lambda zap library Cit...	58 3e-08
	emb AI723907 AI723907 RHIZ1_32_B07.y1_A001 Rhizome1 Sorghum hale...	57 5e-08
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40	emb AJ250663 HVU250663 <i>Hordeum vulgare</i> partial mRNA for putative...	57 5e-08
	emb AI724485 AI724485 RHIZ1_10_F03.y1_A001 Rhizome1 Sorghum hale...	57 5e-08
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	gb L06985 POTPIN1A <i>Solanum tuberosum</i> proteinase inhibitor I mRNA...	43 1e-07
45	gb M13938 TOMWIPIG Tomato (<i>L.esculentum</i>) wound-inducible protein...	42 2e-07
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	emb AI490242 AI490242 EST248568 tomato ovary, TAMU Lycopersicon ...	42 2e-07
	emb AI486930 AI486930 EST245252 tomato ovary, TAMU Lycopersicon ...	42 2e-07
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50	gb K03290 TOMWIPI Tomato leaf wound-induced proteinase inhibitor...	42 2e-07
	emb X67950 STPIN1MR <i>S.tuberosum</i> pin1 mRNA for proteinase inhibit...	41 5e-07
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55	emb AI899242 AI899242 EST268685 tomato ovary, TAMU Lycopersicon ...	41 9e-07
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 10 emb|AI772725|AI772725 EST253825 tomato resistant, Cornell Lycop... 35 5e-06
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 emb|AI774403|AI774403 EST255503 tomato resistant, Cornell Lycop... 35 5e-06
 emb|AI772154|AI772154 EST253254 tomato resistant, Cornell Lycop... 35 5e-06
 emb|AW094311|AW094311 EST287491 tomato mixed elicitor, BTI Lycop... 35 5e-06
 15 emb|AW092125|AW092125 EST285221 tomato mixed elicitor, BTI Lycop... 35 5e-06
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 emb|AW040872|AW040872 EST283736 tomato mixed elicitor, BTI Lycop... 35 5e-06
 emb|AW093509|AW093509 EST286689 tomato mixed elicitor, BTI Lycop... 35 5e-06
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 30 http://www.ncgr.org/cgi-bin/ff?aj001809
 (2247 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

35 Searching.....done

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			(bits) Value
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	emb Z49320 SCYJL045W	S.cerevisiae chromosome X reading frame ORF...	403 0.0
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60	emb AW180257 AW180257	MgA0347fMgA Library Mycosphaerella gramin...	309 4e-83
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 emb|AQ646390|AQ646390 RPCI93-DpnII-29L18.TJ RPCI93-DpnII Trypano... 120 2e-32
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 35 emb|AW736633|AW736633 EST333125 KV3 Medicago truncatula cDNA clo... 128 6e-32
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 45 emb|AW830714|AW830714 sm35c05.y1 Gm-c1028 Glycine max cDNA clone... 81 3e-18
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 55 gb|L36344|YSCGTGMS Saccharomyces cerevisiae tRNA-Met, tRNA-Ser, ... 47 1e-06
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 25. [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005727|/ncgi)
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 (2008 letters).

30. Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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35. Score E
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 emb|AW565896|AW565896 LG1_353_C06.g1_A002 Light Grown 1 (LG1) So... 156 5e-37
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 (938 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AW598595 AW598595 sj93f10.y1 Gm-c1023 Glycine max cDNA clone...	118	5e-26	
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50	Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done		
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	emb AW736643 AW736643 EST333135 KV3 Medicago truncatula cDNA clo...	104	2e-21
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	emb AW568172 AW568172 si57d03.y1 Gm-r1030 Glycine max cDNA clone...	84	2e-15
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 (2703 letters)

Database: plantfungal
 10 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 15 Sequences producing significant alignments: (bits) Value

emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 318 e-148
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 289 3e-96
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 280 8e-93
 20 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 281 3e-92
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 280 1e-91
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 268 1e-91
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 278 3e-91
 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 271 8e-90
 25 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 272 2e-89
 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 221 5e-88
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 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 272 9e-88
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 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 182 6e-84
 35 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 275 2e-82
 emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 129 6e-82
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 50 emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 266 5e-70
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 emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 158 2e-55
 emb|Y16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 133 3e-55
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 35 emb|Z18862|BOSRKRPA B.oleracea encoding S-receptor kinase protein. 93 4e-44
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(1953 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments:

(bits) Value

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emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 330 e-134

gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 224 e-107

gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 215 e-105

gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 297 e-104

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dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 285 e-103

emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 287 e-103

gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 304 e-102

emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 289 e-102

emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 292 e-102

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emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 291 e-101

emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 303 e-101

emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 299 e-101

gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 294 e-101

emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 301 e-101

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emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 302 e-101

dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 287 e-100

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emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 264 3e-93

gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 286 2e-92

emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 199 6e-92

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emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 126 3e-75

emb|AJ245479|BNA245479 Brassica napus SII3, slk, srk, CePP, Fmt,... 126 4e-75

emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 126 2e-74

emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 119 3e-74

emb|X79432|BOSRK3 B.oleracea SRK3 gene. 118 8e-74

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emb|AB024422|AB024422S2 Brassica oleracea SRK13-b gene, exon 2, ... 117 1e-73

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emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 121 8e-73

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emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 116 1e-72

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dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 124 1e-71

emb|AW831390|AW831390 sm22a06.y1 Gm-c1028 Glycine max cDNA clone... 211 3e-71

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 5 emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 124 8e-57
 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 194 2e-56
 emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 91 4e-56
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<http://www.ncgr.org/cgi-bin/ff?x74514>
 (1947 letters)

60

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5	Score	E
Sequences producing significant alignments:	(bits)	Value
emb AF000521 AF000521 <i>Fragaria x ananassa</i> cell wall invertase pr...	413	0.0
emb Z35163 VFCWINV2 <i>V.faba</i> VFCWINV2 mRNA for cell wall invertase...	418	0.0
10 gb M58362 DARBFUC <i>D.carota</i> cell wall beta-fructosidase mRNA, co...	239	0.0
emb X81792 CRCIN1 <i>C.rubrum</i> CIN1 mRNA for extracellular invertase.	181	0.0
emb X81834 NTMRNABDF <i>N.tabacum</i> mRNA for beta-fructosidase.	205	0.0
emb AF030420 AF030420 <i>Triticum aestivum</i> cell wall invertase (IVR...	240	0.0
emb Y11176 CIFRUCTOS <i>C.intybus</i> mRNA for fructosidase.	144	0.0
15 emb Z21486 STBETFRUA <i>S.tuberosum</i> mRNA for invertase gene encodin...	196	e-180
emb AJ272305 LPE272305 <i>Lycopersicon pennellii</i> mRNA for beta-fruc...	190	e-170
emb X85327 PSRNABFRU <i>P.sativum</i> mRNA for beta-fructofuranosidase.	398	e-169
emb AF063246 AF063246 <i>Pisum sativum</i> cell wall invertase (bfruct1...	398	e-169
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20 emb Z22645 STBETFRCA <i>S.tuberosum</i> invertase gene encoding beta-fr...	204	e-166
emb AF000520 AF000520 <i>Fragaria x ananassa</i> cell wall invertase (I...	210	e-164
emb AB004558 AB004558 <i>Lycopersicon esculentum</i> mRNA for acid inve...	200	e-164
emb X69321 DCBFRUCT <i>D.carota</i> (Queen Anne's Lace) Inv*Dc1 gene.	178	e-145
emb X78424 DCINC1 <i>D.carota</i> (Queen Anne's Lace) Inv*Dc2 gene, 343...	161	e-136
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emb AJ133765 STU133765 <i>Solanum tuberosum</i> invGE and invGF genes.	148	e-128
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emb AJ006067 ACE6067 <i>Allium cepa</i> mRNA for invertase.	210	e-126
30 emb A94218 A94218 Sequence 1 from Patent EP0952222.	176	e-122
emb AF002656 AF002656 <i>Asparagus officinalis</i> acid invertase mRNA,...	198	e-120
gb U81520 CIU81520 <i>Cichorium intybus</i> sucrose:sucrose 1-fructosyl...	173	e-120
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emb X75353 DCRNABF <i>D.carota</i> (Nantaise) mRNA for soluble acid b...	203	e-120
35 emb AJ272307 LPE272307 <i>Lycopersicon pennellii</i> lin 5 gene for bet...	145	e-119
emb X75352 DCRNAABF <i>D.carota</i> (Nantaise) mRNA for soluble acid be...	203	e-119
emb X78423 DCINUC1 <i>D.carota</i> (Queen Anne's Lace) Inv*Dc3 gene, 44...	160	e-118
emb A94222 A94222 Sequence 5 from Patent EP0952222.	173	e-117
emb Y09662 CSSS1FT <i>C.scolymus</i> mRNA for sucrose sucrose 1-fructos...	170	e-117
40 emb A86530 A86530 Sequence 1 from Patent WO9839460.	170	e-117
emb AJ272306 LES272306 <i>Lycopersicon esculentum</i> lin 5 gene for be...	145	e-116
emb AJ250634 TOF250634 <i>Taraxacum officinale</i> mRNA for sucrose:suc...	169	e-116
emb Z49831 VFVCINVMR <i>V.faba</i> VFVCINV mRNA for invertase (beta-fru...	199	e-115
gb U92438 PVU92438 <i>Phaseolus vulgaris</i> soluble acid invertase mRN...	198	e-114
45 emb AW686881 AW686881 NF003E07RT1F1000 Developing root Medicago ...	413	e-114
dbj D10265 VIRINVA <i>Vigna radiata</i> mRNA for invertase, complete cds.	194	e-114
emb AJ009757 HTU9757 <i>Helianthus tuberosus</i> sst-1 gene.	171	e-113
emb A52468 A52468 Sequence 1 from Patent WO9621023.	171	e-113
emb X70368 STPAIN1A <i>S.tuberosum</i> PAIN-1 mRNA for beta-fructofuran...	200	e-108
50 emb X67163 DCSBFRU <i>D.carota</i> mRNA for soluble beta-fructosidase.	140	e-107
gb L29099 POTBFRUASE <i>Solanum tuberosum</i> beta-fructosidase mRNA, c...	198	e-107
dbj E07108 E07108 cDNA encoding acid invertase.	198	e-106
dbj D11350 TOMBFSO <i>Tomato</i> mRNA for beta-fructosidase, complete cds.	198	e-106
emb Z12026 LPBFRUCM <i>L.pimpinellifolium</i> beta-fructosidase mRNA fo...	198	e-106
55 emb Z12025 LEBFRUCM <i>L.esculentum</i> beta-fructosidase mRNA for vacu...	198	e-106
gb M81081 TOMACIN <i>Tomato</i> acid invertase (TIV1) mRNA, complete cds.	198	e-106
gb S70040 S70040 acid invertase [<i>Lycopersicon esculentum</i> =tomatoe...	198	e-106
dbj E16293 E16293 cDNA encoding invertase.	198	e-106
dbj E08976 E08976 cDNA encoding tomato invertase.	198	e-106
60 emb AF017082 AF017082 <i>Ipomoea batatas</i> beta-fructofuranosidase (S...	141	e-103
emb Y11124 CIPINVERT <i>C.intybus</i> mRNA for putative invertase.	138	e-102

	emb X97642 TGINV5GEN T.gesneriana mRNA for invertase 5.	180 6e-97
	emb X95651 TGINV11GN T.gesneriana mRNA for invertase.	186 7e-96
	emb X97643 TGINV6GEN T.gesneriana mRNA for invertase 6.	186 2e-94
	emb Y18706 DCA18706 Daucus carota Inv*Dc5 gene.	130 2e-93
5	emb Y18707 DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge...	161 2e-93
	emb AF062735 AF062735 Saccharum officinarum soluble acid inverta...	129 1e-91
	emb AF062734 AF062734 Saccharum robustum soluble acid invertase ...	129 1e-91
	emb AF091549 AF091549 Hamamelis virginiana clone 7 beta-fructofu...	331 9e-90
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10	emb AF091550 AF091550 Hamamelis virginiana clone C beta-fructofu...	330 3e-89
	emb A94220 A94220 Sequence 3 from Patent EP0952222.	161 1e-88
	emb AF091548 AF091548 Hamamelis virginiana clone 3 beta-fructofu...	327 1e-88
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	emb Z12028 LPBFRUCG L.pimpinellifolium gene encoding vacuolar in...	157 6e-88
15	emb Z12027 LEBFRUCG L.esculentum gene for vacuolar invertase.	157 6e-88
	emb AJ009756 HTU9756 Helianthus tuberosus fft-1 gene.	161 2e-87
	emb A52470 A52470 Sequence 3 from Patent WO9621023.	161 2e-87
	emb X81795 BVBIN35 B.vulgaris BIN35 mRNA for extracellular inver...	265 5e-86
	gb BE055183 BE055183 GA_Ea0035H23f Gossypium arboreum 7-10 dpa ...	203 4e-83
20	emb X91392 LELIN8 L.esculentum mRNA for invertase (LIN8).	133 2e-82
	emb AF091547 AF091547 Hamamelis virginiana clone 1 beta-fructofu...	295 3e-81
	emb X81793 CRCIN2 C.rubrum CIN2 mRNA for intracellular invertase.	135 2e-80
	emb X91389 LELIN5 L.esculentum mRNA for invertase (LIN5).	129 1e-78
	emb X91391 LELIN7 L.esculentum mRNA for invertase (LIN7).	133 5e-78
25	emb Y07838 ACY07838 A.cepa mRNA for fructan:fructan 6G-fructosyl...	156 2e-77
	emb X81796 BVBIN44 B.vulgaris BIN44 mRNA for intracellular inver...	149 5e-77
	emb AF014925 AF014925 Citrus unshiu acid invertase (CUAI1) gene,...	138 4e-76
	emb AJ006066 ACE6066 Allium cepa mRNA for sucrose sucrose 1-fruc...	132 2e-75
	emb AF091545 AF091545 Hamamelis virginiana clone 4 beta-fructofu...	196 2e-75
30	emb A48282 A48282 Sequence 3 from Patent WO9601904.	152 4e-75
	emb AW685050 AW685050 NF024F09NR1F1000 Nodulated root Medicago t...	248 5e-75
	emb Z83339 PSZ83339 P.sativum mRNA for cell wall invertase II.	280 2e-74
	emb AF091546 AF091546 Hamamelis virginiana clone 6 beta-fructofu...	193 3e-74
	emb AV407850 AV407850 Lotus japonicus young plants (two...	267 2e-70
35	emb A48284 A48284 Sequence 5 from Patent WO9601904.	130 1e-69
	emb AW666614 AW666614 GA_Ea0005C10 Gossypium arboreum 7-10 dpa ...	207 3e-69
	emb AW730389 AW730389 GA_Ea0023K22 Gossypium arboreum 7-10 dpa ...	141 2e-68
	emb A48280 A48280 Sequence 1 from Patent WO9601904.	82 2e-68
	emb X83233 HVSF6FT Hordeum vulgare mRNA for sucrose:fructan 6-fr...	82 2e-68
40	emb AF069309 AF069309 Triticum aestivum vacuolar invertase (WIVR...	127 5e-67
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	emb AW738685 AW738685 EST340112 tomato flower buds, anthesis, Co...	189 3e-64
	emb X91390 LELIN6 L.esculentum mRNA for invertase (LIN6).	133 5e-64
45	emb AI522941 AI522941 sa92d01.y1 Gm-c1004 Glycine max cDNA clone...	201 1e-63
	emb AW441409 AW441409 EST310805 tomato fruit red ripe, TAMU Lyco...	114 4e-62
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	Sequences producing significant alignments:	(bits) Value
60	emb AF000521 AF000521 Fragaria x ananassa cell wall invertase pr...	
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5 emb|AF030420|AF030420 Triticum aestivum cell wall invertase (IVR... 240 0.0
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emb|Z21486|STBETFRUA S.tuberosum mRNA for invertase gene encodin... 196 e-180
emb|AJ272305|LPE272305 Lycopersicon pennellii mRNA for beta-fruc... 190 e-170
emb|X85327|PSRNABFRU P.sativum mRNA for beta-fructofuranosidase. 398 e-169
10 emb|AF063246|AF063246 Pisum sativum cell wall invertase (bfructl... 398 e-169
emb|AJ272304|LES272304 Lycopersicon esculentum mRNA for beta-fru... 190 e-169
emb|Z22645|STBETFRCA S.tuberosum invertase gene encoding beta-fr... 204 e-166
emb|AF000520|AF000520 Fragaria x ananassa cell wall invertase (I... 210 e-164
emb|AB004558|AB004558 Lycopersicon esculentum mRNA for acid inve... 200 e-164
15 emb|X69321|DCBFRUCT D.carota (Queen Anne's Lace) Inv*Dc1 gene. 178 e-145
emb|X78424|DCINC1 D.carota (Queen Anne's Lace) Inv*Dc2 gene, 343... 161 e-136
emb|Z35162|VFCWINV1 V.faba VFCWINV1 mRNA for cell wall invertase I. 207 e-132
emb|AF030421|AF030421 Triticum aestivum cell wall invertase (IVR... 138 e-130
emb|AJ133765|STU133765 Solanum tuberosum invGE and invGF genes. 148 e-128
20 gb|U87849|CAU87849 Capsicum annuum acid beta-fructosidase mRNA, ... 200 e-126
emb|AJ006067|ACE6067 Allium cepa mRNA for invertase. 210 e-126
emb|A94218|A94218 Sequence 1 from Patent EP0952222. 176 e-122
emb|AF002656|AF002656 Asparagus officinalis acid invertase mRNA,... 198 e-120
gb|U81520|CIU81520 Cichorium intybus sucrose:sucrose 1-fructosyl... 173 e-120
25 emb|X75351|DCRNABF D.carota (Nantaise) mRNA for soluble acid bet... 202 e-120
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emb|X75352|DCRNAABF D.carota (Nantaise) mRNA for soluble acid be... 203 e-119
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30 emb|A94222|A94222 Sequence 5 from Patent EP0952222. 173 e-117
emb|Y09662|CSSSIFT C.scolymus mRNA for sucrose sucrose 1-fructos... 170 e-117
emb|A86530|A86530 Sequence 1 from Patent WO9839460. 170 e-117
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emb|AJ250634|TOF250634 Taraxacum officinale mRNA for sucrose:suc... 169 e-116
35 emb|Z49831|VFVCINVMR V.faba VFVCINV mRNA for invertase (beta-fru... 199 e-115
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emb|AW686881|AW686881 NF003E07RT1F1000 Developing root Medicago ... 413 e-114
dbj|D10265|VIRINVA Vigna radiata mRNA for invertase, complete cds. 194 e-114
emb|AJ009757|HTU9757 Helianthus tuberosus sst-1 gene. 171 e-113
40 emb|A52468|A52468 Sequence 1 from Patent WO9621023. 171 e-113
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gb|L29099|POTBFRUASE Solanum tuberosum beta-fructosidase mRNA, c... 198 e-107
dbj|E07108|E07108 cDNA encoding acid invertase. 198 e-106
45 dbj|D11350|TOMBFSO Tomato mRNA for beta-fructosidase, complete cds. 198 e-106
emb|Z12026|LPBFRUCM L.pimpinellifolium beta-fructosidase mRNA fo... 198 e-106
emb|Z12025|LEBFRUCM L.esculentum beta-fructosidase mRNA for vacu... 198 e-106
gb|M81081|TOMACIN Tomato acid invertase (TIV1) mRNA, complete cds. 198 e-106
gb|S70040|S70040 acid invertase [Lycopersicon esculentum=tomatoe... 198 e-106
50 dbj|E16293|E16293 cDNA encoding invertase. 198 e-106
dbj|E08976|E08976 cDNA encoding tomato invertase. 198 e-106
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emb|X97642|TGINV5GEN T.gesneriana mRNA for invertase 5. 180 6e-97
55 emb|X95651|TGINV11GN T.gesneriana mRNA for invertase. 186 7e-96
emb|X97643|TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94
emb|Y18706|DCA18706 Daucus carota Inv*Dc5 gene. 130 2e-93
emb|Y18707|DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge... 161 2e-93
emb|AF062735|AF062735 Saccharum officinarum soluble acid inverta... 129 1e-91
60 emb|AF062734|AF062734 Saccharum robustum soluble acid invertase ... 129 1e-91
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- emb|AJ000481|CSFF1FRUC *Cynara scolymus* mRNA for fructan fructan ... 162 3e-89
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 emb|Z12027|LEBFRUCG *L. esculentum* gene for vacuolar invertase. 157 6e-88
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 10 emb|X81795|BVBIN35 *B. vulgaris* BIN35 mRNA for extracellular inver... 265 5e-86
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 15 emb|X91389|LELIN5 *L. esculentum* mRNA for invertase (LIN5). 129 1e-78
 emb|X91391|LELIN7 *L. esculentum* mRNA for invertase (LIN7). 133 5e-78
 emb|Y07838|ACY07838 *A. cepa* mRNA for fructan:fructan 6G-fructosyl... 156 2e-77
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 20 emb|AJ006066|ACE6066 *Allium cepa* mRNA for sucrose sucrose 1-fruc... 132 2e-75
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 25 emb|AF091546|AF091546 *Hamamelis virginiana* clone 6 beta-fructofu... 193 3e-74
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 emb|AW666614|AW666614 GA_Ea0005C10 *Gossypium arboreum* 7-10 dpa ... 207 3e-69
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 30 emb|A48280|A48280 Sequence 1 from Patent WO9601904. 82 2e-68
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- 45 Database: plantfungal
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- Searching.....done
- 50 Score E
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- emb|Z69369|SPAC3F10 *S. pombe* chromosome I cosmid c3F10. 314 e-119
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 emb|AL356012|SPBC359 *Schizosaccharomyces pombe* cosmid c359. 291 e-112
 emb|AW278374|AW278374 sf43c10.y1 *Gm-c1009* Glycine max cDNA clone... 383 e-105
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 60 emb|AI781883|AI781883 EST262762 tomato susceptible, Cornell Lyco... 370 e-101
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- emb|X97560|SC32KBF *S.cerevisiae* 32kb DNA fragment of chromosome ... 159 1e-94
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 emb|AW223995|AW223995 EST300806 tomato fruit red ripe, TAMU Lyco... 290 7e-77
 emb|AW222948|AW222948 EST299759 tomato fruit red ripe, TAMU Lyco... 285 2e-75
 emb|AI437711|AI437711 sa38f05.y1 Gm-c1004 Glycine max cDNA clone... 276 7e-73
 10 emb|AW476771|AW476771 ga37g03.y1 Moss EST library PPU Physcomitr... 275 1e-72
 emb|AW100468|AW100468 sd55e07.y1 Gm-c1016 Glycine max cDNA clone... 272 2e-71
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 emb|AI896472|AI896472 EST265903 tomato callus, TAMU Lycopersicon... 267 6e-70
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 15 emb|AW034253|AW034253 EST277824 tomato callus, TAMU Lycopersicon... 265 2e-69
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 20 dbj|E12376|E12376 Nucleotide sequence of scaur2 gene. 170 2e-67
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 35 emb|AI729186|AI729186 BNLGHi12864 Six-day Cotton fiber *Gossypium*... 210 3e-57
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 gb|L29485|LEIPGLYB *Leishmania tarentolae* P-glycoprotein related ... 171 6e-57
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 40 emb|AW459613|AW459613 sh89d10.y1 Gm-c1016 Glycine max cDNA clone... 219 1e-55
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 emb|AW757110|AW757110 sl29c06.y1 Gm-c1027 Glycine max cDNA clone... 208 3e-52
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 emb|AW761593|AW761593 sl69g02.y1 Gm-c1027 Glycine max cDNA clone... 205 2e-51
 45 emb|Z99262|SPAC9E9 *S.pombe* chromosome I cosmid c9E9. 129 2e-51
 emb|Y09354|SPABC1 *S.pombe* ABC1 gene. 129 2e-51
 emb|AL136538|SPAC30 *S.pombe* chromosome I cosmid c30. 144 1e-48
 emb|AI974480|AI974480 T110430e KVO Medicago truncatula cDNA clon... 196 1e-48
 emb|AI495498|AI495498 sa98g09.y1 Gm-c1004 Glycine max cDNA clone... 194 4e-48
 50 emb|AW736468|AW736468 EST332482 KV3 Medicago truncatula cDNA clo... 191 3e-47
 emb|AW677202|AW677202 DG1_6_D10.b1_A002 Dark Grown 1 (DG1) Sorgh... 191 5e-47
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 emb|Z49222|TCPGP2 *T.cruzi* gene for P-glycoprotein. 140 9e-45
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 55 emb|AI777095|AI777095 EST258060 tomato resistant, Cornell Lycope... 177 6e-43
 emb|AQ935847|AQ935847 CpG2684B CpIOWAgDNA1 *Cryptosporidium parvu*... 175 3e-42
 gb|U95956|TCU95956 *Trypanosoma cruzi* P-glycoprotein (tcpgp1A) ge... 130 9e-42
 emb|AW830202|AW830202 sm24a04.y1 Gm-c1028 Glycine max cDNA clone... 172 2e-41
 emb|AL113101|CNS01ALX *Botrytis cinerea* strain T4 cDNA library un... 138 4e-41
 60 emb|AW155943|AW155943 ga22b09.y1 Moss EST library PPU Physcomitr... 167 7e-40
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- emb|AW759534|AW759534 sl44f02.y1 Gm-c1027 Glycine max cDNA clone... 166 9e-40
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 25 emb|AQ646228|AQ646228 RPCI93-DpnII-30J14.TV RPCI93-DpnII Trypano... 141 5e-32
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(2055 letters)

Database: plantfungal

40 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 45 Sequences producing significant alignments: (bits) Value

- emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 356 e-115
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 318 e-100
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 50 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 312 9e-99
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 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 307 4e-95
 55 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 308 1e-93
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 313 2e-93
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 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 310 3e-92
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 60 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 266 1e-90
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- dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 260 1e-89
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5 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 258 3e-87
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emb|Y12530|BOARLKGEN B.oleraceae gene encoding serine/threonine ... 111 1e-83
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emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 109 2e-65
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5 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 161 2e-45
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10 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 65 7e-44
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20 emb|AW597214|AW597214 si71g06.y1 Gm-c1031 Glycine max cDNA clone... 116 1e-40
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gb|U59316|LEU59316 Lycopersicon esculentum serine/threonine prot... 96 2e-40
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http://www.ncgr.org/cgi-bin/ff?ac002387
(1533 letters)

Database: plantfungal
35 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
40 Sequences producing significant alignments: (bits) Value

gb|U82977|CSU82977 Citrus sinensis pectinesterase mRNA, complete... 483 0.0
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45 emb|AF152172|AF152172 Solanum tuberosum cultivar Desiree pectin ... 208 e-111
emb|AF229849|AF229849 Vigna radiata pectin methylesterase isoform... 208 e-107
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55 emb|A17011|A17011 tomato fruit pectin esterase with pPel DNA seq... 190 5e-94
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60 gb|S66607|S66607 Lycopersicon esculentum pectinmethylesterase-li... 190 8e-93
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- emb|A15983|A15983 *L.esculentum* mRNA for pectin esterase. 190 1e-92
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5 emb|A24196|A24196 *L.esculentum* pectin esterase clone pPE1. 188 7e-92
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45 emb|AW758821|AW758821 NXNV_091_A04_F Nsf Xylem Normal wood Verti... 160 8e-62
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emb|AW932254|AW932254 EST358097 tomato fruit mature green, TAMU ... 148 4e-61
50 gb|U82974|CSU82974 *Citrus sinensis* pectinesterase (PECS-1.2) gen... 216 6e-60
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 (825 letters)

30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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35 Score E
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 gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 248 e-112
 40 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase class 4 (p... 201 e-107
 gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 247 1e-97
 dbj|D45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 197 8e-96
 dbj|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 136 6e-95
 dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 136 4e-94
 45 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 227 5e-91
 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 143 5e-91
 emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 164 1e-90
 gb|U52848|DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 137 3e-90
 gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 142 4e-90
 50 emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 158 2e-89
 gb|U52847|DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... 133 4e-89
 emb|X61488|BNCHITIN B.napus mRNA for chitinase. 181 5e-85
 emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 166 2e-84
 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... 164 2e-84
 55 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 185 9e-83
 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 127 8e-80
 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 127 8e-80
 emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 126 2e-78
 gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 167 4e-78
 60 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem Medicago ... 131 5e-78
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- emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 126 2e-77
emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 126 2e-77
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5 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 156 7e-75
emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 215 1e-74
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emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 139 1e-74
10 emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 126 2e-74
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emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 156 4e-72
emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 238 6e-71
emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 126 2e-70
15 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 132 2e-68
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20 emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 215 5e-65
gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 79 2e-64
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25 emb|AI055037|AI055037 coau0002N18 Cotton Boll Abscission Zone cD... 111 3e-60
gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 101 3e-60
gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 100 4e-59
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emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 108 2e-58
30 emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 224 6e-58
emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 224 6e-58
gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 108 2e-57
gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 208 2e-57
emb|AI488583|AI488583 EST246922 tomato ovary, TAMU Lycopersicon ... 126 3e-57
35 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 118 4e-57
emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 221 4e-57
emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 111 1e-56
emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 111 1e-56
emb|AI897391|AI897391 EST266834 tomato ovary, TAMU Lycopersicon ... 126 1e-56
40 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 110 7e-56
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emb|AW676775|AW676775 DG1_14_C09.g1_A002 Dark Grown 1 (DG1) Sorg... 215 3e-55
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45 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 214 7e-55
emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54
emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 110 2e-54
gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 107 5e-54
emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 110 6e-54
50 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 110 7e-54
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gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 105 1e-53
emb|AF043247|AF043247 Solanum tuberosum class I chitinase (ChtC1... 105 1e-53
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gb|L37876|PEACHI2 Pisum sativum chitinase class I (chi2) gene, ... 112 9e-53
emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 112 9e-53
emb|AW029730|AW029730 EST272985 tomato callus, TAMU Lycopersicon... 125 1e-52
gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 205 3e-52
60 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 114 1e-51
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- emb|AF034566|AF034566 *Gossypium hirsutum* class I chitinase mRNA,... 108 2e-51
 emb|AF043248|AF043248 *Solanum tuberosum* class I chitinase (ChtC2... 100 3e-51
 gb|U83592|MSU83592 *Medicago sativa* class I chitinase mRNA, compl... 112 4e-51
 gb|U83591|MSU83591 *Medicago sativa* class I chitinase mRNA, compl... 112 4e-51
 5 emb|Z54234|VVCHIT1MR *V. vinifera* mRNA for chitinase. 102 7e-51
 gb|U02608|STU02608 *Solanum tuberosum* chitinase (chtB4) mRNA, par... 107 1e-50
 emb|X88800|VURNACHI1 *V. unguiculata* mRNA for chitinase class I (p... 107 2e-50
 emb|AF000964|AF000964 *Poa pratensis* chitinase (Chi1) gene, compl... 100 2e-50
 gb|U78888|GHU78888 *Gossypium hirsutum* class I endochitinase mRNA... 103 4e-50
 10 emb|X63899|PSCHITIN *P. sativum* mRNA for chitinase. 94 1e-49
 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 100 7e-49
 gb|BE034450|BE034450 MH05B01 *MH Mesembryanthemum crystallinum* cD... 84 1e-48
 gb|U02287|HVVU02287 *Hordeum vulgare* cultivar NK1558 chitinase gen... 111 3e-48
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 108 6e-48
 15 gb|M15173|TOBECH Tobacco (*N. tabacum*) endochitinase mRNA, partial... 108 6e-48

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 /blast_score 1.00e-166 /ec_number /family /chip nova /gb_link /ncgi
 (825 letters)

Database: plantfungal
 25 661,018 sequences; 426,114,510 total letters

Searching.....done

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|----|---|-------|-------|--------------|
| | | | | (bits) Value |
| 30 | Sequences producing significant alignments: | | | |
| | emb X57187 PVCHITIN <i>P. vulgaris</i> mRNA for chitinase. | 238 | e-123 | |
| | gb U97522 VVU97522 <i>Vitis vinifera</i> class IV endochitinase (VvChi4... | 248 | e-112 | |
| | emb X88803 VURNACHI4 <i>V. unguiculata</i> mRNA for chitinase class 4 (p... | 201 | e-107 | |
| 35 | gb U97521 VVU97521 <i>Vitis vinifera</i> class IV endochitinase (VvChi4... | 247 | 1e-97 | |
| | dbj D45183 D45183 <i>Chenopodium amaranticolor</i> mRNA for chitinase, ... | 197 | 8e-96 | |
| | dbj D45182 D45182 <i>Chenopodium amaranticolor</i> mRNA for chitinase, ... | 136 | 6e-95 | |
| | dbj D45181 D45181 <i>Chenopodium amaranticolor</i> mRNA for chitinase, ... | 136 | 4e-94 | |
| | emb AF112966 AF112966 <i>Triticum aestivum</i> chitinase IV precursor (... | 227 | 5e-91 | |
| 40 | gb U52845 DCU52845 <i>Daucus carota</i> class IV chitinase EP3-1/H5 (EP... | 143 | 5e-91 | |
| | emb AI897733 AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... | 164 | 1e-90 | |
| | gb U52848 DCU52848 <i>Daucus carota</i> class IV chitinase EP3B/E6 (EP3... | 137 | 3e-90 | |
| | gb U52846 DCU52846 <i>Daucus carota</i> class IV chitinase EP3-2/H1 (EP... | 142 | 4e-90 | |
| | emb AI897843 AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... | 158 | 2e-89 | |
| 45 | gb U52847 DCU52847 <i>Daucus carota</i> class IV chitinase EP3-3/E7 (EP... | 133 | 4e-89 | |
| | emb X61488 BNCHITIN <i>B. napus</i> mRNA for chitinase. | 181 | 5e-85 | |
| | emb Z46948 SNCHJET15 <i>S. nigra</i> mRNA for chitinase, pathogenesis-re... | 166 | 2e-84 | |
| | emb AI897217 AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... | 164 | 2e-84 | |
| | gb L25826 BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. | 185 | 9e-83 | |
| 50 | emb X75945 BVCH4RNA <i>B. vulgaris</i> Ch4 mRNA for chitinase. | 127 | 8e-80 | |
| | emb A23392 A23392 <i>B. vulgaris</i> mRNA for chitinase 4 (B15). | 127 | 8e-80 | |
| | emb AI898279 AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... | 126 | 2e-78 | |
| | gb BE034166 BE034166 MG05H02 <i>MG Mesembryanthemum crystallinum</i> cD... | 167 | 4e-78 | |
| | emb AW691007 AW691007 NF036E09ST1F1000 Developing stem <i>Medicago</i> ... | 131 | 5e-78 | |
| 55 | emb AW030814 AW030814 EST274069 tomato callus, TAMU Lycopersicon... | 126 | 1e-77 | |
| | emb AW035013 AW035013 EST279284 tomato callus, TAMU Lycopersicon... | 126 | 2e-77 | |
| | emb AI485982 AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... | 126 | 2e-77 | |
| | gb BE034428 BE034428 MH04G02 <i>MH Mesembryanthemum crystallinum</i> cD... | 170 | 3e-77 | |
| | dbj D45184 D45184 <i>Chenopodium amaranticolor</i> mRNA for chitinase, ... | 136 | 2e-76 | |
| 60 | gb BE034975 BE034975 ML07H10 <i>ML Mesembryanthemum crystallinum</i> cD... | 156 | 7e-75 | |
| | emb AF090336 AF090336 <i>Citrus sinensis</i> chitinase CHI1 (chi1) mRNA... | 215 | 1e-74 | |

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emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 126 2e-74
5 gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 104 3e-74
emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 156 4e-72
emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 238 6e-71
emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 126 2e-70
10 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 132 2e-68
emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 126 3e-68
gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 114 2e-67
emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 154 1e-66
emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 122 5e-66
emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 215 5e-65
15 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 79 2e-64
gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 208 6e-63
emb|AW680953|AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S... 224 7e-63
emb|AI729668|AI729668 BNLGH113889 Six-day Cotton fiber Gossypium... 121 1e-61
emb|AI055037|AI055037 coau0002N18 Cotton Boll Abcission Zone cD... 111 3e-60
20 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 101 3e-60
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emb|AW924422|AW924422 WS1_69_C06.b1_A002 Water-stressed 1 (WS1) ... 171 4e-59
emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 108 2e-58
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25 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 224 6e-58
gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 108 2e-57
gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 208 2e-57
emb|AI488583|AI488583 EST246922 tomato ovary, TAMU Lycopersicon ... 126 3e-57
emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 118 4e-57
30 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 221 4e-57
emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 111 1e-56
emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 111 1e-56
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emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 110 7e-56
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40 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54
emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 110 2e-54
gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 107 5e-54
emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 110 6e-54
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45 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 105 1e-53
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emb|AF043247|AF043247 Solanum tuberosum class I chitinase (ChtC1... 105 1e-53
gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 104 2e-53
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50 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 112 9e-53
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gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 205 3e-52
emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 114 1e-51
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gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 112 4e-51
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60 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 102 7e-51
gb|U02608|STU02608 Solanum tuberosum chitinase (chtB4) mRNA, par... 107 1e-50

emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 107 2e-50
 emb|AF000964|AF000964 Poa pratensis chitinase (Chi1) gene, compl... 100 2e-50
 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 103 4e-50
 emb|X63899|PSCHITIN P.sativum mRNA for chitinase. 94 1e-49
 5 emb|AB015655|AB015655 Cucurbita sp. mRNA for chitinase, complete... 100 7e-49
 gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 84 1e-48
 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 111 3e-48
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 108 6e-48
 10 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 108 6e-48

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 (1788 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AW931942 AW931942	EST357785 tomato fruit mature green, TAMU ...	356 3e-97
30	emb AW218352 AW218352	EST303535 tomato radicle, 5 d post-imbibit...	210 1e-73
	emb AL031966 SPCC1442	S.pombe chromosome III cosmid c1442.	209 6e-69
	emb AW651095 AW651095	EST329549 tomato germinating seedlings, TA...	222 2e-64
	dbj D89256 D89256	Schizosaccharomyces pombe mRNA, partial cds, c...	205 5e-64
	emb AW982499 AW982499	HVSMEg0003G22f Hordeum vulgare pre-anthesi...	215 2e-58
35	emb AW460005 AW460005	si07d11.y1 Gm-c1029 Glycine max cDNA clone...	116 1e-57
	gb U18839 SCE9747	Saccharomyces cerevisiae chromosome V cosmids ...	123 4e-48
	emb X68327 SCTRP2	S.cerevisiae TRP2 gene for anthranilate syntha...	123 4e-48
	emb AW719463 AW719463	LjNEST5b1r Lotus japonicus nodule library,...	184 1e-45
	emb AI736775 AI736775	sb33d01.y1 Gm-c1012 Glycine max cDNA clone...	104 2e-40
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	emb AL032684 SPBP8B7	S.pombe chromosome II p1 p8B7.	95 6e-25
	emb AW509018 AW509018	si39b01.y1 Gm-r1030 Glycine max cDNA clone...	113 5e-24
	gb T14852 T14852	crs299 lambdaZAPST Ricinus communis cDNA clone ...	107 2e-22
	emb AW223881 AW223881	EST300692 tomato fruit red ripe, TAMU Lyco...	103 4e-21
45	emb AF119554 AF119554	Plasmodium falciparum para-aminobenzoic ac...	67 6e-10
	emb AL111470 CNS019CM	Botrytis cinerea strain T4 cDNA library un...	45 2e-05
	emb AI329873 AI329873	b9g02ne.r1 Neurospora crassa evening cDNA ...	48 3e-04
	emb AW224247 AW224247	EST300974 tomato fruit red ripe, TAMU Lyco...	46 7e-04
	emb AF149719 AF149719	Aspergillus fumigatus para aminobenzoic ac...	42 0.012
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	emb AQ160089 AQ160089	mgxb0003G09r CUGI Rice Blast BAC Library P...	39 0.15
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55	emb AQ659747 AQ659747 Sheared DNA-16J5.TR Sheared DNA Trypanosom...	33	9.2
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 (1342 letters)

Database: plantfungal

15 661,018 sequences; 426,114,510 total letters

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25	emb AW729492 AW729492 GA_Ea0025C18 Gossypium arboreum 7-10 dpa ...	291	8e-78	
	emb AW924000 AW924000 WS1_32_E10.b1_A002 Water-stressed 1 (WS1) ...	277	1e-73	
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	emb AW755778 AW755778 sl09c05.y1 Gm-c1036 Glycine max cDNA clone...	248	1e-64	
	emb AW737762 AW737762 EST339189 tomato flower buds, anthesis, Co...	169	1e-60	
30	emb AW621695 AW621695 EST312493 tomato root during/after fruit s...	206	3e-52	
	emb AW350933 AW350933 GM210010B10D11R Gm-r1021 Glycine max cDNA ...	203	3e-51	
	emb AI166669 AI166669 xylem.est.479 Poplar xylem Lambda ZAPII li...	144	3e-50	
	emb AI496468 AI496468 sb08a12.y1 Gm-c1004 Glycine max cDNA clone...	197	2e-49	
35	emb AI774565 AI774565 EST255665 tomato resistant, Cornell Lycopersicon...	192	7e-48	
	emb AW907026 AW907026 EST343253 potato stolon, Cornell Universit...	186	4e-46	
	emb AW423906 AW423906 sh57f06.y1 Gm-c1015 Glycine max cDNA clone...	173	2e-42	
	emb AW458923 AW458923 sh16f03.y1 Gm-c1016 Glycine max cDNA clone...	171	8e-42	
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	emb AW034075 AW034075 EST277570 tomato callus, TAMU Lycopersicon...	150	2e-35	
	emb AI166457 AI166457 xylem.est.288 Poplar xylem Lambda ZAPII li...	145	7e-35	
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5 emb|AF074932|AF074932 Sinapis arvensis 1-aminocyclopropane-1-car... 36 2e-05
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gb|L20634|POTACCSYN Solanum tuberosum 1-aminocyclopropane-1-carb... 36 1e-04
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25 emb|AB033502|AB033502 Populus euphratica peacs-1 mRNA for 1-amin... 42 0.008
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60 emb|AF083814|AF083814 Antirrhinum majus ACC synthase 1 (ACS1) mR... 39 0.11
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(1752 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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emb|AW567653|AW567653 si77b05.y1 Gm-cl031 Glycine max cDNA clone... 55 2e-06
emb|AT000874|AT000874 AT000874 Brassica rapa guard cell Brassica... 46 7e-04
emb|AI563090|AI563090 EST00214 watermelon lambda zap library Cit... 37 0.010
emb|Z74921|BOK8A2 B.oleracea mRNA (unknown). 31 0.26
10 emb|AZ221382|AZ221382 Gm_UMB001_002_A13R UMN Soybean BAC Library... 33 0.65
gb|BE035329|BE035329 MM06C12 MM Mesembryanthemum crystallinum cD... 36 0.71
emb|AW186503|AW186503 se68f07.y1 Gm-cl019 Glycine max cDNA clone... 36 0.97
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emb|AW693662|AW693662 NF067A11ST1F1084 Developing stem Medicago ... 35 1.3
15 emb|AW688978|AW688978 NF014A05ST1F1000 Developing stem Medicago ... 35 1.3
emb|AI374173|AI374173 T6346 MVAT4 bloodstream form of serodeme W... 35 1.3
emb|AW689953|AW689953 NF027B09ST1F1000 Developing stem Medicago ... 35 1.3
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emb|X96770|SCLACHXVI S.cerevisiae chromosome XVI, left arm DNA. 35 1.8
20 emb|X05498|SCSNR17B Yeast SNR17B gene for U3 small nuclear RNA. 35 1.8
emb|Z73500|SCYPL144W S.cerevisiae chromosome XVI reading frame O... 35 1.8
gb|U43703|SCU43703 Saccharomyces cerevisiae chromosome XVI cosmi... 35 1.8
emb|Z73499|SCYPL143W S.cerevisiae chromosome XVI reading frame O... 35 1.8
emb|AJ242498|CCL242498 Candida cloacae mRNA for long chain fatty... 35 1.8
25 emb|AQ949106|AQ949106 Sheared DNA-49L9.TR Sheared DNA Trypanosom... 35 2.5
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emb|Z74965|SCYOR057W S.cerevisiae chromosome XV reading frame OR... 34 3.5
emb|AC007061|AC007061 Leishmania major chromosome 3 clone L1559 ... 34 3.5
30 emb|AQ642037|AQ642037 RPCI93-DpnII-29K3.TJ RPCI93-DpnII Trypanos... 34 3.5
emb|AQ445280|AQ445280 GSSTc01558 Trypanosoma cruzi random genom... 34 3.5
emb|Z70678|SCXV55KB S.cerevisiae chromosome XV DNA, 54.7 kb region. 34 3.5
emb|AQ659145|AQ659145 Sheared DNA-16H2.TF Sheared DNA Trypanosom... 34 3.5
gb|U88830|SCU88830 Saccharomyces cerevisiae Sgt1p (SGT1) gene, c... 34 3.5
35 emb|AC005927|AC005927 Leishmania major chromosome 3 clone L3561 ... 34 3.5
emb|AQ637975|AQ637975 927P1-6A12.TV 927P1 Trypanosoma brucei gen... 34 3.5
emb|AL031744|PFMAL1P1 Plasmodium falciparum chromosome 1 strain ... 29 4.5
emb|AF091345|AF091345 Schizosaccharomyces pombe N-terminal serin... 34 4.7
emb|AC013353|AC013353 Trypanosoma brucei chromosome VI clone RPC... 34 4.7
40 emb|AQ948416|AQ948416 Sheared DNA-38M22.TR Sheared DNA Trypanoso... 34 4.7
emb|AW257222|AW257222 EST305359 KV2 Medicago truncatula cDNA clo... 34 4.7
emb|Y13973|CACIP1 Candida sp. CIP1 gene. 34 4.7
emb|AL031263|SPBC17F3 S.pombe chromosome II cosmid c17F3... 34 4.7
emb|AF152552|AF152552 Sorghum bicolor chalcone synthase 5 (CHS5)... 34 4.7
45 emb|AQ655690|AQ655690 Sheared DNA-9G1.TR Sheared DNA Trypanosoma... 34 4.7
emb|AZ212373|AZ212373 Sheared DNA-101E1.TF Sheared DNA Trypanoso... 34 4.7
emb|AJ250726|TBR250726 Trypanosoma brucei HSP100 gene, GPI-PLC g... 34 4.7
gb|M17420|YSTHEP Saccharomyces cerevisiae heptapeptide repeat re... 33 6.5
emb|AI730517|AI730517 BNLGHi6942 Six-day Cotton fiber Gossypium ... 33 6.5
50 emb|Z49511|SCYJR011C S.cerevisiae chromosome X reading frame ORF... 33 6.5
gb|U59312|HVVU59312 Hordeum vulgare (1,4)-beta-xylan endohydrolas... 33 6.5
emb|Z74188|SCYDL140C S.cerevisiae chromosome IV reading frame OR... 33 6.5
emb|X87611|SCXCOSM83 S.cerevisiae chromosome X DNA (cosmid 83). 33 6.5
emb|AA003500|AA003500 T3189 MVAT4 bloodstream form of serodeme W... 33 6.5
55 emb|AQ951709|AQ951709 Sheared DNA-51E22.TF Sheared DNA Trypanoso... 33 6.5

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gb|aac36163.1| (ac005314) putative serpin [arabidopsis thaliana]
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60 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005314|/ncgi
http://www.ncgr.org/cgi-bin/ff?ac005314

(1125 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5

Searching.....done

	Score	E	(bits)	Value
10	Sequences producing significant alignments:			
	emb Y11486 TASERPIN T.aestivum mRNA for serpin WZS3.	112	2e-68	
	emb AJ245879 TAE245879 Triticum aestivum mRNA for serpin (WSZ2a ...	113	7e-66	
	emb AJ245878 TAE245878 Triticum aestivum mRNA for serpin (WSZ1c ...	116	2e-65	
	emb Y11485 TAESERPIN T.aestivum mRNA for serpin WZS2.	116	2e-62	
15	emb Z49890 TAWZCISPIN T.aestivum WZCI mRNA for serpin.	109	3e-60	
	emb X95277 HVSEH H.vulgare mRNA for serpin.	98	6e-58	
	emb AW458573 AW458573 sh10h03.y1 Gm-cl016 Glycine max cDNA clone...	115	6e-55	
	emb X97636 HVSEH H.vulgare mRNA for serpin.	96	2e-44	
	emb AW598408 AW598408 sj91a11.y1 Gm-cl023 Glycine max cDNA clone...	144	2e-43	
20	gb BE058355 BE058355 sn15a03.y1 Gm-cl016 Glycine max cDNA clone ...	134	3e-40	
	emb AW688254 AW688254 NF005C03ST1F1000 Developing stem Medicago ...	127	7e-38	
	emb Z15116 HVPAXXG H.vulgare pazx gene encoding protein zx.	80	6e-32	
	emb AF118560 AF118560 Avena fatua barley protein Z homolog mRNA,...	73	7e-32	
	emb AW394511 AW394511 sh33b01.y1 Gm-cl017 Glycine max cDNA clone...	81	2e-31	
25	emb AI730301 AI730301 BNLGHi6607 Six-day Cotton fiber Gossypium ...	77	8e-31	
	emb AI725411 AI725411 BNLGHi11751 Six-day Cotton fiber Gossypium...	55	9e-30	
	emb AV420945 AV420945 AV420945 Lotus japonicus young plants (two...	126	4e-28	
	emb AI772215 AI772215 EST253315 tomato resistant, Cornell Lycopersicon...	116	6e-27	
	emb X51726 HVPAXZ1 Barley Paz1 gene for protein Z.	76	3e-26	
30	emb AW219573 AW219573 EST302055 tomato root during/after fruit s...	83	4e-26	
	emb AI726323 AI726323 BNLGHi5614 Six-day Cotton fiber Gossypium ...	112	8e-26	
	emb AW926241 AW926241 HVSMeg0006L04 Hordeum vulgare pre-anthesis...	117	2e-25	
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	emb AW725528 AW725528 GA_Ea0018H14 Gossypium arboreum 7-10 dpa ...	73	6e-24	
35	emb AV408545 AV408545 AV408545 Lotus japonicus young plants (two...	68	9e-22	
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	emb AW983183 AW983183 HVSMeg0008J04f Hordeum vulgare pre-anthesi...	64	2e-21	
	emb AW728267 AW728267 GA_Ea0016C18 Gossypium arboreum 7-10 dpa ...	102	4e-21	
	emb AW099940 AW099940 sd18f07.y2 Gm-cl012 Glycine max cDNA clone...	57	5e-18	
40	emb AW720162 AW720162 LjNEST16a4r Lotus japonicus nodule library...	84	1e-15	
	emb AW598800 AW598800 ga88d04.y1 Moss EST library PPU Physcomit...	84	3e-15	
	gb BE058596 BE058596 sn18b11.y1 Gm-cl016 Glycine max cDNA clone ...	48	7e-14	
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	emb AQ917127 AQ917127 T233156b Medicago truncatula BAC library M...	47	3e-09	
	emb AW306929 AW306929 sf50e08.y1 Gm-cl009 Glycine max cDNA clone...	56	4e-08	
50	emb AW010023 AW010023 ST01E04 Pine TriplEx shoot tip library Pin...	41	1e-07	
	emb X51727 HVPAXPSE Barley DNA for pseudogene PAZ.	51	3e-07	
	gb BE022668 BE022668 sm75h09.y1 Gm-cl015 Glycine max cDNA clone ...	56	7e-07	
	emb X05902 HVPROTZ Barley mRNA fragment for protein Z.	46	8e-07	
	emb AW102228 AW102228 sd85a05.y1 Gm-cl009 Glycine max cDNA clone...	48	7e-06	
55	emb AI779352 AI779352 EST260231 tomato susceptible, Cornell Lyco...	51	1e-05	
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	emb AW599056 AW599056 gb01e09.y1 Moss EST library PPN Physcomit...	50	3e-05	
	emb AV414917 AV414917 AV414917 Lotus japonicus young plants (two...	50	3e-05	
60	emb AW738877 AW738877 gb03f10.y1 Moss EST library PPN Physcomit...	42	0.002	
	emb AW693477 AW693477 NF065F09ST1F1000 Developing stem Medicago ...	42	0.010	

- emb|AW905918|AW905918 EST342091 potato stolon, Cornell Universit... 35 0.81
 emb|Z49939|SC9959 *S.cerevisiae* chromosome XIII cosmid 9959. 35 1.5
 gb|BE059186|BE059186 sn27d04.y1 *Gm-c1016 Glycine max* cDNA clone ... 35 1.5
 5 emb|AW119311|AW119311 A57 *Neospora caninum* Lambda Zap cDNA libra... 34 2.1
 emb|AL114606|CNS01BRQ *Botrytis cinerea* strain T4 cDNA library un... 34 2.1
 emb|AL114185|CNS01BG1 *Botrytis cinerea* strain T4 cDNA library un... 34 2.1
 emb|AL114991|CNS01C2F *Botrytis cinerea* strain T4 cDNA library un... 34 2.1
 emb|AQ367717|AQ367717 tox0002L20r CUGI Tomato BAC Library Lycop... 34 2.1
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 10 emb|AL115273|CNS01CA9 *Botrytis cinerea* strain T4 cDNA library un... 34 2.1
 emb|AL113815|CNS01B5R *Botrytis cinerea* strain T4 cDNA library un... 34 2.1
 emb|AI490380|AI490380 EST248706 tomato ovary, TAMU Lycopersicon ... 34 2.9
 emb|AL116919|CNS01DJZ *Botrytis cinerea* strain T4 cDNA library un... 34 2.9
 gb|U68716|BFU68716 *Botryotinia fuckeliana* endopolygalacturonase ... 33 4.0
 15 gb|L25681|HYBRG18S *Hydnora africana* Thunb. 18S ribosomal RNA (18... 33 4.0
 emb|AI165169|AI165169 A077P18U Hybrid aspen plasmid library Popu... 33 4.0
 gb|BE020501|BE020501 sm44e08.y1 *Gm-c1028 Glycine max* cDNA clone ... 33 5.5
 gb|M55639|AURRR16S *Aureobasidium pullulans* 16S-like ribosomal RN... 33 5.5
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 20 emb|AI494738|AI494738 sb14f02.y1 *Gm-c1004 Glycine max* cDNA clone... 33 5.5
 gb|M35065|BLYPROZ *Barley* protein Z mRNA, partial cds. 33 5.5
 emb|AV409233|AV409233 *Lotus japonicus* young plants (two... 26 6.2
 emb|AJ273043|AJ273043 AJ273043 *Metarhizium anisopliae* ARSEF 2575... 32 7.5
 emb|AF106529|AF106529 *Monacrosporium leptosporum* 18S small subun... 32 7.5
 25 emb|AW569360|AW569360 si86a11.y1 *Gm-c1031 Glycine max* cDNA clone... 32 7.5
 emb|X51599|NTCHN50 Tobacco CHN50 gene for endochitinase. 32 7.5
 emb|AL356192|NCB24B19 *Neurospora crassa* DNA linkage group II BAC... 32 7.5
 emb|AF123288|AF123288 *Lagynion scherffellii* small subunit ribosom... 32 7.5
 emb|AW180275|AW180275 MgA0367f MgA Library *Mycosphaerella gramin...* 32 7.5
 30 emb|AL356172|NCB23L21 *Neurospora crassa* DNA linkage group II BAC... 32 7.5
 emb|AI779615|AI779615 EST260494 tomato susceptible, Cornell Lyco... 32 7.5
 emb|X64519|NTCHN50G *N.tabacum* chitinase gene 50 for class I chit... 32 7.5
 emb|AF123299|AF123299 *Chrysosphaera parvula* small subunit riboso... 32 7.5
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 emb|A72838|A72838 Sequence 1 from Patent WO9505467. 314 e-138
 emb|X77110|NTCHIVR *N.tabacum* chi-V mRNA for chitinase class V. 312 e-137
 55 emb|AF088885|AF088885 *Nicotiana tabacum* receptor-like kinase CHR... 189 3e-84
 emb|X77111|NTCHIVD *N.tabacum* chi-V gene. 204 1e-69
 emb|A72844|A72844 Sequence 7 from Patent WO9505467. 204 7e-69
 emb|AW690230|AW690230 NF030F05ST1F1000 Developing stem *Medicago* ... 139 4e-66
 emb|AF108893|AF108893 AF108893 *Capsicum annuum* root 1st-branched... 201 7e-51
 60 emb|AW032116|AW032116 EST275570 tomato callus, TAMU Lycopersicon... 186 2e-46
 emb|AW560415|AW560415 EST315463 DSIR *Medicago truncatula* cDNA cl... 169 3e-41

- emb|AW351251|AW351251 GM210011A20A4R Gm-r1021 Glycine max cDNA 3... 145 6e-34
- emb|AV423067|AV423067 AV423067 Lotus japonicus young plants (two... 129 2e-32
- emb|AV412385|AV412385 AV412385 Lotus japonicus young plants (two... 129 4e-29
- 5 emb|AV411642|AV411642 AV411642 Lotus japonicus young plants (two... 84 3e-28
- emb|AI495953|AI495953 sb18c04.y1 Gm-c1004 Glycine max cDNA clone... 111 1e-23
- emb|AV422006|AV422006 AV422006 Lotus japonicus young plants (two... 75 3e-21
- emb|AF188932|AF188932 Hypocrea rufa strain Hy9 42 kDa endochitin... 68 1e-20
- emb|AF188921|AF188921 Trichoderma atroviride strain DAOM 165782 ... 70 3e-20
- 10 gb|U49455|THU49455 Trichoderma harzianum endochitinase (chi1) mR... 69 3e-20
- emb|AF188918|AF188918 Hypocrea koningii 42 kDa endochitinase gen... 71 3e-20
- emb|AF188930|AF188930 Trichoderma asperellum strain CBS 361.97, ... 68 6e-20
- emb|AF188926|AF188926 Trichoderma asperellum strain GJS 90-14 42... 68 6e-20
- emb|AF188923|AF188923 Hypocrea rufa strain GJS 89-142 42 kDa end... 68 8e-20
- 15 emb|X79381|THECH42 T.harzianum (IMI 206040) ech-42 gene. 68 9e-20
- gb|L14614|TRREDOCHI Trichoderma harzianum endochitinase mRNA, c... 68 9e-20
- emb|AF188920|AF188920 Trichoderma atroviride strain DAOM 165779 ... 68 9e-20
- emb|AF188929|AF188929 Trichoderma asperellum strain CBS 433.97, ... 68 9e-20
- emb|AF188933|AF188933 Trichoderma asperellum strain BBA 68646R 4... 68 9e-20
- 20 gb|S78423|S78423 chit42=endochitinase [Trichoderma harzianum, mR... 67 9e-20
- gb|U88560|THU88560 Trichoderma hamatum endochitinase gene, compl... 68 1e-19
- emb|AF188931|AF188931 Hypocrea vinosa 42 kDa endochitinase gene, ... 68 1e-19
- emb|AF188927|AF188927 Trichoderma viride strain GJS 90-20 42 kDa... 68 2e-19
- gb|U33265|CIU33265 Coccidioides immitis complement fixation/chit... 60 2e-19
- 25 gb|U60807|CIU60807 Coccidioides immitis complement fixation-chit... 60 3e-19
- emb|AF188924|AF188924 Trichoderma viride strain ATCC 32630, syno... 68 4e-19
- emb|AF188928|AF188928 Trichoderma viride strain BBA 66069R 42 kD... 68 4e-19
- emb|AF188925|AF188925 Trichoderma viride strain Tr6 42 kDa endoc... 68 4e-19
- emb|AF188919|AF188919 Trichoderma viride strain ATCC 18652, syno... 66 2e-18
- 30 emb|AF188922|AF188922 Hypocrea rufa strain GJS 89-127 42 kDa end... 66 3e-18
- emb|AF050098|AF050098 Trichoderma virens chitinase gene, complet... 65 2e-17
- emb|X64104|AACH11A A.album chi1 gene for chitinase. 65 3e-17
- emb|AJ243014|MFL243014 Metarhizium flavoviride mRNA for chitinas... 62 8e-17
- emb|AF027498|AF027498 Metarhizium anisopliae chitinase CHIT42 (C... 60 9e-16
- 35 emb|AF027497|AF027497 Metarhizium anisopliae chitinase CHIT42 (C... 60 9e-16
- emb|AI967677|AI967677 Ljirnp08-687-g4 Ljirnp Lambda HybriZap ... 72 5e-14
- emb|AV421624|AV421624 AV421624 Lotus japonicus young plants (two... 63 2e-13
- emb|AI899627|AI899627 EST269070 tomato susceptible, Cornell Lyco... 75 1e-12
- dbj|D87894|D87894 Rhizopus oligosporus DNA for chitinase, comple... 59 2e-10
- 40 emb|AV407063|AV407063 AV407063 Lotus japonicus young plants (two... 68 2e-10
- emb|AF009354|AF009354 Leishmania donovani chitinase (Chi-1) gene... 57 4e-09
- emb|AA786967|AA786967 m7d11a1.r1 Aspergillus nidulans 24hr asexu... 54 5e-09
- emb|AA966331|AA966331 w4a12a1.r1 Aspergillus nidulans 24hr asexu... 54 5e-09
- emb|AI212420|AI212420 x5f11a1.r1 Aspergillus nidulans 24hr asexu... 43 6e-08
- 45 emb|AI210660|AI210660 k0b03a1.r1 Aspergillus nidulans 24hr asexu... 53 1e-07
- emb|AA785435|AA785435 g7d04a1.r1 Aspergillus nidulans 24hr asexu... 54 2e-07
- emb|AA787768|AA787768 r1d06a1.r1 Aspergillus nidulans 24hr asexu... 46 2e-06
- emb|AA784794|AA784794 g2d07a1.r1 Aspergillus nidulans 24hr asexu... 43 2e-06
- gb|L41663|COICTS1CHI Coccidioides immitis chitinase (cts1) gene, ... 44 5e-06
- 50 gb|U51271|CIU51271 Coccidioides immitis complement-fixation anti... 44 5e-06
- gb|U60806|CIU60806 Coccidioides immitis complement-fixation chit... 44 5e-06
- emb|AI213337|AI213337 z1b11a1.r1 Aspergillus nidulans 24hr asexu... 50 7e-06
- emb|AI211269|AI211269 o0h07a1.r1 Aspergillus nidulans 24hr asexu... 43 1e-05
- emb|AW334147|AW334147 S31A10 AGS-1 Pneumocystis carinii f. sp. c... 51 1e-05
- 55 emb|Z71415|THENDOCHS T.hamatum endochitinase gene. 50 3e-05
- emb|AA786295|AA786295 l3d02a1.r1 Aspergillus nidulans 24hr asexu... 31 6e-05
- emb|AI209456|AI209456 a0h06a1.r1 Aspergillus nidulans 24hr asexu... 43 6e-05
- gb|M11815|YSKGL1A Plasmid pGKL1 from killer yeast (K.lactis), c... 39 1e-04
- emb|X01095|KLKILL1L Yeast DNA killer plasmid pGKL1. 39 1e-04
- 60 emb|X00762|KLKILL05 Kluyveromyces lactis (killer strain) plasmid... 39 1e-04
- emb|X07127|KLKIP Kluyveromyces lactis killer plasmid k1 DNA. 39 1e-04

	emb X89212	MADNACHIA M.anisopliae DNA for ChiA gene.	48	1e-04
	emb A86212	A86212 Sequence 871 from Patent EP0866129.	48	2e-04
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20	emb AW108998	AW108998 gate0002M02f Gossypium arboreum 7-10 dpa f...	34	2.1
	emb AI727383	AI727383 BNLGHi7901 Six-day Cotton fiber Gossypium ...	34	2.1
	emb AL353817	NC1A9 Neurospora crassa DNA linkage group V Cosmid ...	34	2.9
	emb AI730373	AI730373 BNLGHi6756 Six-day Cotton fiber Gossypium ...	34	2.9
	emb AJ273533	AJ273533 Metarhizium anisopliae ARSEF 2575...	33	4.0
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	emb AF006311	AF006311 Cookeina tricholoma 18S ribosomal RNA gene...	32	4.2
	emb AW625979	AW625979 EST319874 tomato radicle, 5 d post-imbibit...	33	5.5
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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45	emb AI894928	AI894928 EST264371 tomato callus, TAMU Lycopersicon...	59	4e-11
	emb AW621748	AW621748 EST312546 tomato root during/after fruit s...	62	1e-08
	emb AW991081	AW991081 SsS0293 Suaeda salsa ZAP cDNA library Suae...	58	3e-07
	emb AI896054	AI896054 EST265497 tomato callus, TAMU Lycopersicon...	55	2e-06
	emb AW932874	AW932874 EST358717 tomato fruit mature green, TAMU ...	54	3e-06
50	emb AW035961	AW035961 EST282820 tomato callus, TAMU Lycopersicon...	53	5e-06
	emb AW217271	AW217271 EST295985 tomato callus, TAMU Lycopersicon...	51	3e-05
	emb AI736949	AI736949 sb35a01.y1 Gm-c1013 Glycine max cDNA clone...	45	6e-05
	emb AI729969	AI729969 BNLGHi5823 Six-day Cotton fiber Gossypium ...	41	8e-05
	gb BE033853	BE033853 MG01B02 MG Mesembryanthemum crystallinum cD...	49	1e-04
55	emb AZ124241	AZ124241 T223105b Medicago truncatula BAC library M...	47	4e-04
	emb AI729861	AI729861 BNLGHi5428 Six-day Cotton fiber Gossypium ...	44	0.005
	emb AW623353	AW623353 EST321298 tomato flower buds 3-8 mm, Come...	44	0.005
	emb AZ124239	AZ124239 T223103b Medicago truncatula BAC library M...	44	0.005
	emb AI166315	AI166315 xylem.est.16 Poplar xylem Lambda ZAPII lib...	42	0.013
60	emb AW219421	AW219421 EST301999 tomato root during/after fruit s...	42	0.013
	emb AI974296	AI974296 T110298e KV0 Medicago truncatula cDNA clon...	42	0.013

	emb AI054990 AI054990 coau0002L09 Cotton Boll Abscission Zone cD...	40	0.037
	emb AW929405 AW929405 EST338193 tomato flower buds 8 mm to pre-a...	39	0.17
	emb AW649475 AW649475 EST327929 tomato germinating seedlings, TA...	39	0.17
	emb AW222512 AW222512 EST299323 tomato fruit red ripe, TAMU Lyco...	38	0.23
5	emb AW222518 AW222518 EST299329 tomato fruit red ripe, TAMU Lyco...	38	0.23
	emb AI781303 AI781303 EST262182 tomato susceptible, Cornell Lyco...	38	0.23
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20	emb AW283124 AW283124 LG1_224_H10.g1_A002 Light Grown 1 (LG1) So...	35	1.6
	emb AI054715 AI054715 coau0001M19 Cotton Boll Abscission Zone cD...	35	1.6
	emb Y10579 VFPOTCHAN V.faba mRNA for potassium channel.	29	1.7
	emb AQ935638 AQ935638 CpG2573A CplOWAgDNA1 Cryptosporidium parvu...	35	2.1
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25	emb X73850 BNPNL3 B.napus (pNL3) mRNA for acyl-ACP-thioesterase.	35	2.9
	emb AL096797 SPBC146 S.pombe chromosome II cosmid c146.	35	2.9
	emb X87842 BNDNAFATA B.napus FatA gene.	35	2.9
	emb AF073683 073693S155 Tinguarra sicula internal transcribed sp...	35	2.9
	dbj D30788 YSPCUT3B Schizosaccharomyces pombe gene for cut3 prot...	35	2.9
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35	emb AA680502 AA680502 T3691 Bloodstream form of serodeme ILTat1....	34	4.0
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40	emb AW145916 AW145916 ga35g12.y1 Moss EST library PPN Physcomitr...	34	5.5
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55	emb AW694856 AW694856 NF080G09ST1F1071 Developing stem Medicago ...	33	7.6
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(864 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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emb|AI485362|AI485362 EST243683 tomato ovary, TAMU Lycopersicon ... 67 1e-25

emb|AI483886|AI483886 EST249757 tomato ovary, TAMU Lycopersicon ... 68 1e-25

emb|AW030869|AW030869 EST274159 tomato callus, TAMU Lycopersicon... 68 5e-24

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emb|AI897376|AI897376 EST266819 tomato ovary, TAMU Lycopersicon ... 68 5e-22

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15 emb|AW729218|AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ... 51 1e-13
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 (1890 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AW560074 AW560074 EST315122 DSIR Medicago truncatula cDNA cl...	84	6e-23
	emb AI855891 AI855891 sc30h08.y1 Gm-c1014 Glycine max cDNA clone...	100	4e-21
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	emb AW736866 AW736866 NXNV_083_H05_F Nsf Xylem Normal wood Verti...	52	2e-05
	emb AW775153 AW775153 EST334304 KV3 Medicago truncatula cDNA clo...	51	4e-05
55	emb AV411498 AV411498 AV411498 Lotus japonicus young plants (two...	47	5e-04
	emb AW934555 AW934555 EST353447 tomato flower buds 0-3 mm, Corné...	36	9e-04
	emb AW010126 AW010126 ST02C06 Pine TriplEx shoot tip library Pin...	46	0.001
	emb AW031593 AW031593 EST275047 tomato callus, TAMU Lycopersicon...	31	0.001
	emb AW746715 AW746715 WS1_55_B02.b1_A002 Water-stressed 1 (WS1)...	39	0.001
60	emb AW720513 AW720513 LjNEST18e1r Lotus japonicus nodule library...	46	0.001
	emb AW773847 AW773847 EST332833 KV3 Medicago truncatula cDNA clo...	35	0.004

	emb AZ051219 AZ051219 Gm_UMb001_062_F16R UMN Soybean BAC Library...	38	0.006
	emb AW684275 AW684275 NF014H05NR1F1000 Nodulated root Medicago t...	43	0.007
	emb AW043221 AW043221 ST30G04 Pine TriplEx shoot tip library Pin...	43	0.007
	emb AW687647 AW687647 NF011F10RT1F1090 Developing root Medicago ...	35	0.019
5	emb AW560122 AW560122 EST315170 DSIR Medicago truncatula cDNA cl...	35	0.019
	emb AW687408 AW687408 NF009C08RT1F1065 Developing root Medicago ...	35	0.019
	emb AW980840 AW980840 EST391993 GVN Medicago truncatula cDNA clo...	35	0.019
	emb AW560121 AW560121 EST315169 DSIR Medicago truncatula cDNA cl...	35	0.019
	gb BE123705 BE123705 NXNV_151_H02_F Nsf Xylem Normal wood Vertic...	41	0.032
10	emb AI781175 AI781175 EST262054 tomato susceptible, Cornell Lyco...	40	0.060
	emb AW616497 AW616497 EST322908 L. hirsutum trichome, Cornell Un...	31	0.063
	emb AZ214029 AZ214029 Sheared DNA-77H12.TF Sheared DNA Trypanoso...	40	0.083
	emb AW693887 AW693887 NF070B08ST1F1064 Developing stem Medicago ...	40	0.083
	emb AZ214023 AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso...	38	0.22
15	emb AI487450 AI487450 EST245772 tomato ovary, TAMU Lycopersicon ...	37	0.41
	emb AI780239 AI780239 EST261118 tomato susceptible, Cornell Lyco...	37	0.41
	emb AI485040 AI485040 EST243320 tomato ovary, TAMU Lycopersicon ...	37	0.41
	emb AW618666 AW618666 EST320652 L. pennellii trichome, Cornell U...	28	0.52
	emb AZ213147 AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso...	35	0.53
20	emb AW698283 AW698283 NXNV_071_C12_F Nsf Xylem Normal wood Verti...	33	0.53
	emb AW690496 AW690496 NF035B12ST1F1000 Developing stem Medicago ...	37	0.56
	emb AW693913 AW693913 NF070E02ST1F1017 Developing stem Medicago ...	37	0.56
	emb AW686233 AW686233 NF035E09NR1F1000 Nodulated root Medicago t...	37	0.56
	emb AW257090 AW257090 EST305227 KV2 Medicago truncatula cDNA clo...	37	0.56
25	emb AW573732 AW573732 EST316323 GVN Medicago truncatula cDNA clo...	37	0.56
	emb AW559393 AW559393 EST314441 DSIR Medicago truncatula cDNA cl...	37	0.56
	emb AW329638 AW329638 N200899e rootphos(-) Medicago truncatula c...	36	0.77
	gb BE123796 BE123796 NXNV_156_E06_F Nsf Xylem Normal wood Vertic...	27	0.96
	emb AW257266 AW257266 EST305403 KV2 Medicago truncatula cDNA clo...	36	1.1
30	emb AW317531 AW317531 sg51e11.y1 Gm-c1025 Glycine max cDNA clone...	33	1.3
	emb AC009259 AC009259 Trypanosoma brucei chromosome VI clone RPC...	35	1.4
	emb AW702888 AW702888 TgESTzz91a12.y1 TgRH*-Tachyzoite cDNA Toxo...	35	1.4
	emb AF013339 AF013339 Cucurbita moschata clone 3 internal transc...	35	1.4
	emb AW704685 AW704685 sk39c02.y1 Gm-c1028 Glycine max cDNA clone...	35	1.4
35	emb AQ650196 AQ650196 Sheared DNA-18B3.TF Sheared DNA Trypanosom...	35	1.4
	emb AW685575 AW685575 NF029B05NR1F1000 Nodulated root Medicago t...	35	2.0
	emb AW773999 AW773999 EST332985 KV3 Medicago truncatula cDNA clo...	35	2.0
	emb Z38060 Z38060 S.cerevisiae chromosome IX sequence derived fr...	35	2.0
	emb AW033298 AW033298 EST276869 tomato callus, TAMU Lycopersicon ...	35	2.0
40	gb L36822 SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas...	35	2.0
	emb AQ952285 AQ952285 Sheared DNA-39M20.TF Sheared DNA Trypanoso...	35	2.0
	emb AI812757 AI812757 18G10 Pine Lambda Zap Xylem library Pinus ...	30	2.3
	emb AI441832 AI441832 sa47h09.y1 Gm-c1004 Glycine max cDNA clone...	35	2.7
	emb AW694970 AW694970 NF082B02ST1F1015 Developing stem Medicago ...	31	3.1
45	emb AW685287 AW685287 NF027B11NR1F1000 Nodulated root Medicago t...	31	3.1
	emb AW932856 AW932856 EST358699 tomato fruit mature green, TAMU ...	34	3.8
	emb AF013320 AF013320 Cucurbita fraterna clone 2 internal transc...	34	3.8
	emb AW719424 AW719424 LjNEST4d11r Lotus japonicus nodule library...	29	4.2
	emb X90770 LEMSREPRG L.esculentum microsatellite repeat DNA region.	34	5.2
50	emb AW133354 AW133354 se17h02.y1 Gm-c1013 Glycine max cDNA clone...	34	5.2
	emb AI967637 AI967637 Ljirmp08-639-b9 Ljirmp Lambda HybriZap ...	34	5.2
	emb AW156054 AW156054 ga24c05.y1 Moss EST library PPU Physcomitr...	34	5.2
	emb AF053127 AF053127 Malus domestica leucine-rich receptor-like...	34	5.2
	emb AB000394 AB000394 Ipomoea purpurea DNA, LTR retrotransposon ...	34	5.2
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	from this gene." /blast_score 9.00e-78 /ec_number /family /chip nova		
60	/gb_link http://www3.ncbi.nlm.nih.gov/htbin-		
	post/entrez/query?db=n&form=6&dopt=g&uid=gb x91919 /ncgi		

<http://www.ncgr.org/cgi-bin/ff?x91919>
(762 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E		(bits)	Value
10	Sequences producing significant alignments:				
	emb AJ224519 CAR224519	Cicer arietinum mRNA for LEA protein (clo...	148	6e-35	
	emb X15348 BNLEA76	Brassica napus LEA76 mRNA for late embryogene...	135	4e-31	
	emb AF117884 AF117884	Glycine max seed maturation protein PM30 (...	88	1e-30	
15	emb AJ224518 CAR224518	Cicer arietinum mRNA for LEA protein (clo...	126	2e-28	
	emb AW472097 AW472097	si20a05.y1 Gm-c1029 Glycine max cDNA clone...	86	9e-27	
	emb AW395529 AW395529	sg72c09.y1 Gm-c1007 Glycine max cDNA clone...	88	7e-24	
	emb AW507599 AW507599	si53h08.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24	
	emb AW318205 AW318205	sg62d04.y1 Gm-c1007 Glycine max cDNA clone...	88	7e-24	
20	emb AW568476 AW568476	si59c06.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24	
	emb AW567816 AW567816	si66b10.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24	
	emb AW706800 AW706800	sk03e03.y1 Gm-c1023 Glycine max cDNA clone...	88	1e-23	
	emb AW509384 AW509384	si22d10.y1 Gm-c1029 Glycine max cDNA clone...	86	2e-23	
	emb AW746690 AW746690	WS1_54_F07.g1_A002 Water-stressed 1 (WS1) ...	106	2e-22	
25	emb AW096396 AW096396	EST289576 tomato mixed elicitor, BTI Lycop...	103	1e-21	
	emb X78205 HVHVA1	H. vulgare (Himalaya) HVA1 gene.	77	1e-20	
	emb X13498 HVABAIP	Barley pHVA1 mRNA for an ABA-inducible protein.	77	1e-20	
	gb M36000 BLYABA	Barley abscisic acid (ABA) mRNA, complete cds.	77	1e-20	
	emb AW680076 AW680076	WS1_3_C03.g1_A002 Water-stressed 1 (WS1) S...	100	2e-20	
30	emb AW397921 AW397921	sg69h06.y1 Gm-c1007 Glycine max cDNA clone...	57	3e-20	
	emb AW747095 AW747095	WS1_65_C09.g1_A002 Water-stressed 1 (WS1) ...	95	4e-19	
	gb BE034388 BE034388	MH04B06 MH Mesembryanthemum crystallinum cD...	73	1e-18	
	emb X13201 GHLEA7	Cotton set 5A Lea gene for seed protein D-7.	61	1e-18	
	emb X15086 GHLEA29R	Cotton set 5A Lea mRNA for seed protein D-29.	61	1e-18	
35	emb X56882 TA3LEA	Wheat mRNA for a group 3 late embryogenesis ab...	75	1e-18	
	emb AW746385 AW746385	WS1_49_G03.g1_A002 Water-stressed 1 (WS1) ...	93	2e-18	
	emb AW680063 AW680063	WS1_3_B02.g1_A002 Water-stressed 1 (WS1) S...	91	1e-17	
	emb AF255052 AF255052	Triticum aestivum cold-responsive LEA/RAB-...	85	6e-17	
	emb AF139915 AF139915	Triticum aestivum ABA-inducible protein WR...	85	6e-17	
40	emb AW164114 AW164114	Ljirmp20-575-b9 Ljirmp Lambda HybriZap ...	88	7e-17	
	emb Y10779 SSY10779	S.stapfianus pSD.42 mRNA.	86	3e-16	
	emb AW569002 AW569002	si62c03.y1 Gm-r1030 Glycine max cDNA clone...	62	4e-16	
	emb AW508284 AW508284	si52b01.y1 Gm-r1030 Glycine max cDNA clone...	62	4e-16	
	gb BE034389 BE034389	MH04B07 MH Mesembryanthemum crystallinum cD...	72	7e-16	
45	emb AW681055 AW681055	WS1_8_F06.b1_A002 Water-stressed 1 (WS1) S...	75	7e-13	
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	emb AW678335 AW678335	WS1_14_F02.g1_A002 Water-stressed 1 (WS1) ...	75	7e-13	
	emb AW678291 AW678291	WS1_14_D10.g1_A002 Water-stressed 1 (WS1) ...	74	1e-12	
	emb AW679525 AW679525	WS1_29_F04.g1_A002 Water-stressed 1 (WS1) ...	74	1e-12	
50	emb Z18891 BPBP8GEN	Betula pendula BP8 gene.	74	1e-12	
	emb AW432699 AW432699	sh85b12.y1 Gm-c1016 Glycine max cDNA clone...	74	1e-12	
	emb AW678194 AW678194	WS1_13_E06.g1_A002 Water-stressed 1 (WS1) ...	72	5e-12	
	emb AW459847 AW459847	sh96a04.y1 Gm-c1016 Glycine max cDNA clone...	70	2e-11	
	emb X13203 GHLEA29	Cotton set 5A Lea gene for seed protein D-29.	62	5e-09	
55	emb Z49713 PMDORORF6	P.menziesii mRNA (open reading frame) (DF77B).	59	3e-08	
	emb Z49712 PMDORORF5	P.menziesii mRNA (open reading frame) (DF77A).	59	3e-08	
	emb AJ225460 AJ225460	AJ225460 Abscisic acid-treated protonemata...	59	5e-08	
	emb X89041 RFLASPPRO	R.fluitans mRNA for landform specific protein.	58	6e-08	
	gb M80664 SOYLEAB	Soybean late embryogenesis abundant (LEA) prot...	58	9e-08	
60	emb AF166485 AF166485	Glycine max maturation protein pPM32 (PM32...	57	2e-07	
	gb M19388 COTSPG	G.hirsutum (cotton) storage protein (late embry...	57	2e-07	

- gb|U47096|DCU47096 *Daucus carota* LEA protein mRNA, somatic embry... 57 2e-07
 gb|U02966|GMU02966 *Glycine max* Shi-shi 51 kDa seed maturation pr... 56 3e-07
 emb|Z49715|PMDORORF8 *P.menziesii* mRNA (open reading frame) (DF77D). 56 4e-07
 gb|L47932|L47932 BNAF1873 Mustard flower buds *Brassica rapa* cDNA... 56 4e-07
 5 emb|Z49714|PMDORORF7 *P.menziesii* mRNA (open reading frame) (DF77C). 55 8e-07
 emb|AW746616|AW746616 WS1_54_F07.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW678229|AW678229 WS1_14_F02.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW924822|AW924822 WS1_72_A12.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW924712|AW924712 WS1_71_A12.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 10 emb|AW679366|AW679366 WS1_24_E04.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW746766|AW746766 WS1_55_D06.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW678206|AW678206 WS1_14_D10.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW747038|AW747038 WS1_65_C09.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW678115|AW678115 WS1_13_E06.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 15 emb|AW679354|AW679354 WS1_24_G08.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AI305014|AI305014 EST00119 mRNP Lambda ZapII Express Library... 51 8e-06
 emb|AF009953|AF009953 *Glycine max* 35 kDa seed maturation protein... 51 8e-06
 emb|Z22872|GMLEAPROA *G.max* Lea protein mRNA, complete CDS. 51 1e-05
 emb|X92955|BOPC15 *B.oleracea* mRNA for pollen coat protein. 51 1e-05
 20 emb|AW680922|AW680922 WS1_8_F06.g1_A002 Water-stressed 1 (WS1) S... 51 1e-05
 emb|AW678045|AW678045 WS1_13_A03.b1_A002 Water-stressed 1 (WS1) ... 50 2e-05
 gb|L33614|L33614 BNAESTF503 Mustard flower buds *Brassica rapa* cD... 50 2e-05
 emb|X79466|HVES2A *H.vulgare* (Dbg 567) ES2A mRNA. 39 4e-05
 emb|AJ000100|HVAJ100 *Hordeum vulgare* mRNA for cold-regulated pro... 39 4e-05
 25 emb|AJ130888|FSY130888 *Fagus sylvatica* mRNA for ABA-inducible pr... 49 4e-05
 emb|AW703962|AW703962 sk14e10.y1 Gm-c1023 *Glycine max* cDNA clone... 49 5e-05
 emb|AW509514|AW509514 ga73a10.y1 Moss EST library PPU Physcomitr... 49 5e-05
 emb|AW679440|AW679440 WS1_24_C05.g1_A002 Water-stressed 1 (WS1) ... 48 1e-04
 gb|L46517|L46517 BNAF1718 Mustard flower buds *Brassica rapa* cDNA... 47 1e-04
 30 emb|AW185164|AW185164 se87g01.y1 Gm-c1023 *Glycine max* cDNA clone... 38 2e-04
 emb|AW679430|AW679430 WS1_24_G08.g1_A002 Water-stressed 1 (WS1) ... 46 5e-04
 emb|X16131|DCDC8 *D. carota* DC8 gene for an embryonic-specific 66... 41 8e-04
 emb|AW754854|AW754854 PC06D01 Pine TriplEx pollen cone library P... 45 9e-04
 emb|AW679001|AW679001 WS1_21_C11.g1_A002 Water-stressed 1 (WS1) ... 44 0.002
 35 emb|AW679463|AW679463 WS1_24_E04.g1_A002 Water-stressed 1 (WS1) ... 44 0.002
 emb|AW981579|AW981579 PC14C08 Pine TriplEx pollen cone library P... 43 0.002
 emb|AF255053|AF255053 *Triticum aestivum* cold-responsive LEA/RAB-... 39 0.004
 emb|AW680686|AW680686 WS1_6_H05.g1_A002 Water-stressed 1 (WS1) S... 42 0.004
 emb|AW747334|AW747334 WS1_67_C01.g1_A002 Water-stressed 1 (WS1) ... 42 0.004
 40 emb|AW747282|AW747282 WS1_67_C01.b1_A002 Water-stressed 1 (WS1) ... 42 0.004
 emb|AW983308|AW983308 HVSMEg0010C18f *Hordeum vulgare* pre-anthesi... 35 0.005
 emb|AW679087|AW679087 WS1_22_A07.b1_A002 Water-stressed 1 (WS1) ... 42 0.006
 emb|AW981621|AW981621 PC14G04 Pine TriplEx pollen cone library P... 42 0.006
 emb|AJ225515|AJ225515 AJ225515 Absciscic acid-treated protonemata... 37 0.017
 45 emb|AW754577|AW754577 PC03H06 Pine TriplEx pollen cone library P... 40 0.021
 emb|AW458460|AW458460 sh09e04.y1 Gm-c1016 *Glycine max* cDNA clone... 39 0.040
 emb|AW981729|AW981729 PC18A04 Pine TriplEx pollen cone library P... 39 0.055
 gb|BE033848|BE033848 MG01A05 MG Mesembryanthemum crystallinum cD... 38 0.076
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 55 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&nid=gb|z99708|/ncgi)
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 (885 letters)

- 60 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	(bits)	Value
5	Sequences producing significant alignments:			
	emb AI486681 AI486681	EST245003	tomato ovary, TAMU Lycopersicon ...	414 e-115
	emb AI488706 AI488706	EST247045	tomato ovary, TAMU Lycopersicon ...	373 e-102
	emb AW185116 AW185116	se87a08.y1 Gm-c1023	Glycine max cDNA clone...	364 e-100
10	emb AW776370 AW776370	EST335435	DSIL Medicago truncatula cDNA cl...	316 1e-85
	emb AW441466 AW441466	EST310862	tomato fruit red ripe, TAMU Lyco...	311 4e-84
	emb AW775237 AW775237	EST331959	GVN Medicago truncatula cDNA clo...	278 4e-74
	emb AW564397 AW564397	LG1_292_F08.b1_A002	Light Grown 1 (LG1) So...	275 2e-73
	emb AW648604 AW648604	EST327154	tomato germinating seedlings, TA...	275 3e-73
15	emb AW309188 AW309188	sg05d07.y1 Gm-c1019	Glycine max cDNA clone...	274 8e-73
	emb AW329561 AW329561	N200812e	rootphos(-) Medicago truncatula c...	204 3e-69
	emb AI897460 AI897460	EST266903	tomato ovary, TAMU Lycopersicon ...	158 7e-67
	emb AI775112 AI775112	EST256212	tomato resistant, Cornell Lycope...	248 4e-65
	emb AI898201 AI898201	EST267644	tomato ovary, TAMU Lycopersicon ...	118 1e-51
20	emb AW011189 AW011189	ST17G07	Pine TriplEx shoot tip library Pin...	172 4e-48
	emb AW622515 AW622515	EST313315	tomato root during/after fruit s...	189 3e-47
	emb AW933718 AW933718	EST359561	tomato fruit mature green, TAMU ...	188 7e-47
	emb AI897919 AI897919	EST267362	tomato ovary, TAMU Lycopersicon ...	102 6e-45
	emb AW623431 AW623431	EST321376	tomato flower buds 3-8 mm, Corne...	179 2e-44
25	emb AI967352 AI967352	Ljimp01-065-f5 Ljimp	Lambda HybriZap ...	167 5e-44
	emb AW496876 AW496876	ga49e04.y1 Moss	EST library PPU Physcomitr...	175 5e-43
	emb AW616498 AW616498	EST322909	L. hirsutum trichome, Cornell Un...	174 1e-42
	emb AW687128 AW687128	NF006C08RT1F1065	Developing root Medicago ...	156 1e-41
	emb AW191300 AW191300	T113619e	KV2 Medicago truncatula cDNA clon...	167 1e-40
30	emb AW257178 AW257178	EST305315	KV2 Medicago truncatula cDNA clo...	144 7e-34
	emb AW699388 AW699388	gb07g07.y1 Moss	EST library PPN Physcomitr...	139 2e-32
	emb AV421449 AV421449	AV421449	Lotus japonicus young plants (two...	132 4e-30
	emb AW626193 AW626193	EST320100	tomato radicle, 5 d post-imbibit...	132 5e-30
	emb AL109608 SPCC23B6	S.pombe	chromosome III cosmid c23B6.	99 3e-28
35	emb AV426790 AV426790	AV426790	Lotus japonicus young plants (two...	123 2e-27
	emb AI778049 AI778049	EST258928	tomato susceptible, Cornell Lyco...	116 2e-25
	emb AW626687 AW626687	NXNV068E07	Nsf Xylem Normal wood Vertical ...	114 1e-24
	emb AW929355 AW929355	EST338143	tomato flower buds 8 mm to pre-a...	106 2e-22
	emb AW719259 AW719259	LjNEST1h10r	Lotus japonicus nodule library...	105 4e-22
40	emb Z69381 SCCXIV39K	S.cerevisiae	38,855 bp segment of chromosom...	60 1e-17
	emb Z71507 SCYNL231C	S.cerevisiae	chromosome XIV reading frame O...	60 1e-17
	emb AB001995 AB001995	Schizosaccharomyces	pombe gene for Tellp, ...	82 6e-17
	emb AI442227 AI442227	sa49c11.y1 Gm-c1004	Glycine max cDNA clone...	85 8e-16
	emb AI725484 AI725484	BNLGH112268	Six-day Cotton fiber Gossypium...	54 2e-15
45	emb X92494 SCBNI1	S.cerevisiae	BNI1, N0647, APL1, N0665, N0670, ...	46 5e-13
	emb Z71540 SCYNL264C	S.cerevisiae	chromosome XIV reading frame O...	46 5e-13
	emb AI731920 AI731920	BNLGH11386	Six-day Cotton fiber Gossypium...	44 2e-12
	emb AI729569 AI729569	BNLGH113678	Six-day Cotton fiber Gossypium...	44 6e-11
	emb AI728685 AI728685	BNLGH11318	Six-day Cotton fiber Gossypium...	45 3e-10
50	emb AI725979 AI725979	BNLGH113788	Six-day Cotton fiber Gossypium...	45 6e-10
	emb AJ273110 AJ273110	AJ273110	Metarhizium anisopliae ARSEF 2575...	52 6e-09
	emb AQ655616 AQ655616	Sheared DNA-2J3.TR	Sheared DNA Trypanosoma...	61 1e-08
	emb AQ501933 AQ501933	V11E10 mTn-3xHA/lacZ	Insertion Library Sac...	60 2e-08
	emb X97320 CGSEC14GN	C.glabrata	SEC14 gene.	55 7e-08
55	emb Z49259 SC9582X	S.cerevisiae	chromosome XIII cosmid 9582.	55 9e-08
	emb X15483 SCSEC14G	Yeast	SEC14 gene for cytosolic factor.	55 9e-08
	gb BE053932 BE053932	GA_Ea0031D10f	Gossypium arboreum 7-10 dpa ...	46 6e-07
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55 Database: plantfungal
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(1140 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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	emb AI776903 AI776903 EST258003 tomato resistant, Cornell Lycope...	47	3e-07		
	emb AW092951 AW092951 EST286131 tomato mixed elicitor, BTI Lycop...	47	3e-07		
20	emb AW203388 AW203388 sf29f06.y1 Gm-c1028 Glycine max cDNA clone...	50	3e-07		
	emb AW597294 AW597294 si71c07.y1 Gm-c1031 Glycine max cDNA clone...	50	3e-07		
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60 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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 /chip nova /gb_link
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 (2196 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb Y18260 BOY18260 Brassica oleracea mRNA for SRK15 protein, pa...	332	e-105
	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	339	e-105
	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein.	330	e-105
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	333	e-104
50	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par...	332	e-104
	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds.	328	e-103
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	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	321	1e-99
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	316	2e-98
55	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	323	2e-98
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	324	4e-98
	emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial.	195	4e-97
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	312	4e-95
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 (2631 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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15 emb|AI895365|AI895365 EST264808 tomato callus, TAMU Lycopersicon... 184 2e-45
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emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 132 9e-42
35 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 115 2e-41
emb|AW036763|AW036763 EST252152 tomato ovary, TAMU Lycopersicon ... 164 2e-41
emb|AW036762|AW036762 EST252151 tomato ovary, TAMU Lycopersicon ... 164 2e-41
emb|AW668493|AW668493 GA_Ea0014C20 Gossypium arboreum 7-10 dpa ... 127 4e-41
gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 110 4e-41
40 emb|AW776704|AW776704 EST335769 DSIL Medicago truncatula cDNA cl... 113 2e-40
emb|AF131222|AF131222 Lophopyrum elongatum protein serine/threon... 97 2e-40
emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 133 2e-40
emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 111 3e-40
emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 105 3e-40
45 emb|AW615998|AW615998 EST325448 tomato flower buds 0-3 mm, Corne... 117 3e-40
emb|AW218745|AW218745 EST301225 tomato root during/after fruit s... 120 5e-40
emb|AI731501|AI731501 BNLGHi9983 Six-day Cotton fiber Gossypium ... 98 6e-40
gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 108 9e-40
emb|AF121448|AF121448 Capsicum annuum protein kinase homolog C11... 95 2e-39
50 emb|AI771280|AI771280 EST252296 tomato ovary, TAMU Lycopersicon ... 165 2e-39
emb|AI486547|AI486547 EST244868 tomato ovary, TAMU Lycopersicon ... 123 2e-39
emb|AW094468|AW094468 EST287648 tomato mixed elicitor, BTI Lycop... 156 2e-39
emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 108 3e-39
emb|AI771841|AI771841 EST252941 tomato ovary, TAMU Lycopersicon ... 164 4e-39
55 emb|AI485090|AI485090 EST243394 tomato ovary, TAMU Lycopersicon ... 164 4e-39
emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber Gossypium ... 78 4e-39
emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 111 4e-39
emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 107 6e-39
emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 107 6e-39
60 emb|AW267961|AW267961 EST306183 DSIR Medicago truncatula cDNA cl... 94 7e-39
emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 107 1e-38

- emb|AI486766|AI486766 EST245088 tomato ovary, TAMU Lycopersicon ... 89 1e-38
 emb|AI485862|AI485862 EST244183 tomato ovary, TAMU Lycopersicon ... 162 1e-38
 emb|AI487456|AI487456 EST245778 tomato ovary, TAMU Lycopersicon ... 123 2e-38
 gb|BE060160|BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis... 75 2e-38
 5 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 107 3e-38
 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 78 3e-38
 emb|AW617255|AW617255 EST323666 L. hirsutum trichome, Cornell Un... 148 4e-38
 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 71 4e-38
 emb|AW774790|AW774790 EST333941 KV3 Medicago truncatula cDNA clo... 95 5e-38
 10 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 105 5e-38
 emb|AW726024|AW726024 GA_Ea0020G24 Gossypium arboreum 7-10 dpa ... 124 6e-38
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 gb|BE020963|BE020963 sm54a06.y1 Gm-cl028 Glycine max cDNA clone ... 125 3e-37
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 15 emb|AF085167|AF085167 Hordeum vulgare receptor-like kinase ARK1A... 81 7e-37
 emb|AW687267|AW687267 NF007G07RT1F1055 Developing root Medicago ... 140 8e-37
 emb|AW648736|AW648736 EST327106 tomato germinating seedlings, TA... 98 1e-36
 emb|AW650851|AW650851 EST329305 tomato germinating seedlings, TA... 126 2e-36

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 dbj|baa82810.1|(ab023448) basic endochitinase [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
 (1008 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

- 30 Score E
 Sequences producing significant alignments: (bits) Value
- emb|AF135130|AF135130 Arabis holboellii from Denmark class I chi... 438 0.0
 emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 491 e-158
 35 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 494 e-158
 gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 490 e-158
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 493 e-158
 emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 541 e-153
 emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 541 e-153
 40 emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 482 e-151
 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 442 e-150
 gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 443 e-150
 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 442 e-149
 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 440 e-148
 45 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 467 e-148
 gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 310 e-146
 gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 310 e-146
 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 309 e-146
 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 472 e-146
 50 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 463 e-146
 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 286 e-145
 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 305 e-144
 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 466 e-144
 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 332 e-144
 55 emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 333 e-144
 emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 469 e-144
 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 435 e-143
 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 284 e-143
 emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase classe 1 (p... 296 e-143
 60 gb|U02287|HVVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 459 e-141
 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 455 e-140

- gb|M94105|ALCCHITIN *Allium sativum* chitinase mRNA, 3' end. 448 e-140
 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 286 e-139
 emb|AF000964|AF000964 *Poa pratensis* chitinase (Chi1) gene, compl... 408 e-139
 gb|L34211|BLYCHI33A *Hordeum vulgare* chitinase (CHI33) gene, comp... 448 e-138
 5 gb|U02608|STU02608 *Solanum tuberosum* chitinase (chtB4) mRNA, par... 408 e-137
 emb|X63899|PSCHITIN *P. sativum* mRNA for chitinase. 270 e-135
 emb|AF061805|AF061805 *Elaeagnus umbellata* acidic chitinase mRNA,... 430 e-134
 emb|AF202731|AF202731 *Glycine max* endochitinase homolog (Chn1) m... 273 e-134
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 10 emb|A37990|A37990 Sequence 9 from Patent EP0616035. 475 e-133
 gb|M62904|BLYCHI H. vulgare L. 26kD chitinase mRNA, complete cds. 475 e-133
 emb|AF098302|AF098302 *Brassica juncea* chitinase mRNA, complete cds. 265 e-132
 gb|U30324|TCU30324 *Theobroma cacao* class I chitinase gene, compl... 238 e-131
 emb|X95610|CSHITIB *C. sativa* mRNA for chitinase Ib. 259 e-130
 15 gb|U48687|CSU48687 *Castanea sativa* endochitinase mRNA, complete ... 259 e-130
 emb|AF141372|AF141372 *Petroselinum crispum* chitinase precursor (... 463 e-130
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 emb|AF061806|AF061806 *Elaeagnus umbellata* basic chitinase mRNA, ... 297 e-128
 emb|AB023464|AB023464 *Arabis gemmifera* ChiB gene for basic endoc... 455 e-127
 20 emb|AF135152|AF135152 *Arabis parishii* country USA class I chitin... 455 e-127
 emb|AF135141|AF135141 *Arabis gunnisoniana* class I chitinase gene... 455 e-127
 emb|AF135135|AF135135 *Arabis drummondii* class I chitinase gene, ... 455 e-127
 emb|AF135143|AF135143 *Arabis lemmonii* country USA class I chitin... 452 e-126
 emb|X67693|STMREN *S. tuberosum* mRNA for endochitinase. 452 e-126
 25 emb|AF135132|AF135132 *Arabis gunnisoniana* from USA class I chiti... 452 e-126
 emb|AF135144|AF135144 *Arabis lemmonii* country USA class I chitin... 451 e-126
 emb|AF135140|AF135140 *Arabis glabra* country USA class I chitinas... 449 e-125
 gb|U30465|LEU30465 *Lycopersicon esculentum* class II chitinase (C... 447 e-125
 emb|AF135153|AF135153 *Arabis parishii* country USA class I chitin... 445 e-124
 30 gb|L22032|ULMCHITIN *Ulmus americana* chitinase (PHS2) mRNA, compl... 295 e-124
 emb|AF135148|AF135148 *Arabis lyallii* class I chitinase gene, par... 444 e-124
 emb|AF135151|AF135151 *Arabis microphylla* country USA class I chi... 444 e-124
 emb|AF135150|AF135150 *Arabis microphylla* country USA class I chi... 443 e-124
 emb|AF135147|AF135147 *Arabis lignifera* country USA class I chiti... 443 e-124
 35 emb|AF135136|AF135136 *Arabis fecunda* country USA class I chitina... 443 e-124
 emb|AF135145|AF135145 *Arabis lignifera* country USA class I chiti... 443 e-123
 emb|AF135146|AF135146 *Arabis lignifera* country USA class I chiti... 441 e-123
 emb|AF135149|AF135149 *Arabis microphylla* class I chitinase gene,... 441 e-123
 emb|AF043247|AF043247 *Solanum tuberosum* class I chitinase (ChtC1... 431 e-122
 40 emb|AF043248|AF043248 *Solanum tuberosum* class I chitinase (ChtC2... 431 e-122
 emb|Z15138|LECH114 *L. esculentum* mRNA for chitinase (partial). 439 e-122
 emb|AF135142|AF135142 *Halimolobos perplexa* var. *perplexa* class I... 435 e-121
 emb|AF135134|AF135134 *Arabis blepharophylla* class I chitinase ge... 434 e-121
 gb|U01660|U01660 *Populus trichocarpa* x *Populus deltoides* acidic ... 207 e-121
 45 emb|AF135138|AF135138 *Arabis glabra* country USA class I chitinas... 431 e-120
 emb|AF135133|AF135133 *Arabis blepharophylla* country USA class I... 423 e-118
 gb|M95835|BNACH25A *Brassica napus* (clone BnCh25) endochitinase g... 422 e-117
 emb|AW034530|AW034530 EST278146 tomato callus, TAMU *Lycopersicon*... 418 e-116
 emb|AW560048|AW560048 EST315096 DSIR *Medicago truncatula* cDNA cl... 350 e-112
 50 emb|AW687771|AW687771 NF013C08RT1F1065 Developing root *Medicago* ... 311 e-111
 emb|AW033115|AW033115 EST276674 tomato callus, TAMU *Lycopersicon*... 391 e-108
 emb|AW034645|AW034645 EST278376 tomato callus, TAMU *Lycopersicon*... 366 e-106
 emb|AF082713|AF082713 *Capsicum annuum* leaf mRNA *Capsicu*... 364 e-106
 emb|AW738053|AW738053 EST339480 tomato flower buds, anthesis, Co... 379 e-104
 55 emb|AF141373|AF141373 *Petroselinum crispum* chitinase precursor (... 237 e-104
 emb|Z70032|CSACHIT2 *C. sinensis* mRNA for class II acidic chitinase. 197 e-104
 emb|AW030745|AW030745 EST274000 tomato callus, TAMU *Lycopersicon*... 360 e-104
 emb|AF141374|AF141374 *Petroselinum crispum* chitinase precursor (... 237 e-104
 emb|AW033034|AW033034 EST276593 tomato callus, TAMU *Lycopersicon*... 367 e-103
 60 emb|AW216454|AW216454 EST295084 tomato callus, TAMU *Lycopersicon*... 373 e-102
 emb|AW267781|AW267781 EST305909 DSIR *Medicago truncatula* cDNA cl... 316 e-102

emb|AW033757|AW033757 EST277328 tomato callus, TAMU Lycopersicon... 285 e-101
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 emb|AW216787|AW216787 EST295501 tomato callus, TAMU Lycopersicon... 364 e-100
 5 emb|AI771248|AI771248 EST252264 tomato ovary, TAMU Lycopersicon ... 363 1e-99
 emb|AW031102|AW031102 EST274409 tomato callus, TAMU Lycopersicon... 275 1e-98
 emb|X15349|HVENDCHT Barley (H.vulgare) mRNA for endochitinase. 359 2e-98
 emb|AW622028|AW622028 EST312826 tomato root during/after fruit s... 269 9e-97
 emb|Z15139|LECHI17 L.esculentum mRNA for chitinase. 242 2e-96
 10 emb|AW032161|AW032161 EST275615 tomato callus, TAMU Lycopersicon... 334 2e-96
 emb|AW560177|AW560177 EST315225 DSIR Medicago truncatula cDNA cl... 295 1e-95

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 (1881 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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25	Sequences producing significant alignments:			
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	emb AB006809 AB006809 Cucurbita sp. mRNA for PV72, complete cds. .	780	0.0	
	emb AW267745 AW267745 EST305873 DSIR Medicago truncatula cDNA cl...	453	e-126	
	emb AW931583 AW931583 EST357426 tomato fruit mature green, TAMU ...	308	e-112	
30	emb AW309187 AW309187 sg05d06.y1 Gm-c1019 Glycine max cDNA clone...	405	e-112	
	gb BE054150 BE054150 GA_Ea0034H17f Gossypium arboreum 7-10 dpa ...	398	e-110	
	emb AW622833 AW622833 EST306903 tomato flower buds 3-8 mm, Corne...	387	e-106	
	emb AW689392 AW689392 NF018F12ST1F1000 Developing stem Medicago ...	371	e-102	
	emb AW737948 AW737948 EST339375 tomato flower buds, anthesis, Co...	342	3e-94	
35	emb AW774434 AW774434 EST333585 KV3 Medicago truncatula cDNA clo...	263	2e-90	
	emb AW932529 AW932529 EST358372 tomato fruit mature green, TAMU ...	326	3e-88	
	emb AW615949 AW615949 EST325315 tomato flower buds 0-3 mm, Corne...	216	1e-87	
	emb AI728635 AI728635 BNLGH11276 Six-day Cotton fiber Gossypium...	281	8e-84	
	emb AI782787 AI782787 EST263666 tomato susceptible, Cornell Lyco...	307	2e-82	
40	emb AI443067 AI443067 sa47a01.y1 Gm-c1004 Glycine max cDNA clone...	305	6e-82	
	emb AW747297 AW747297 WS1_67_G06.b1_A002 Water-stressed 1 (WS1) ...	292	8e-78	
	emb AI727826 AI727826 BNLGH19195 Six-day Cotton fiber Gossypium ...	280	1e-77	
	emb AI484571 AI484571 EST242801 tomato ovary, TAMU Lycopersicon ...	284	1e-75	
	emb AW685785 AW685785 NF030C07NR1F1000 Nodulated root Medicago t...	166	1e-71	
45	emb AV406766 AV406766 AV406766 Lotus japonicus young plants (two...	260	2e-68	
	emb AW509740 AW509740 ga63h11.y1 Moss EST library PPU Physcomitr...	232	1e-65	
	emb AV428420 AV428420 AV428420 Lotus japonicus young plants (two...	249	4e-65	
	emb AW695542 AW695542 NF096C05ST1F1037 Developing stem Medicago ...	124	1e-58	
	emb AW289687 AW289687 NXNV004E04F Nsf Xylem Normal wood Vertical...	226	4e-58	
50	emb AW064744 AW064744 ST35C06 Pine TriplEx shoot tip library Pin...	198	2e-56	
	emb AW309191 AW309191 sg05d10.y1 Gm-c1019 Glycine max cDNA clone...	171	3e-52	
	emb AW096632 AW096632 EST289812 tomato mixed elicitor, BTI Lycop...	165	7e-52	
	emb AW568619 AW568619 si60a11.y1 Gm-r1030 Glycine max cDNA clone...	205	1e-51	
	emb AF209910 AF209910 Prunus dulcis vacuolar sorting receptor pr...	160	5e-51	
55	emb AW623959 AW623959 EST321904 tomato flower buds 3-8 mm, Corne...	75	1e-50	
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	emb AW256542 AW256542 EST304679 KV2 Medicago truncatula cDNA clo...	151	2e-50	
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	emb AW690002 AW690002 NF026G04ST1F1000 Developing stem Medicago ...	109	2e-43
	emb AW290400 AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical...	177	3e-43
	emb AI162330 AI162330 A016P01U Hybrid aspen plasmid library Popu...	131	2e-39
	emb AI161766 AI161766 A006P54U Hybrid aspen plasmid library Popu...	93	3e-38
5	emb AW737369 AW737369 EST338892 tomato flower buds, anthesis, Co...	149	5e-35
	gb BE125908 BE125908 DG1_59_E01.b1_A002 Dark Grown 1 (DG1) Sorgh...	149	5e-35
	emb AW201441 AW201441 sf03b09.y1 Gm-c1027 Glycine max cDNA clone...	113	1e-34
	emb AW398931 AW398931 EST309431 L. pennellii trichome, Cornell U...	95	2e-34
	gb BE049814 BE049814 NXNV_144_F04_F Nsf Xylem Normal wood Vertic...	143	6e-33
10	emb AW126100 AW126100 N100297e rootphos(-) Medicago truncatula c...	100	5e-30
	emb AW508719 AW508719 si35f03.y1 Gm-r1030 Glycine max cDNA clone...	125	1e-27
	gb L38113 L38113 BNAF0628E Mustard flower buds Brassica rapa cDN...	117	4e-26
	emb AW317388 AW317388 sg48g10.y1 Gm-c1025 Glycine max cDNA clone...	80	1e-25
	emb AW706755 AW706755 sk02f10.y1 Gm-c1023 Glycine max cDNA clone...	118	2e-25
15	emb AA660955 AA660955 00852 MRHE Medicago truncatula cDNA 5' si...	74	7e-25
	emb AW616461 AW616461 EST322872 L. hirsutum trichome, Cornell Un...	69	2e-24
	emb AW348825 AW348825 GM210003B11E6R Gm-r1021 Glycine max cDNA 3...	68	8e-24
	emb AW932524 AW932524 EST358367 tomato fruit mature green, TAMU ...	80	1e-23
	emb AW774190 AW774190 EST333273 KV3 Medicago truncatula cDNA clo...	101	2e-20
20	emb AW125944 AW125944 N100139e rootphos(-) Medicago truncatula c...	66	6e-20
	emb AW093844 AW093844 EST287024 tomato mixed elicitor, BTI Lycop...	96	7e-19
	emb AW906386 AW906386 EST342508 potato stolon, Cornell Universit...	67	2e-16
	gb BE060808 BE060808 HVSMEg0013H06f Hordeum vulgare pre-anthesis...	87	4e-16
	emb AW620693 AW620693 sj08d10.y1 Gm-c1032 Glycine max cDNA clone...	76	1e-15
25	emb AW256398 AW256398 EST304465 KV2 Medicago truncatula cDNA clo...	74	6e-14
	emb AW037563 AW037563 EST278890 tomato mixed elicitor, BTI Lycop...	79	8e-14
	emb AW691052 AW691052 NF037B05ST1F1000 Developing stem Medicago ...	72	4e-13
	emb AW686287 AW686287 NF040A08NR1F1000 Nodulated root Medicago t...	77	4e-13
	emb AW685952 AW685952 NF036G09NR1F1000 Nodulated root Medicago t...	46	2e-11
30	emb AW760128 AW760128 sl58d09.y1 Gm-c1027 Glycine max cDNA clone...	58	1e-10
	emb AW119909 AW119909 sd54d08.y1 Gm-c1016 Glycine max cDNA clone...	66	8e-10
	emb AI794754 AI794754 sb68f11.y1 Gm-c1019 Glycine max cDNA clone...	64	4e-09
	emb AW774852 AW774852 EST334003 KV3 Medicago truncatula cDNA clo...	64	4e-09
	emb AW127457 AW127457 M110648 DSIL Medicago truncatula cDNA clon...	58	3e-07
35	emb AW443352 AW443352 EST308282 tomato mixed elicitor, BTI Lycop...	56	1e-06
	emb AW747372 AW747372 WS1_67_G06.gl_A002 Water-stressed 1 (WS1) ...	55	2e-06
	emb AI939286 AI939286 sc69h02.y1 Gm-c1016 Glycine max cDNA clone...	46	0.001
	emb AF198615 AF198615 Neospora caninum microneme protein Nc-P38 ...	43	0.009
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40	gb BE035779 BE035779 MO16H05 MO Mesembryanthemum crystallinum cD...	36	0.025
	emb AI822869 AI822869 L30-712T3 Ice plant Lambda Uni-Zap XR expr...	36	0.025
	emb AI822754 AI822754 L0-128T73 Ice plant Lambda Uni-Zap XR expr...	36	0.025
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45	emb AU036628 AU036628 Schizosaccharomyces pombe genomic clone ha...	40	0.083
	emb AA948752 AA948752 L0-271M13R Ice plant Lambda Uni-Zap XR exp...	35	0.086
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55	gb BE036036 BE036036 MO18H02 MO Mesembryanthemum crystallinum cD...	36	0.76
	gb C95899 C95899 C95899 Marchantia polymorpha immature sex organ...	36	1.0
	emb AA966307 AA966307 v8c01a1.r1 Aspergillus nidulans 24hr asexu...	36	1.0
	emb AI759219 AI759219 EtESTea26c02.y1 Eimeria S5-2 Sporozoite st...	28	1.3
	gb U11583 YSCH9196 Saccharomyces cerevisiae chromosome VIII cosm...	35	1.4
60	emb AQ639257 AQ639257 927P1-10E12.TV 927P1 Trypanosoma brucei ge...	35	1.4
	emb AQ943504 AQ943504 Sheared DNA-43F22.TF Sheared DNA Trypanoso...	35	1.4

emb|AW623282|AW623282 EST321227 tomato flower buds 3-8 mm, Corne... 35 1.4
dbj|D85226|D85226 Brassica campestris DNA for S glycoprotein, pa... 28 1.6
emb|AF001525|AF001525 Musa acuminata ripening-associated protein... 35 2.0

5 Query= X84728.6_s_at 12349_s_at /id_source genbank /description
gb|aa17993.1| (m91192) phenylalanine ammonia-lyase [trifolium
subterraneum] /blast_score 0 /ec_number /family /chip nova /gb_link
/ncgi

(1962 letters)

10

Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

15

Score E
Sequences producing significant alignments: (bits) Value

20 gb|L11747|POPPALGA Populus tricocarpa X Populus deltoides (hybri... 354 0.0
emb|X99997|BFPAL B.finlaysoniana mRNA for phenylalanine ammonia-... 352 0.0
emb|X58180|MSPAL M.sativa PAL mRNA for phenylalanine ammonia-lyase. 351 0.0
gb|U43338|CLU43338 Citrus limon phenylalanine ammonia-lyase (pal... 350 0.0
gb|L36822|SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas... 350 0.0
emb|AF036948|AF036948 Prunus avium phenylalanine ammonia-lyase (... 349 0.0
25 emb|AJ250836|CAR250836 Cicer arietinum mRNA for phenylalanine am... 349 0.0
emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 349 0.0
emb|X81158|PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 349 0.0
emb|X81159|PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 348 0.0
dbj|D83075|D83075 Lithospermum erythrorhizon mRNA for phenylalan... 348 0.0
30 emb|AF237955|AF237955 Rubus idaeus phenylalanine ammonia-lyase 2... 348 0.0
emb|AJ002221|DLJ002221 Digitalis lanata mRNA for phenylalanine a... 347 0.0
gb|M29232|IPBPAL Sweet potato phenylalanine ammonia-lyase mRNA (... 345 0.0
dbj|D26596|CMEPAL Camellia sinensis mRNA for phenylalanine ammon... 344 0.0
dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase,... 344 0.0
35 emb|X78269|NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine ... 343 0.0
dbj|D83076|D83076 Lithospermum erythrorhizon mRNA for phenylalan... 343 0.0
dbj|D78640|IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni... 342 0.0
emb|Y12461|HAPHAMLY Helianthus annuus mRNA for phenylalanine amm... 341 0.0
emb|AB042520|AB042520 Catharanthus roseus mRNA for phenylalanine... 339 0.0
40 emb|AF237954|AF237954 Rubus idaeus phenylalanine ammonia-lyase 1... 330 0.0
dbj|D10001|PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase... 349 0.0
emb|X63103|STPAL1 S.tuberosum PAL-1 gene for phenylalanine ammon... 353 0.0
emb|AJ238754|CCL238754 Citrus clementina X Citrus reticulata mRN... 350 0.0
emb|AJ238753|CCL238753 Citrus clementina X Citrus reticulata mRN... 353 0.0
45 dbj|D10003|PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas... 349 0.0
dbj|E04042|E04042 cDNA sequence coding for pea phenylalanine amm... 349 0.0
emb|AF165998|AF165998 Vigna unguiculata phenylalanine ammonia-ly... 355 0.0
gb|U16130|PAU16130 Persea americana phenylalanine ammonia lyase ... 331 0.0
dbj|D30656|POPPALA Populus kitakamiensis gene for phenylalanine ... 356 0.0
50 gb|M84466|TOBTPA1A Tobacco phenylalanine ammonia-lyase (tpal) gen... 352 0.0
emb|AB008200|AB008200 Nicotiana tabacum palB gene for phenylalan... 352 0.0
dbj|D85850|D85850 Daucus carota gDcPAL1 gene for phenylalanine a... 347 0.0
emb|X52953|DMPAL1 Glycine max PAL1 gene for phenylalanine ammoni... 355 0.0
emb|X99705|TAPALGEN1 T.aestivum PAL gene. 342 0.0
55 gb|M91192|TRFPAL1X Trifolium subterraneum phenylalanine ammonia-... 345 0.0
gb|M90692|TOMPAL5A Lycopersicon esculentum phenylalanine ammonia... 347 0.0
emb|AB008199|AB008199 Nicotiana tabacum palA gene for phenylalan... 344 0.0
emb|Y07654|PCPAL1 P.crispum pal1 gene. 350 0.0
emb|X16772|PCPAL1EX2 P.crispum PAL-1 gene for phenylalanine ammo... 350 0.0
60 dbj|D43803|POPPALG4B Populus kitakamiensis gene for phenylalanin... 336 0.0
gb|M83314|TOMPHEAMLY Lycopersicon esculentum phenylalanine ammon... 353 0.0

- emb|X76130|CMPAL C.melo (cantaloupe) pal mRNA. 318 0.0
 dbj|D30657|POPPALB Populus kitakamiensis gene for phenylalanine ... 333 0.0
 dbj|D43802|POPPALG2BA Populus kitakamiensis gene for phenylalani... 336 0.0
 emb|AF081215|AF081215 Capsicum chinense phenylalanine ammonia-ly... 346 0.0
 5 dbj|D10002|PEAPAL1 P.sativum gene for phenylalanine ammonia-lyas... 349 0.0
 emb|Z49147|HVPAL7RM H.vulgare partial PAL mRNA for phenylalanine... 342 0.0
 emb|X63104|STPAL2 S.tuberosum PAL-2 gene for phenylalanine ammon... 353 0.0
 gb|U39792|PTU39792 Pinus taeda phenylalanine ammonia-lyase (IpPA... 311 0.0
 gb|M11939|PHVPAL Phaseolus vulgaris L. phenylalanine ammonia-lya... 354 0.0
 10 dbj|E04043|E04043 cDNA sequence coding for kidney bean phenylala... 354 0.0
 emb|AB015871|AB015871 Vitis vinifera gene for phenylalanine ammo... 350 0.0
 emb|Z49145|HVPAL2MR H.vulgare partial PAL mRNA for phenylalanine... 341 0.0
 emb|Z49146|HVPAL3MR H.vulgare partial PAL mRNA for phenylalanine... 311 0.0
 emb|X75967|VVPAL V.vinifera PAL mRNA for phenylalanine ammonia l... 350 0.0
 15 gb|S46988|S46988 phenylalanine ammonia-lyase [soybeans, mRNA, 14... 344 0.0
 emb|AF206634|AF206634 Prunus persica cultivar Loring phenylalani... 336 0.0
 emb|AF167487|AF167487 Eucalyptus globulus phenylalanine ammonia ... 334 e-178
 emb|X99725|TAPALGEN2 T.aestivum PAL gene, coding region. 300 e-137
 emb|AW218834|AW218834 EST301314 tomato root during/after fruit s... 347 e-134
 20 emb|AW031612|AW031612 EST275066 tomato callus, TAMU Lycopersicon... 327 e-132
 emb|AJ289609|BPE289609 Betula pendula partial pal gene for pheny... 205 e-128
 emb|AJ278116|BPE278116 Betula pendula partial pal1 gene for phen... 205 e-128
 emb|AW219303|AW219303 EST301785 tomato root during/after fruit s... 339 e-126
 emb|AW726548|AW726548 GA__Ea0022A01 Gossypium arboreum 7-10 dpa ... 323 e-124
 25 emb|AI166817|AI166817 xylem.est.611 Poplar xylem Lambda ZAPII li... 251 e-117
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 emb|AW776946|AW776946 EST336011 DSIL Medicago truncatula cDNA cl... 280 e-114
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 30 emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanin... 247 e-105
 emb|AW216505|AW216505 EST295219 tomato callus, TAMU Lycopersicon... 209 e-104
 emb|AI166477|AI166477 xylem.est.305 Poplar xylem Lambda ZAPII li... 291 e-100
 emb|AV428905|AV428905 AV428905 Lotus japonicus young plants (two... 243 1e-98
 emb|AW220322|AW220322 EST302805 tomato root during/after fruit s... 255 2e-98
 35 emb|AW734312|AW734312 sk81e07.y1 Gm-c1016 Glycine max cDNA clone... 324 6e-98
 emb|AW034774|AW034774 EST278810 tomato callus, TAMU Lycopersicon... 325 3e-93
 emb|AW329762|AW329762 N201031e rootphos(-) Medicago truncatula c... 337 1e-91
 emb|AI777483|AI777483 EST258362 tomato susceptible, Cornell Lyco... 294 3e-90
 emb|AW621418|AW621418 EST312216 tomato root during/after fruit s... 330 2e-89
 40 emb|AW443181|AW443181 EST308111 tomato mixed elicitor, BTI Lycop... 329 6e-89
 emb|AW781748|AW781748 sl90e11.y1 Gm-c1037 Glycine max cDNA clone... 326 3e-88
 emb|X68126|MSPALMR Malus sp. PAL mRNA for phenylalanine ammonia-... 324 1e-87
 emb|AW760268|AW760268 sl48b08.y1 Gm-c1027 Glycine max cDNA clone... 323 3e-87
 emb|AW278641|AW278641 sf63c08.y1 Gm-c1013 Glycine max cDNA clone... 316 4e-85
 45 emb|AF218454|AF218454 Coffea arabica clone 430.4 phenylalanine a... 243 6e-85
 emb|AI899698|AI899698 EST269141 tomato susceptible, Cornell Lyco... 314 2e-84
 emb|AW455294|AW455294 EST311832 tomato root during/after fruit s... 313 3e-84
 emb|AW685111|AW685111 NF026A05NR1F1000 Nodulated root Medicago t... 236 6e-84
 emb|AW667320|AW667320 GA__Ea0008P06 Gossypium arboreum 7-10 dpa ... 189 2e-83
 50 gb|BE021354|BE021354 sm57e05.y1 Gm-c1028 Glycine max cDNA clone ... 308 9e-83
 emb|AI772657|AI772657 EST253757 tomato resistant, Cornell Lycope... 299 2e-80
 emb|AI894514|AI894514 EST263957 tomato callus, TAMU Lycopersicon... 294 1e-78
 gb|L11883|WHTWALJ4A Triticum aestivum phenylalanine ammonia-lyas... 87 4e-16
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- 55 Query= AL022347.131_at 12360_at /id_source genbank /description
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 /gb_link [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022347|/ncgi)
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 60 <http://www.ncgr.org/cgi-bin/ff?al022347>
 (1554 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5 Searching.....done

Score E

Sequences producing significant alignments:

(bits) Value

- 10 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 251 1e-65
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 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 231 1e-59
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 230 2e-59
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 227 1e-58
- 15 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 226 4e-58
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 225 7e-58
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 225 7e-58
 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 224 1e-57
 gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 186 1e-57
- 20 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 222 6e-57
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 221 8e-57
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 221 2e-56
 gb|BE057261|BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ... 220 3e-56
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 219 6e-56
- 25 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 218 8e-56
 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 216 3e-55
 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 215 5e-55
 emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 213 3e-54
 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 211 1e-53
- 30 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 116 6e-53
 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 207 2e-52
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 117 1e-51
 dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 204 1e-51
 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 198 4e-51
- 35 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 202 7e-51
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 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 196 2e-49
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- 40 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 196 4e-49
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- 45 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 112 3e-47
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 emb|X79432|BOSRK3 B.oleracea SRK3 gene. 107 6e-47
 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 108 6e-47
 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 111 2e-46
- 50 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 120 3e-46
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 emb|AW039406|AW039406 EST281663 tomato mixed elicitor, BTI Lycop... 107 3e-45
 emb|AJ245479|BNA245479 Brassica napus Sl13, slk, srk, CePP, Fmt,... 106 4e-45
- 55 emb|AW034624|AW034624-EST278308 tomato callus, TAMU Lycopersicon... 182 6e-45
 dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 109 9e-45
 emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 116 1e-43
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- 60 emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 171 9e-42
 emb|AW706972|AW706972 sk20a03.y1 Gm-c1028 Glycine max cDNA clone... 171 9e-42

emb|Z18861|BOSRKPA B.oleracea encoding S-receptor kinase relate... 111 4e-41
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emb|AW154835|AW154835 EST290228 tomato root deficiency, Cornell ... 169 6e-41
5 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 97 3e-40
emb|AI898854|AI898854 EST268297 tomato ovary, TAMU Lycopersicon ... 163 4e-39
emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 162 7e-39
emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 160 4e-38
emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 96 2e-37
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emb|Y16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 116 5e-37
emb|AW455306|AW455306 EST311844 tomato root during/after fruit s... 124 9e-37
emb|AI730535|AI730535 BNLGHI7007 Six-day Cotton fiber Gossypium ... 80 1e-36
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15 emb|AW223870|AW223870 EST300681 tomato fruit red ripe, TAMU Lyco... 96 6e-36
emb|AW224241|AW224241 EST300968 tomato fruit red ripe, TAMU Lyco... 96 6e-36
emb|AI486766|AI486766 EST245088 tomato ovary, TAMU Lycopersicon ... 110 8e-36
emb|AW934655|AW934655 EST353547 tomato flower buds 0-3 mm, Come... 87 1e-34
emb|AW617954|AW617954 EST314028 L. pennellii trichome, Cornell U... 87 1e-34
20 dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 100 2e-34
dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 100 2e-34
emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 88 3e-34
emb|Z18862|BOSRKRPD B.oleracea encoding S-receptor kinase protein. 80 5e-34
emb|AI896183|AI896183 EST265626 tomato callus, TAMU Lycopersicon... 96 5e-34
25 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 120 1e-33
emb|AI055189|AI055189 coau0003E19 Cotton Boll Abscission Zone cD... 91 1e-33
emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 144 2e-33
emb|AV422094|AV422094 AV422094 Lotus japonicus young plants (two... 102 2e-33
emb|AI937984|AI937984 sc06e07.y1 Gm-c1012 Glycine max cDNA clone... 144 2e-33
30 emb|AW756743|AW756743 sl26f10.y1 Gm-c1027 Glycine max cDNA clone... 143 3e-33
emb|AW290044|AW290044 NXNV009D10F Nsf Xylem Normal wood Vertical... 91 4e-33
emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 93 6e-33
emb|AI772117|AI772117 EST253217 tomato resistant, Cornell Lycope... 142 6e-33
emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 117 8e-33
emb|A67797|A67797 Sequence 2 from Patent WO9743427. 76 2e-32
35 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor... 76 2e-32
emb|AW221202|AW221202 EST297671 tomato fruit mature green, TAMU ... 85 4e-32
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40 emb|AW697111|AW697111 NF112D03ST1F1028 Developing stem Medicago ... 83 7e-32
emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 138 8e-32
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45 emb|AI729170|AI729170 BNLGHI12834 Six-day Cotton fiber Gossypium... 88 2e-31
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emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 88 7e-31
emb|Z18863|BOSRKPGA B.oleracea S-receptor kinase pseudogene. 74 9e-31
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/gb_link /ncgi
(1323 letters)

55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

60 Score E
Sequences producing significant alignments: (bits) Value

- emb|AW031251|AW031251 EST274626 tomato callus, TAMU Lycopersicon... 372 e-102
emb|AW032461|AW032461 EST276020 tomato callus, TAMU Lycopersicon... 363 2e-99
emb|AI938425|AI938425 sc45a04.y1 Gm-c1015 Glycine max cDNA clone... 347 1e-94
5 emb|AW930806|AW930806 EST356649 tomato fruit mature green, TAMU ... 346 2e-94
emb|AW930422|AW930422 EST340795 tomato fruit mature green, TAMU ... 346 3e-94
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emb|AW776450|AW776450 EST335515 DSIL Medicago truncatula cDNA cl... 324 1e-87
emb|AW034511|AW034511 EST278127 tomato callus, TAMU Lycopersicon... 323 2e-87
10 emb|AI965412|AI965412 sc71d05.y1 Gm-c1016 Glycine max cDNA clone... 322 3e-87
emb|AW185064|AW185064 se86c08.y1 Gm-c1023 Glycine max cDNA clone... 321 6e-87
emb|AI813025|AI813025 2H4 Pine Lambda Zap Xylem library Pinus ta... 321 6e-87
emb|AI895246|AI895246 EST264689 tomato callus, TAMU Lycopersicon... 317 1e-85
emb|AI896622|AI896622 EST266065 tomato callus, TAMU Lycopersicon... 312 3e-84
15 gb|BE021087|BE021087 sm55c04.y1 Gm-c1028 Glycine max cDNA clone ... 277 2e-78
emb|AW746042|AW746042 WS1_39_B06.b1_A002 Water-stressed 1 (WS1) ... 277 1e-73
gb|BE021086|BE021086 sm55c03.y1 Gm-c1028 Glycine max cDNA clone ... 276 2e-73
emb|AW934118|AW934118 EST359961 tomato fruit mature green, TAMU ... 274 1e-72
emb|AW649568|AW649568 EST328022 tomato germinating seedlings, TA... 264 1e-69
20 emb|AW694276|AW694276 NF074C12ST1F1097 Developing stem Medicago ... 261 1e-68
emb|AW719214|AW719214 LjNEST1c1r Lotus japonicus nodule library,... 257 1e-67
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30 emb|AW686159|AW686159 NF034F08NR1F1000 Nodulated root Medicago t... 231 7e-60
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35 emb|AI728658|AI728658 BNLGHi11350 Six-day Cotton fiber Gossypium... 222 5e-57
emb|AW348121|AW348121 GM210001A11H6R Gm-r1021 Glycine max cDNA 3... 161 6e-56
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40 emb|AW220836|AW220836 EST297305 tomato fruit mature green, TAMU ... 204 1e-51
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45 emb|AI779032|AI779032 EST259911 tomato susceptible, Cornell Lyco... 198 1e-49
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emb|AI440607|AI440607 sa68d03.y1 Gm-c1004 Glycine max cDNA clone... 190 2e-47
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50 emb|AW290830|AW290830 NXNV047E02F Nsf Xylem Normal wood Vertical... 188 6e-47
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emb|AW931325|AW931325 EST357168 tomato fruit mature green, TAMU ... 185 8e-46
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55 emb|AW096584|AW096584 EST289764 tomato mixed elicitor, BTI Lycop... 181 1e-44
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emb|AW220837|AW220837 EST297306 tomato fruit mature green, TAMU ... 180 2e-44
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emb|AW677446|AW677446 DG1_7_D07.b1_A002 Dark Grown 1 (DG1) Sorgh... 178 7e-44
60 emb|AW559359|AW559359 EST314407 DSIR Medicago truncatula cDNA cl... 178 9e-44
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- emb|AW310207|AW310207 sf32g10.x1 Gm-c1028 Glycine max cDNA clone... 176 4e-43
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 5 emb|AI775651|AI775651 EST256751 tomato resistant, Cornell Lycopersicon... 168 1e-40
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 10 emb|AW277663|AW277663 sf85a06.y1 Gm-c1019 Glycine max cDNA clone... 155 1e-36
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 15 emb|AI778980|AI778980 EST259859 tomato susceptible, Cornell Lyco... 138 1e-31
 emb|AI773172|AI773172 EST254272 tomato resistant, Cornell Lycopersicon... 133 2e-30
 gb|BE054249|BE054249 GA_Ea0033L21f Gossypium arboreum 7-10 dpa ... 120 3e-30
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 20 emb|AI725556|AI725556 BNLGHI12118 Six-day Cotton fiber Gossypium... 125 7e-28
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 emb|AW649713|AW649713 EST328167 tomato germinating seedlings, TA... 114 2e-24
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 25 emb|AW091914|AW091914 EST285094 tomato mixed elicitor, BTI Lycopersicon... 112 5e-24
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 30 emb|AT000037|AT000037 AT000037 Apple young fruit cDNA library Ma... 101 1e-20
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 emb|AW423725|AW423725 sh50h06.y1 Gm-c1017 Glycine max cDNA clone... 98 1e-19
 emb|AW278733|AW278733 sf96f12.y1 Gm-c1019 Glycine max cDNA clone... 95 8e-19
 35 emb|AW495793|AW495793 NXNV_065_E02_FF Nsf Xylem Normal wood Vert... 94 2e-18
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 emb|AI974654|AI974654 T113109e KV2 Medicago truncatula cDNA clon... 79 4e-16
 emb|AW255631|AW255631 ML690 peppermint glandular trichome Mentha... 86 7e-16
 40 emb|AW102109|AW102109 sd83c02.y1 Gm-c1009 Glycine max cDNA clone... 83 6e-15
 emb|X68950|TRUOCAN T.repens gene for urocanase. 58 5e-14

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Database: plantfungal
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Score E
 Sequences producing significant alignments: (bits) Value

- 55 emb|AB012932|AB012932 Vigna radiata mRNA for Ca²⁺/H⁺ exchanger, ... 324 e-141
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 60 emb|AB018526|AB018526 Ipomoea nil mRNA for H⁺/Ca²⁺ exchanger 2, ... 262 4e-86
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	emb AW668567 AW668567 GA_Ea0014K15 Gossypium arboreum 7-10 dpa ...	141	1e-61
5	emb AW648038 AW648038 EST326492 tomato germinating seedlings, TA...	230	2e-59
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	emb AW399625 AW399625 EST310125 L. pennellii trichome, Cornell U...	154	4e-49
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10	emb Z74176 SCYDL128W S.cerevisiae chromosome IV reading frame OR...	195	5e-49
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	emb AW459585 AW459585 sh89a07.y1 Gm-c1016 Glycine max cDNA clone...	164	1e-39
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30	emb AW737653 AW737653 EST339080 tomato flower buds, anthesis, Co...	140	3e-32
	emb AI900767 AI900767 sb93a03.y1 Gm-c1017 Glycine max cDNA clone...	83	3e-31
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	emb AW695100 AW695100 NF091E10ST1F1082 Developing stem Medicago ...	98	1e-30
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35	emb AI899610 AI899610 EST269053 tomato susceptible, Cornell Lyco...	121	7e-30
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	emb AW689061 AW689061 NF014H11ST1F1000 Developing stem Medicago ...	87	3e-27
40	emb AW691346 AW691346 NF043G04ST1F1000 Developing stem Medicago ...	85	4e-27
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	emb AW694830 AW694830 NF080D09ST1F1077 Developing stem Medicago ...	85	1e-26
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45	emb AW394839 AW394839 sh36a06.y1 Gm-c1017 Glycine max cDNA clone...	118	1e-25
	emb AW119664 AW119664 sd50f07.y1 Gm-c1016 Glycine max cDNA clone...	117	1e-25
	emb AW181027 AW181027 MgA0398r MgA Library Mycosphaerella gramin...	116	3e-25
	emb AI771453 AI771453 EST252553 tomato ovary, TAMU Lycopersicon ...	84	3e-24
	emb AW695020 AW695020 NF082E03ST1F1021 Developing stem Medicago ...	76	7e-24
50	emb AI211368 AI211368 o6g04a1.f1 Aspergillus nidulans 24hr asexu...	111	9e-24
	emb AW692971 AW692971 NF057G06ST1F1000 Developing stem Medicago ...	85	1e-23
	emb AI966081 AI966081 sc27a12.y1 Gm-c1013 Glycine max cDNA clone...	110	3e-23
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	emb AW690067 AW690067 NF027E05ST1F1000 Developing stem Medicago ...	58	8e-22
55	emb AW218225 AW218225 EST303406 tomato radicle, 5 d post-imbibit...	105	1e-21
	emb AW696232 AW696232 NF104B05ST1F1044 Developing stem Medicago ...	61	1e-19
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	emb AW693419 AW693419 NF064H07ST1F1000 Developing stem Medicago ...	58	5e-18
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- emb|AW310634|AW310634 sg22e01.x1 Gm-c1024 Glycine max cDNA clone... 82 1e-14
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 5 emb|AW923051|AW923051 DG1_48_G08.g1_A002 Dark Grown 1 (DG1) Sorg... 74 2e-12
 emb|AW695860|AW695860 NF099D07ST1F1061 Developing stem Medicago ... 74 3e-12
 emb|AW704472|AW704472 sk53e05.y1 Gm-c1019 Glycine max cDNA clone... 74 3e-12
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 10 emb|AI756356|AI756356 EtESTea42h07.y1 Eimeria S5-2 Sporozoite st... 67 3e-10
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 emb|AI488088|AI488088 EST246410 tomato ovary, TAMU Lycopersicon ... 59 7e-08
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 15 emb|AW694277|AW694277 NF074D01ST1F1012 Developing stem Medicago ... 58 1e-07
 emb|AI812387|AI812387 1G6 Pine Lambda Zap Xylem library Pinus ta... 54 3e-06
 emb|AW985137|AW985137 NXNV_133_D09_F Nsf Xylem Normal wood Verti... 52 8e-06
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 20 emb|AI043540|AI043540 L30-547T3 Ice plant Lambda Uni-Zap XR expr... 48 2e-04
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 25 emb|AV424693|AV424693 AV424693 Lotus japonicus young plants (two... 46 7e-04
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 30 emb|AQ855371|AQ855371 CpG1905B CpIOWAgDNA1 Cryptosporidium parvu... 40 0.030
 emb|AW038228|AW038228 EST279885 tomato mixed elicitor, BTI Lycop... 40 0.030
 emb|AL114296|CNS01BJ4 Botrytis cinerea strain T4 cDNA library un... 40 0.057
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- emb|Z71753|NPPME3MR N.plumbaginifolia mRNA for pectin methyleste... 142 3e-34
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 55 emb|AW429110|AW429110 EST306566 tomato flower buds 0-3 mm, Corne... 135 5e-32
 emb|AW429158|AW429158 EST306614 tomato flower buds 0-3 mm, Corne... 135 5e-32
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 emb|AI780635|AI780635 EST261610 tomato susceptible, Cornell Lyco... 135 5e-32
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 60 emb|AW220185|AW220185 EST302668 tomato root during/after fruit s... 134 1e-31
 emb|AW154926|AW154926 EST290291 tomato root deficiency, Cornell ... 134 1e-31

- emb|X94443|VRPECMEST V.radiata mRNA for pectinmethylesterase. 133 2e-31
- emb|AW458218|AW458218 sh79h10.y1 Gm-cl016 Glycine max cDNA clone... 133 2e-31
- emb|AF152172|AF152172 Solanum tuberosum cultivar Desiree pectin ... 132 3e-31
- emb|AJ249786|NTA249786 Nicotiana tabacum partial mRNA for pectin... 132 3e-31
- 5 emb|AI494978|AI494978 sa93d09.y1 Gm-cl004 Glycine max cDNA clone... 132 3e-31
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- emb|AW623150|AW623150 EST321095 tomato flower buds 3-8 mm, Corne... 131 6e-31
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- 10 emb|X97762|STBPE1 S.tuberosum mRNA BPE1 for pectin methylesterase. 131 7e-31
- emb|X67425|PSPMEAG Pisum sativum pmeA gene for pectinesterase. 131 1e-30
- emb|AF056493|AF056493 Pisum sativum pectin methylesterase mRNA, ... 131 1e-30
- emb|AF081457|AF081457 Pisum sativum pectin methylesterase (rcpme... 131 1e-30
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- 15 emb|AW257345|AW257345 EST305482 KV2 Medicago truncatula cDNA clo... 130 2e-30
- emb|AI781140|AI781140 EST262019 tomato susceptible, Cornell Lyco... 129 3e-30
- emb|AI441604|AI441604 sa68e03.y1 Gm-cl004 Glycine max cDNA clone... 129 3e-30
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- emb|X68029|PVVPE2 P.vulgaris PvVPE2 mRNA for pectin esterase. 128 8e-30
- 20 emb|AW784073|AW784073 NXNV_117_D06_F Nsf Xylem Normal wood Verti... 126 2e-29
- emb|AW429112|AW429112 EST306568 tomato flower buds 0-3 mm, Corne... 126 3e-29
- emb|AW888107|AW888107 NXNV_129_C06_F Nsf Xylem Normal wood Verti... 125 5e-29
- emb|AW774488|AW774488 EST333639 KV3 Medicago truncatula cDNA clo... 124 9e-29
- emb|AF152171|AF152171 Solanum tuberosum cultivar Desiree pectin ... 121 8e-28
- 25 emb|A17010|A17010 tomato fruit pectin esterase seq ID no1. 121 1e-27
- emb|AW930691|AW930691 EST356534 tomato fruit mature green, TAMU ... 121 1e-27
- emb|AW934244|AW934244 EST360087 tomato fruit mature green, TAMU ... 121 1e-27
- emb|AW930330|AW930330 EST340883 tomato fruit mature green, TAMU ... 121 1e-27
- gb|S66607|S66607 Lycopersicon esculentum pectinmethylesterase-li... 121 1e-27
- 30 emb|AW221911|AW221911 EST298722 tomato fruit red ripe, TAMU Lyco... 121 1e-27
- emb|AW221863|AW221863 EST298674 tomato fruit red ripe, TAMU Lyco... 121 1e-27
- emb|X74638|LEPEC1 L.esculentum mRNA for pectin esterase. 121 1e-27
- emb|AW696177|AW696177 NF103C11ST1F1085 Developing stem Medicago ... 121 1e-27
- emb|AW760550|AW760550 sl51g07.y1 Gm-cl027 Glycine max cDNA clone... 120 2e-27
- 35 emb|AW289642|AW289642 NXNV003F09F Nsf Xylem Normal wood Vertical... 119 3e-27
- gb|U50986|SLU50986 Solanum lycopersicum pectin methylesterase PM... 119 4e-27
- gb|U70675|LEU70675 Lycopersicon esculentum fruit-specific pectin... 118 6e-27
- gb|U70676|LEU70676 Lycopersicon esculentum pectin methylesteras... 118 6e-27
- emb|Z71751|NPPME1MR N.plumbaginifolia mRNA for pectin methyleste... 118 8e-27
- 40 emb|AW932254|AW932254 EST358097 tomato fruit mature green, TAMU ... 118 8e-27
- emb|AF229849|AF229849 Vigna radiata pectin methylesterase isofor... 118 8e-27
- gb|U70677|LEU70677 Lycopersicon esculentum (LePME1) gene, partia... 118 8e-27
- gb|U82974|CSU82974 Citrus sinensis pectinesterase (PECS-I.2) gen... 117 1e-26
- emb|AI897776|AI897776 EST267219 tomato ovary, TAMU Lycopersicon ... 117 2e-26
- 45 gb|U50985|SLU50985 Solanum lycopersicum pectin methylesterase PM... 116 3e-26
- emb|AW758821|AW758821 NXNV_091_A04_F Nsf Xylem Normal wood Verti... 116 3e-26
- emb|A17011|A17011 tomato fruit pectin esterase with pPel DNA seq... 116 3e-26
- emb|X74639|LEPEC2 L.esculentum mRNA for pectin esterase clone. 116 3e-26
- emb|X07910|LEPECES Tomato mRNA for pectin esterase. 116 3e-26
- 50 emb|A15983|A15983 L.esculentum mRNA for pectin esterase. 116 3e-26
- emb|AW623570|AW623570 EST321515 tomato flower buds 3-8 mm, Corne... 116 3e-26
- emb|AW221834|AW221834 EST298645 tomato fruit red ripe, TAMU Lyco... 115 5e-26
- emb|X97763|STBPE2 S.tuberosum mRNA BPE2 for pectin methylesterase. 115 5e-26
- emb|A24196|A24196 L.esculentum pectin esterase clone pPE1. 113 2e-25
- 55 emb|AW687047|AW687047 NF005D06RT1F1057 Developing root Medicago... 113 2e-25
- emb|AW424141|AW424141 sh61d11.y1 Gm-cl015 Glycine max cDNA clone... 112 6e-25
- emb|AW398532|AW398532 EST309032 L. pennellii trichome, Cornell U... 111 8e-25
- emb|AW666622|AW666622 GA_Ea0005C20 Gossypium arboreum 7-10 dpa ... 110 2e-24
- emb|AW163926|AW163926 Ljirmp17-358-e10 Ljirmp Lambda HybriZap... 110 2e-24
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- emb|AI440753|AI440753 sa53f07.y1 Gm-cl004 Glycine max cDNA clone... 108 7e-24

- gb|U82977|CSU82977 Citrus sinensis pectinesterase mRNA, complete... 84 2e-23
 emb|AI731654|AI731654 BNLGH10367 Six-day Cotton fiber Gossypium... 106 4e-23
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 5 gb|BE123534|BE123534 NXNV_149_D04_F Nsf Xylem Normal wood Vertic... 103 2e-22
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 10 emb|Y07899|CPSPE1 C.papaya mRNA for pectinesterase. 97 3e-20
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 emb|AW220222|AW220222 EST302705 tomato root during/after fruit s... 62 4e-10

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 30 [post/entrez/query?db=n&form=6&dopt=g&uid=gb|al079344|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al079344|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al079344>
 (1386 letters).

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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| | emb AW563733 AW563733 LG1_248_C01.g1_A002 Light Grown 1 (LG1) So... | 205 | 5e-52 | |
| | gb BE053112 BE053112 GA_Ea0031A01f Gossypium arboreum 7-10 dpa ... | 166 | 2e-50 | |
| | emb AV409759 AV409759 AV409759 Lotus japonicus young plants (two... | 165 | 4e-44 | |
| 45 | emb AW704801 AW704801 sk55f12.y1 Gm-c1019 Glycine max cDNA clone... | 148 | 3e-43 | |
| | emb AL034352 SPBC725 S.pombe chromosome II cosmid c725. | 87 | 6e-42 | |
| | gb C96280 C96280 C96280 Marchantia polymorpha immature sex organ... | 89 | 9e-37 | |
| | emb AW599232 AW599232 gb12b03.y1 Moss EST library PPN Physcomitr... | 154 | 1e-36 | |
| | emb AW306350 AW306350 se49e12.y1 Gm-c1017 Glycine max cDNA clone... | 116 | 2e-33 | |
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	emb AF130334 AF130334 Bruguiera cylindrica internal transcribed ...	35	1.9
20	gb B13384 B13384 jd152 Trypanosome Shotgun M13 genomic Trypanoso...	34	2.7
	emb AQ500377 AQ500377 V40F1 mTn-3xHA/lacZ Insertion Library Sacc...	34	2.7
	emb AW102097 AW102097 sd83a09.y1 Gm-c1009 Glycine max cDNA clone...	34	2.7
	emb AW334235 AW334235 S32B4 AGS-1 Pneumocystis carinii f. sp. ca...	34	3.6
	emb AW648115 AW648115 EST326569 tomato germinating seedlings, TA...	34	3.6
25	emb AQ500705 AQ500705 V33B7 mTn-3xHA/lacZ Insertion Library Sacc...	34	3.6
	emb AW220222 AW220222 EST302705 tomato root during/after fruit s...	34	3.6
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	gb M55447 BLYRCAA2 Hordeum vulgare rubisco activase (RcaA2) mRNA...	34	3.6
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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

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	emb X94986 MEBGLA M.esculenta bgIA gene.	94	6e-20
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	gb U39228 AU39228 Prunus avium beta-glucosidase mRNA, partial cds.	93	8e-20
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/gb_link <http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af024504|/ncgi>
<http://www.ncgr.org/cgi-bin/ff7af024504>
 (1374 letters)

5

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

10

Searching.....done

15

Score E
 Sequences producing significant alignments: (bits) Value

emb|AW216758|AW216758 EST295472 tomato callus, TAMU Lycopersicon... 119 3e-34
 15 emb|AW219044|AW219044 EST301526 tomato root during/after fruit s... 108 7e-33
 emb|AW031258|AW031258 EST274633 tomato callus, TAMU Lycopersicon... 108 7e-33
 emb|AI772760|AI772760 EST253860 tomato resistant, Cornell Lycopen... 108 7e-33
 emb|AI486533|AI486533 EST244854 tomato ovary, TAMU Lycopersicon ... 71 5e-29
 emb|AI898645|AI898645 EST268088 tomato ovary, TAMU Lycopersicon ... 71 6e-28
 20 emb|AW686482|AW686482 NF041H08NR1F1000 Nodulated root Medicago t... 112 8e-28
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 emb|AW759958|AW759958 sl56c04.y1 Gm-c1027 Glycine max cDNA clone... 115 7e-25
 emb|AW126130|AW126130 N100327e rootphos(-) Medicago truncatula c... 115 1e-24
 25 emb|AI776363|AI776363 EST257463 tomato resistant, Cornell Lycopen... 114 1e-24
 emb|AI731720|AI731720 BNLGHi10579 Six-day Cotton fiber Gossypium... 112 5e-24
 emb|AW034441|AW034441 EST278012 tomato callus, TAMU Lycopersicon... 103 5e-24
 emb|AI896076|AI896076 EST265519 tomato callus, TAMU Lycopersicon... 102 1e-23
 emb|AI898707|AI898707 EST268150 tomato ovary, TAMU Lycopersicon ... 71 2e-22
 30 emb|AW310471|AW310471 sf36e11.x1 Gm-c1028 Glycine max cDNA clone... 105 6e-22
 emb|AW219445|AW219445 EST302023 tomato root during/after fruit s... 105 8e-22
 emb|AW648110|AW648110 EST326564 tomato germinating seedlings, TA... 105 1e-21
 emb|AW831572|AW831572 sm34h08.y1 Gm-c1028 Glycine max cDNA clone... 100 2e-20
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 35 emb|AW671843|AW671843 LG1_352_B09.b1_A002 Light Grown 1 (LG1) So... 64 2e-18
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 40 emb|AW565825|AW565825 LG1_352_B09.g1_A002 Light Grown 1 (LG1) So... 57 8e-14
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 45 emb|AW398760|AW398760 EST309260 L. pennellii trichome, Cornell U... 54 2e-12
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 emb|AW394635|AW394635 sh33h09.y1 Gm-c1017 Glycine max cDNA clone... 55 3e-12
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 50 emb|AI728748|AI728748 BNLGHi11497 Six-day Cotton fiber Gossypium... 57 4e-12
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 55 emb|AW734790|AW734790 sk88g11.y1 Gm-c1035 Glycine max cDNA clone... 42 5e-09
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 60 emb|AW282482|AW282482 LG1_313_B10.g1_A002 Light Grown 1 (LG1) So... 57 3e-07
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- emb|AT000645|AT000645 AT000645 Brassica rapa guard cell Brassica... 56 6e-07
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 5 emb|AW154916|AW154916 EST290281 tomato root deficiency, Cornell ... 40 6e-05
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 emb|AI490477|AI490477 EST248846 tomato ovary, TAMU Lycopersicon ... 44 1e-04
 emb|AI895257|AI895257 EST264700 tomato callus, TAMU Lycopersicon... 47 4e-04
 10 emb|AW564044|AW564044 LG1_281_A09.b1_A002 Light Grown 1 (LG1) So... 47 4e-04
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 15 emb|AI486814|AI486814 EST245136 tomato ovary, TAMU Lycopersicon ... 46 5e-04
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 20 emb|AI728904|AI728904 BNLGH11968 Six-day Cotton fiber Gossypium... 41 0.002
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 25 emb|AI485669|AI485669 EST243990 tomato ovary, TAMU Lycopersicon ... 44 0.003
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- Query= AC006920.138_at 12642_at /id_source genbank /description
 55 gb|aad22285.1|ac006920_9 (ac006920) unknown protein [arabidopsis
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 http://www.ncgr.org/cgi-bin/ff?ac006920
 60 (1512 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments: (bits) Value

- emb|AF223643|AF223643 Pisum sativum xyloglucan fucosyltransferas... 311 e-147
- 10 emb|AW719438|AW719438 LjNEST4f10r Lotus japonicus nodule library... 164 1e-64
- emb|AA660464|AA660464 00349 MtRHE Medicago truncatula cDNA 5', m... 128 6e-38
- emb|AW693268|AW693268 NF064A03ST1F1000 Developing stem Medicago ... 109 5e-32
- emb|AW508697|AW508697 si35c12.y1 Gm-r1030 Glycine max cDNA clone... 77 6e-31
- emb|AW689377|AW689377 NF018E07ST1F1000 Developing stem Medicago ... 78 2e-30
- 15 gb|BE058474|BE058474 sn16f08.y1 Gm-c1016 Glycine max cDNA clone ... 102 6e-21
- emb|AW704030|AW704030 sk27a04.y1 Gm-c1028 Glycine max cDNA clone... 64 5e-20
- emb|AU089974|AU089974 AU089974 Hordeum vulgare subsp. vulgare Up... 45 1e-19
- emb|AW720399|AW720399 LjNEST22c8r Lotus japonicus nodule library... 83 1e-18
- emb|AU089968|AU089968 AU089968 Hordeum vulgare subsp. vulgare Up... 45 5e-17
- 20 emb|AV417193|AV417193 AV417193 Lotus japonicus young plants (two... 88 2e-16
- emb|AQ855554|AQ855554 CpG1646A CpIOWAgDNA1 Cryptosporidium parvu... 35 1.1
- emb|Z37536|LTND9 L.tarentolae ND9 mRNA encoding putative NADH de... 35 2.1
- emb|AW934637|AW934637 EST353529 tomato flower buds 0-3 mm, Corne... 35 2.1
- emb|AF050740|AF050740 Plasmodium falciparum variant-specific sur... 35 2.1
- 25 emb|AI329848|AI329848 b8h09ne.r1 Neurospora crassa evening cDNA ... 35 2.1
- emb|AW035275|AW035275 EST280638 tomato callus, TAMU Lycopersicon... 35 2.1
- emb|AW933190|AW933190 EST359033 tomato fruit mature green, TAMU ... 35 2.1
- emb|AL109832|SPAC630 S.pombe chromosome I cosmid c630. 34 2.9
- emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 34 4.0
- 30 emb|A85491|A85491 Sequence 150 from Patent EP0866129. 34 4.0
- emb|AC004688|AC004688 Plasmodium falciparum chromosome 12 clone ... 34 4.0
- emb|AA786891|AA786891 m7a05a1.r1 Aspergillus nidulans 24hr asexu... 34 4.0
- gb|BE124954|BE124954 EST393989 GVN Medicago truncatula cDNA clon... 27 4.7
- emb|AL356172|NCB23L21 Neurospora crassa DNA linkage group II BAC... 33 5.5
- 35 emb|AW617216|AW617216 EST323627 L. hirsutum trichome, Cornell Un... 33 5.5
- emb|AL160493|LMFLCHR26 Leishmania major Friedlin assembled chrom... 33 7.6
- emb|AF056622|AF056622 Vitis vinifera putative Cu/Zn superoxide d... 33 7.6
- gb|BE053037|BE053037 GA__Ea0031O23f Gossypium arboreum 7-10 dpa ... 33 7.6
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- (1488 letters)
- 45 Database: plantfungal
- 661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments: (bits) Value

- emb|AW203670|AW203670 sf36h04.y1 Gm-c1028 Glycine max cDNA clone... 334 1e-90
- 55 emb|AW268012|AW268012 EST306234 DSIR Medicago truncatula cDNA cl... 246 2e-83
- emb|AW041000|AW041000 EST283864 tomato mixed elicitor, BTI Lycop... 307 1e-82
- emb|AW472433|AW472433 si25b07.y1 Gm-c1029 Glycine max cDNA clone... 306 3e-82
- emb|AW560118|AW560118 EST315166 DSIR Medicago truncatula cDNA cl... 166 3e-64
- emb|AW394771|AW394771 sh35b02.y1 Gm-c1017 Glycine max cDNA clone... 213 3e-54
- 60 emb|AW622568|AW622568 EST313368 tomato root during/after fruit s... 181 5e-51
- emb|AW737712|AW737712 EST339139 tomato flower buds, anthesis, Co... 162 1e-45

- emb|AW694002|AW694002 NF071F03ST1F1029 Developing stem Medicago ... 135 2e-45
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 emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 114 1e-38
 5 emb|AL111746|CNS019KA Botrytis cinerea strain T4 cDNA library un... 123 2e-38
 emb|AL111744|CNS019K8 Botrytis cinerea strain T4 cDNA library un... 123 3e-37
 emb|AW922483|AW922483 DG1_19_A10.g1_A002 Dark Grown 1 (DG1) Sorg... 155 8e-37
 emb|Z49211|SC9711X S.cerevisiae chromosome XIII cosmid 9711. 113 3e-36
 gb|U34636|SCU34636 Saccharomyces cerevisiae cytochrome P450 gene... 113 3e-36
 emb|AW928489|AW928489 EST337277 tomato flower buds 8 mm to pre-a... 149 5e-35
 10 emb|AL033396|CAC35A5 C.albicans cosmid Ca35A5. 117 2e-34
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 15 emb|AU012887|AU012887 AU012887 Schizosaccharomyces pombe late lo... 71 1e-12
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 25 emb|AA556134|AA556134 TENF0475 T.cruzi epimastigote normalized c... 61 2e-08
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 40 emb|AW728587|AW728587 GA_Ea0017C12 Gossypium arboreum 7-10 dpa ... 37 2e-05
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 60 emb|AW255346|AW255346 ML357 peppermint glandular trichome Mentha... 37 1e-04
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30	emb AI728374 AI728374 BNLGHI10609 Six-day Cotton fiber Gossypium...	43	0.005
	emb AI485472 AI485472 EST243793 tomato ovary, TAMU Lycopersicon ...	43	0.005

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 40 (417 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

45 Searching.....done

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	emb AI728590 AI728590 BNLGHI11133 Six-day Cotton fiber Gossypium...	60	7e-13
	emb AI731959 AI731959 BNLGHI11511 Six-day Cotton fiber Gossypium...	60	7e-13
	emb AI775217 AI775217 EST256317 tomato resistant, Cornell Lycope...	59	7e-13
55	emb AW458973 AW458973 sh17e01.y1 Gm-c1016 Glycine max cDNA clone...	61	3e-12
	emb AW132527 AW132527 se05c02.y1 Gm-c1013 Glycine max cDNA clone...	61	3e-12
	emb AW102493 AW102493 sd88b04.y1 Gm-c1009 Glycine max cDNA clone...	61	4e-12
	emb AV421249 AV421249 AV421249 Lotus japonicus young plants (two...	62	2e-09
	emb AW691065 AW691065 NF040H08ST1F1000 Developing stem Medicago ...	61	3e-09
60	emb AW349295 AW349295 GM210004B12D12R Gm-r1021 Glycine max cDNA ...	46	8e-08
	emb AW101242 AW101242 sd97a09.y1 Gm-c1013 Glycine max cDNA clone...	56	2e-07

	emb AI898360 AI898360 EST267803 tomato ovary, TAMU Lycopersicon ...	39	6e-07
	emb AI496321 AI496321 sb05c05.y1 Gm-cl004 Glycine max cDNA clone...	50	9e-06
	emb AW208239 AW208239 M110892e GVSN Medicago truncatula cDNA clo...	48	3e-05
	emb AI489067 AI489067 EST247406 tomato ovary, TAMU Lycopersicon ...	45	3e-04
5	emb AI771636 AI771636 EST252736 tomato ovary, TAMU Lycopersicon ...	45	3e-04
	emb AW219417 AW219417 EST301995 tomato root during/after fruit s...	45	3e-04
	emb AI898830 AI898830 EST268273 tomato ovary, TAMU Lycopersicon ...	45	3e-04
	emb AI489478 AI489478 EST247817 tomato ovary, TAMU Lycopersicon ...	45	3e-04
	emb AI489770 AI489770 EST248109 tomato ovary, TAMU Lycopersicon ...	45	3e-04
10	emb AW672287 AW672287 LG1_358_A02.b1_A002 Light Grown 1 (LG1) So...	44	5e-04
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	emb AI488844 AI488844 EST247183 tomato ovary, TAMU Lycopersicon ...	44	7e-04
	emb AJ238740 CRO238740 Catharanthus roseus mRNA for AP2-domain D...	43	0.001
	emb AV424732 AV424732 AV424732 Lotus japonicus young plants (two...	42	0.002
15	emb AW040122 AW040122 EST282621 tomato mixed elicitor, BTI Lycop...	33	0.002
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25	emb AI731460 AI731460 BNLGH19812 Six-day Cotton fiber Gossypium ...	42	0.003
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30	emb AI795106 AI795106 sb76f04.y1 Gm-cl010 Glycine max cDNA clone...	41	0.004
	emb AW694919 AW694919 NF081D08ST1F1073 Developing stem Medicago ...	41	0.004
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40	emb AW318239 AW318239 sg62g03.y1 Gm-cl007 Glycine max cDNA clone...	40	0.007
	emb AW706818 AW706818 sk03g11.y1 Gm-cl023 Glycine max cDNA clone...	40	0.009
	emb AI166481 AI166481 xylem.est.309 Poplar xylem Lambda ZAPII li...	40	0.013
	emb AW759250 AW759250 sl38g10.y1 Gm-cl027 Glycine max cDNA clone...	39	0.018
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50	emb AW031292 AW031292 EST274667 tomato callus, TAMU Lycopersicon...	39	0.018
	emb AI487841 AI487841 EST246163 tomato ovary, TAMU Lycopersicon ...	39	0.018
	emb AW032262 AW032262 EST275716 tomato callus, TAMU Lycopersicon...	39	0.018
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55	emb AI988644 AI988644 sd05h06.y1 Gm-cl020 Glycine max cDNA clone...	39	0.024
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60	emb AW030386 AW030386 EST273641 tomato callus, TAMU Lycopersicon...	39	0.024
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- emb|AI973653|AI973653 sd07h05.y1 Gm-c1020 Glycine max cDNA clone... 39 0.024
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 emb|AI899237|AI899237 EST268680 tomato ovary, TAMU Lycopersicon ... 38 0.046
 emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 38 0.046
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 25 emb|AI895984|AI895984 EST265427 tomato callus, TAMU Lycopersicon... 38 0.046
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 35 (1161 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

- 40 Searching.....done

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| | Sequences producing significant alignments: | (bits) | Value |
| 45 | emb AW185155 AW185155 se87e11.y1 Gm-c1023 Glycine max cDNA clone... | 134 | 2e-30 |
| | emb AW278569 AW278569 sf46b12.y1 Gm-c1009 Glycine max cDNA clone... | 131 | 1e-29 |
| | emb AW683973 AW683973 NF004E08NR1F1000 Nodulated root Medicago t... | 97 | 2e-19 |
| | emb AI055338 AI055338 coau0003L11 Cotton Boll Abscission Zone cD... | 56 | 2e-07 |
| | emb AW693058 AW693058 NF059E03ST1F1021 Developing stem Medicago ... | 49 | 9e-05 |
| 50 | emb AW686062 AW686062 NF033A11NR1F1000 Nodulated root Medicago t... | 49 | 9e-05 |
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| | gb M86518 PFAHMGPL Plasmodium falciparum high mobility group-lik... | 35 | 1.1 |
| 55 | emb AQ952389 AQ952389 Sheared DNA-32H3.TF Sheared DNA Trypanosom... | 35 | 1.1 |
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| 60 | emb AL049183 PFMAL13P6 Plasmodium falciparum chromosome 13 strai... | 33 | 2.8 |
| | emb AF108883 AF108883 Capsicum annuum small GTP-binding protein ... | 28 | 3.6 |

emb|X75082|STCITS *S.tuberosum* mRNA for mitochondrial citrate-syn... 33 3.9
 emb|A46545|A46545 Sequence 1 from Patent WO9524487. 33 3.9
 emb|X07693|SPNUC2 Fission yeast nuc2 gene encoding nuclear scaff... 33 3.9
 emb|X83997|CPEAPC *C.parasitica* eapC gene. 33 3.9

5 emb|AF143971|AF143971 *Pinus taeda* microsatellite PtTX3026 sequence. 33 3.9
 emb|AW667663|AW667663 GA_Ea0010C16 *Gossypium arboreum* 7-10 dpa ... 33 5.0
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10 emb|AW761626|AW761626 gb27h09.y1 Moss EST library PPN Physcomitr... 32 6.9
 emb|AI055163|AI055163 coau0003D12 Cotton Boll Abscission Zone cD... 32 6.9
 emb|AW761333|AW761333 sl66b07.y1 Gm-c1027 Glycine max cDNA clone... 32 6.9
 emb|AI822729|AI822729 L0-1261T3 Ice plant Lambda Uni-Zap XR expr... 32 6.9
 emb|AW931465|AW931465 EST357308 tomato fruit mature green, TAMU ... 32 7.3

15 emb|AA555413|AA555413 CpEST.644 uniZAPCpIOWAsporoLib3 Cryptospor... 32 7.3
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 emb|AQ640247|AQ640247 927P1-18B12.TV 927P1 *Trypanosoma brucei* ge... 32 7.3
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20 emb|AF143965|AF143965 *Pinus taeda* microsatellite PtTX3011 sequence. 32 7.3
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 emb|AJ225402|AJ225402 AJ225402 Absciscic acid-treated protonemata... 32 9.4

25 emb|AW735860|AW735860 EST336628 tomato flower buds 0-3 mm, Corne... 32 9.4
 emb|AW756470|AW756470 sl21g05.y1 Gm-c1036 Glycine max cDNA clone... 32 9.4

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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002521|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002521|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002521|/ncgi)
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 (999 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

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	Score	E
Sequences producing significant alignments:	(bits)	Value
emb AI727718 AI727718 BNLGHi8830 Six-day Cotton fiber <i>Gossypium</i> ...	405	e-112
45 emb AI894939 AI894939 EST264382 tomato callus, TAMU <i>Lycopersicon</i> ...	405	e-112
emb AI727173 AI727173 BNLGHi7479 Six-day Cotton fiber <i>Gossypium</i> ...	404	e-112
emb AW091566 AW091566 EST284842 tomato mixed elicitor, BTI <i>Lycop</i> ...	364	e-100
emb AW201381 AW201381 sf02d09.y1 Gm-c1027 Glycine max cDNA clone...	301	1e-98
emb AW397167 AW397167 sg67f10.y1 Gm-c1007 Glycine max cDNA clone...	287	1e-94
50 emb AW038822 AW038822 EST280778 tomato mixed elicitor, BTI <i>Lycop</i> ...	282	3e-75
emb AI488594 AI488594 EST246933 tomato ovary, TAMU <i>Lycopersicon</i> ...	280	2e-74
emb AW926055 AW926055 HVSMEg0006C20 <i>Hordeum vulgare</i> pre-anthesis...	160	2e-71
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emb AW329252 AW329252 N200470e rootphos(-) <i>Medicago truncatula</i> c...	246	2e-64
55 emb AW932653 AW932653 EST358496 tomato fruit mature green, TAMU ...	246	2e-64
emb AW508528 AW508528 si33a06.y1 Gm-r1030 Glycine max cDNA clone...	177	8e-60
emb AW201152 AW201152 se98d11.y1 Gm-c1027 Glycine max cDNA clone...	137	1e-49
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 emb|AL096796|SPBC839 *S.pombe* chromosome II cosmid c839. 65 2e-25
 emb|AL021816|SPBC24E9 *S.pombe* chromosome II cosmid c24E9. 65 2e-25
 5 emb|AW395997|AW395997 sh08a03.y1 *Gm-c1016 Glycine max* cDNA clone... 114 1e-24
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 10 emb|AQ449927|AQ449927 500006A04.x1 CpIOWAM13mp18gDNA1 Cryptospor... 65 1e-09
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 emb|AW932638|AW932638 EST358481 tomato fruit mature green, TAMU ... 36 0.37
 emb|AQ845544|AQ845544 LMAJFV1_1m26h01.y1 *Leishmania major* FV1 ra... 35 0.70
 emb|AC007862|AC007862 Trypanosoma brucei chromosome II clone RPC... 35 0.97
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 25 emb|Z38062|SC9687 *S.cerevisiae* chromosome IX cosmid 9687. 35 1.3
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 emb|AW596179|AW596179 si99a03.y1 *Gm-c1032 Glycine max* cDNA clone... 33 4.7
 emb|AJ055366|AJ055366 coau0003M17 Cotton Boll Abscission Zone cD... 33 4.7
 emb|AW696344|AW696344 NF106H09ST1F1079 Developing stem *Medicago* ... 31 5.0
 50 gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 32 6.5
 emb|X58396|HVEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 32 6.5
 emb|AL121851|LMFL2581 *Leishmania major* Friedlin chromosome 23 co... 32 6.5
 emb|AW731480|AW731480 GA_Ea0030L23 *Gossypium arboreum* 7-10 dpa ... 32 6.5
 gb|BE058697|BE058697 sn19e12.y1 *Gm-c1016 Glycine max* cDNA clone ... 32 6.5
 55 emb|AL031324|SPCC1672 *S.pombe* chromosome III cosmid c1672. 32 6.5
 emb|AC007865|AC007865 Trypanosoma brucei chromosome II clone RPC... 28 6.8
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 emb|AW255452|AW255452 ML474 peppermint glandular trichome *Mentha*... 26 7.0
 emb|AI490316|AI490316 EST248642 tomato ovary, TAMU *Lycopersicon* ... 28 7.2
 60 emb|AF124817|AF124817 *Mentha x piperita* cytochrome p450 isoform ... 26 8.9
 emb|AJ133001|CPL133001 *Craterostigma plantagineum* mRNA for phosp... 32 8.9

- emb|AW348239|AW348239 GM210001B12D9R Gm-r1021 Glycine max cDNA 3... 32 8.9
 emb|AQ903735|AQ903735 GSSTc04776 Trypanosome cruzi random genom... 32 8.9
 emb|AB014483|AB014483 Nicotiana tabacum NtHSF1 mRNA for heat sho... 32 8.9
 emb|AF016328|AF016328 Hordeum vulgare Barperm2 (perm2) mRNA, par... 32 8.9
 5 emb|AW696053|AW696053 NF102A09ST1F1068 Developing stem Medicago ... 32 8.9
 emb|AW691566|AW691566 NF046E03ST1F1000 Developing stem Medicago ... 32 8.9
 emb|AW309484|AW309484 sf20a10.x1 Gm-c1028 Glycine max cDNA clone... 32 8.9
 emb|AI442542|AI442542 sa32h01.y1 Gm-c1004 Glycine max cDNA clone... 32 8.9
 10 emb|X55347|LPHSF24 Tomato mRNA for heat stress transcription fac... 32 8.9
 emb|X54488|CRAH2 Chlamydomonas reinhardtii CAH2 gene for carbon... 32 8.9
 emb|A85864|A85864 Sequence 523 from Patent EP0866129. 32 8.9
 emb|AF020814|AF020814 Pisum sativum glucose-6-phosphate/phosphat... 32 8.9
 emb|AW184970|AW184970 se84g02.y1 Gm-c1023 Glycine max cDNA clone... 32 8.9
 emb|Z46871|SOEXG1 S.occidentalis gene for exo-1,3-beta-glucanase... 32 8.9
 15 emb|AI163250|AI163250 A038p15u Hybrid aspen plasmid library Popu... 32 8.9
 emb|AL023592|SPCC550 S.pombe chromosome III cosmid c550. 32 8.9
 emb|AW668371|AW668371 GA_Ea0013L20 Gossypium arboreum 7-10 dpa ... 26 9.3
 emb|AW255363|AW255363 ML376 peppermint glandular trichome Menth... 26 9.5
 gb|C96116|C96116 Marchantia polymorpha immature sex organ... 27 9.6
 20 emb|AW255126|AW255126 ML1418 peppermint glandular trichome Menth... 26 9.8

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 25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000348|/ncgi)
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 (1869 letters)

- 30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

- 35 Score E
 Sequences producing significant alignments: (bits) Value

- emb|AW622865|AW622865 EST306935 tomato flower buds 3-8 mm, Corne... 246 3e-64
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 40 emb|AW596038|AW596038 si97b04.y1 Gm-c1032 Glycine max cDNA clone... 98 4e-28
 emb|AW774367|AW774367 EST333518 KV3 Medicago truncatula cDNA clo... 101 1e-25
 emb|AW459521|AW459521 sh42e12.y1 Gm-c1017 Glycine max cDNA clone... 96 5e-24
 emb|AW777159|AW777159 Str2-E4 Sugar Beet germination cDNA libr... 82 1e-20
 emb|AW694460|AW694460 NF076E10ST1F1082 Developing stem Medicago ... 95 1e-18
 45 emb|AW651335|AW651335 EST329789 tomato germinating seedlings, TA... 82 8e-15
 gb|BE052602|BE052602 GA_Ea0032J02f Gossypium arboreum 7-10 dpa ... 50 2e-13
 emb|AW928691|AW928691 EST337479 tomato flower buds 8 mm to pre-a... 50 2e-09
 emb|AW226419|AW226419 ST82B05 Pine TripleEx shoot tip library Pin... 62 2e-08
 emb|AW398212|AW398212 EST298059 L. pennellii trichome, Cornell U... 60 4e-08
 50 emb|AT002124|AT002124 AT002124 Flower bud cDNA Brassica rapa sub... 44 0.004
 emb|AW666214|AW666214 sk33g11.y1 Gm-c1028 Glycine max cDNA clone... 40 0.040
 gb|U51033|YSCP9513 Saccharomyces cerevisiae chromosome XVI cosmi... 38 0.19
 emb|AI725302|AI725302 1168 PtIFG2 Pinus taeda cDNA clone 9253r, ... 38 0.19
 emb|AB035928|AB035928 Malus transitoria mRNA for St-RNase, compl... 36 0.50
 55 emb|Z48618|SCCHVII35 S.cerevisiae genes for RAD54, ACE1(CUP2), P... 36 0.68
 emb|Z72673|SCYGL151W S.cerevisiae chromosome VII reading frame O... 36 0.68
 emb|AF126872|AF126872 Magnaporthe grisea magnaporin mRNA, comple... 36 0.68
 emb|AF044679|AF044679 Leishmania major thiol specific antioxidan... 31 1.0
 emb|AC011617|AC011617 Leishmania major chromosome 35 clone L2993... 36 1.3
 60 emb|AB002141|AB002141 Pyrus pyrifolia mRNA for S5-RNase, complet... 35 1.3
 dbj|D88282|D88282 Pyrus serotina mRNA for S5-RNase, complete cds. 35 1.3

- emb|AB025421|AB025421 *Pyrus pyrifolia* gene for S3-RNase, complet... 35 1.3
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 emb|AL357592|LMFL5856 *Leishmania major* Friedlin chromosome 5 cos... 35 1.3
 5 emb|AW180136|AW180136 MgA0212f MgA Library *Mycosphaerella gramin...* 35 1.8
 emb|AW677734|AW677734 WS1_10_E07.g1_A002 Water-stressed 1 (WS1) ... 35 1.8
 emb|AI780435|AI780435 EST261314 tomato susceptible, Cornell Lyco... 34 2.4
 emb|AL355928|NCB1D4 *Neurospora crassa* DNA linkage group II BAC c... 34 2.4
 emb|AF188714|AF188714 *Emericella nidulans* chromosome VIII cosmid... 34 2.4
 10 emb|AF138284|AF138284 *Emericella nidulans* molybdopterin synthase... 34 2.4
 gb|M23080|BLYHORA *Hordeum vulgare* alpha-hordothionin (Hth-1) gen... 26 3.3
 emb|AQ989014|AQ989014 35CID04NE.R1 *C. parvum* Lambda Zap Express ... 34 3.3
 emb|X55685|LEEXTEN5 Tomato extensin mRNA (clone uG-18). 34 3.3
 emb|AB001337|AB001337 *Saccharum officinarum* mRNA for Sucrose-Pho... 34 3.3
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 15 emb|AL035064|SPAC1687 *S.pombe* chromosome I cosmid c1687. 34 3.3
 emb|AJ223010|SCP223010 *Schizosaccharomyces pombe* pmt2 gene. 34 3.3
 emb|AL356456|LMFLUNK01 *Leishmania major* Friedlin cosmid clones L... 34 3.3
 emb|AW683291|AW683291 NF010B07LF1F1060 Developing leaf Medicago ... 34 3.3
 emb|X63357|HVNREHTH *H.vulgare* Hth-1 gene (promoter region). 26 3.3
 20 emb|AW710511|AW710511 e4c05ne.fl *Neurospora crassa* evening cDNA ... 34 4.4
 emb|AQ411888|AQ411888 CpG0892A CpIOWAgDNA1 *Cryptosporidium parvu...* 34 4.4
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 emb|AF128526|AF128526 *Theileria lestoquardi* sporozoite antigen S... 33 4.6
 25 gb|M76671|TOMEXTENB *L.esculentum* extensin (class II) gene, compl... 33 4.6
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 emb|AC004145|AC004145 *Leishmania major* chromosome 3 clone LS801 ... 32 4.8
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 30 emb|AW725958|AW725958 GA_Ea0020E02 *Gossypium arboreum* 7-10 dpa ... 33 6.1
 emb|X91837|SCCHVIEU *S.cerevisiae* G1301, G1304, G1307, G1315, G1... 33 6.1
 emb|Z72717|SCYGL195W *S.cerevisiae* chromosome VII reading frame O... 33 6.1
 emb|X55694|LEEXTEN14 Tomato extensin mRNA (clone w10-1 L). 33 6.3
 emb|X55693|LEEXTEN13 Tomato mRNA for a glycine-rich protein (clo... 33 6.3
 35 emb|AV427911|AV427911 AV427911 *Lotus japonicus* young plants (two... 33 6.3
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 emb|AW690872|AW690872 NF039H07ST1F1000 Developing stem Medicago ... 33 6.3
 emb|AW688252|AW688252 NF005C01ST1F1000 Developing stem Medicago ... 33 6.3
 gb|L38908|TOBEXTE *Nicotiana tabacum* extensin gene, complete cds. 33 6.3
 40 dbj|D13951|TOBEXTS Tobacco gene for extensin, complete cds. 33 6.3
 dbj|E05393|E05393 DNA sequence encoding *Nicotiana tabacum* extensin. 33 6.3
 emb|AA901958|AA901958 NCC2C12T7 Conidial *Neurospora crassa* cDNA ... 33 8.3
 emb|AW704352|AW704352 sk18c03.y1 Gm-cl028 Glycine max cDNA clone... 33 8.3
 emb|AF085735|AF085735 *Trypanosoma triglae* kinetoplast minicircle... 33 8.3
 45 emb|AW457944|AW457944 sh97h02.y1 Gm-cl016 Glycine max cDNA clone... 33 8.3
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 emb|AQ941354|AQ941354 Sheared DNA-19O3.TR Sheared DNA *Trypanosom...* 32 8.6
 emb|AF046120|AF046120 *Candida glabrata* ATP-binding cassette tran... 32 8.6
 50 emb|AW725268|AW725268 GA_Ea0015L23 *Gossypium arboreum* 7-10 dpa ... 32 8.6
 emb|X77955|NCERG3 *N.crassa* (74-OR23-1VA) erg3 gene. 27 8.8

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 55 /blast_score 1.00e-103 /ec_number /family /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022605|/ncgi)
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 (645 letters)

60

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5	Score	E
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	emb AW351246 AW351246 GM210011A20F7R Gm-r1021 Glycine max cDNA 3...	114 3e-43
10	emb AW222063 AW222063 EST298874 tomato fruit red ripe, TAMU Lyco...	103 4e-40
	emb AW218145 AW218145 EST303326 tomato radicle, 5 d post-imbibit...	103 1e-39
	emb AW398260 AW398260 EST298107 L. pennellii trichome, Cornell U...	101 3e-39
	emb AW477271 AW477271 ga44c12.y1 Moss EST library PPU Physcomitr...	94 1e-38
	emb AW568049 AW568049 si56g06.y1 Gm-r1030 Glycine max cDNA clone...	102 1e-36
15	emb AW565775 AW565775 LG1_349_D04.g1_A002 Light Grown 1 (LG1) So...	108 5e-35
	emb AW218146 AW218146 EST303327 tomato radicle, 5 d post-imbibit...	108 5e-26
	emb AI488047 AI488047 EST246369 tomato ovary, TAMU Lycopersicon ...	78 3e-24
	emb AW671633 AW671633 LG1_349_D04.b1_A002 Light Grown 1 (LG1) So...	111 4e-24
	emb AI495965 AI495965 sb18d07.y1 Gm-c1004 Glycine max cDNA clone...	102 3e-21
20	emb AT002115 AT002115 AT002115 Flower bud cDNA Brassica rapa sub...	52 1e-09
	emb AT001714 AT001714 AT001714 Flower bud cDNA Brassica rapa sub...	52 3e-09
	emb AW621058 AW621058 sj95d05.y1 Gm-c1023 Glycine max cDNA clone...	52 3e-08
	emb AW099304 AW099304 sd38a08.y1 Gm-c1016 Glycine max cDNA clone...	33 0.092
	emb AI774719 AI774719 EST255819 tomato resistant, Cornell Lycope...	35 0.12
25	emb AW040524 AW040524 EST283484 tomato mixed elicitor, BTI Lycop...	35 0.12
	emb AB003068 AB003068 Trypanosoma cruzi clone TcCE5-9-1 mRNA, pa...	36 0.22
	emb AI781680 AI781680 EST262559 tomato susceptible, Cornell Lyco...	33 0.29
	emb AI778418 AI778418 EST259297 tomato susceptible, Cornell Lyco...	33 0.29
	emb AI775731 AI775731 EST256831 tomato resistant, Cornell Lycope...	35 0.78
30	emb AF047694 AF047694 Vernicia fordii glutaredoxin mRNA, complet...	34 1.1
	emb AW599677 AW599677 ga91d04.y1 Moss EST library PPN Physcomitr...	34 1.1
	emb AW039130 AW039130 EST281103 tomato mixed elicitor, BTI Lycop...	31 1.3
	emb AB003073 AB003073 Trypanosoma cruzi clone CE5-9-5 mRNA, part...	34 1.5
	emb AI899521 AI899521 EST268964 tomato susceptible, Cornell Lyco...	30 1.8
35	emb AI055583 AI055583 coau0004G11 Cotton Boll Abscission Zone cD...	33 2.0
	emb AI776180 AI776180 EST257280 tomato resistant, Cornell Lycope...	30 2.4
	emb AL110509 SPAC1250 S.pombe chromosome I cosmid c1250.	33 2.8
	emb Z74775 SCYOL033W S.cerevisiae chromosome XV reading frame OR...	33 2.8
	gb BE034215 BE034215 MH01C08 MH Mesembryanthemum crystallinum cD...	33 2.8
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	gb L39015 YSCMSE1G Saccharomyces cerevisiae nuclear-encoded mito...	33 2.8
	emb AI398391 AI398391 NCSM1H10T7 Subtracted Mycelial Neurospora ...	33 2.8
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	gb M97956 TRBBEALTU Trypanosoma cruzi beta tubulin and alpha tub...	31 7.2
60	emb AW686835 AW686835 NF043H11NR1F1000 Nodulated root Medicago t...	31 9.9
	emb AI304976 AI304976 EST00081 mRNP Lambda ZapII Express Library...	31 9.9

- emb|AF026421|AF026421 Chlamydomonas reinhardtii clone CD191 star... 31 9.9
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 emb|AW624834|AW624834 EST313651 tomato radicle, 5 d post-imbibit... 31 9.9
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 5 emb|X64601|ANNIMTMR A.nidulans nimT mRNA for tyrosine phosphatase. 31 9.9

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 (1761 letters)

15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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20 Score E
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- emb|AV411445|AV411445 AV411445 Lotus japonicus young plants (two... 198 1e-49
 25 emb|AV415235|AV415235 AV415235 Lotus japonicus young plants (two... 190 3e-47
 emb|AV415282|AV415282 AV415282 Lotus japonicus young plants (two... 190 3e-47
 emb|AW906097|AW906097 EST342218 potato stolon, Cornell Universit... 162 8e-39
 emb|AV413830|AV413830 AV413830 Lotus japonicus young plants (two... 161 1e-38
 emb|AV419573|AV419573 AV419573 Lotus japonicus young plants (two... 82 5e-36
 emb|AA660119|AA660119 EST00006 watermelon lambda zap express lib... 148 7e-36
 30 emb|AI507855|AI507855 sa88a07.y1 Gm-c1004 Glycine max cDNA clone... 91 2e-35
 emb|AW160273|AW160273 EST290131 L. pennellii trichome, Cornell U... 146 4e-34
 emb|AV428532|AV428532 AV428532 Lotus japonicus young plants (two... 80 3e-30
 emb|AV424557|AV424557 AV424557 Lotus japonicus young plants (two... 128 1e-28
 emb|AW668007|AW668007 GA_Ea0012E04 Gossypium arboreum 7-10 dpa ... 117 2e-25
 35 emb|AW922981|AW922981 DG1_48_B03.b1_A002 Dark Grown 1 (DG1) Sorg... 105 8e-22
 emb|AW432282|AW432282 sh71f09.y1 Gm-c1015 Glycine max cDNA clone... 100 3e-20
 emb|AW621610|AW621610 EST312408 tomato root during/after fruit s... 100 5e-20
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 emb|AI937949|AI937949 sc06a10.y1 Gm-c1012 Glycine max cDNA clone... 88 3e-16
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 emb|AW497095|AW497095 ga53g06.y1 Moss EST library PPU Physcomitr... 42 3e-06
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 55 gb|BE124825|BE124825 EST393860 GVN Medicago truncatula cDNA clon... 35 1.8
 emb|AW684862|AW684862 NF022D06NR1F1000 Nodulated root Medicago t... 35 1.8
 emb|AW686248|AW686248 NF039F10NR1F1000 Nodulated root Medicago t... 35 1.8
 emb|AW696000|AW696000 NF100H02ST1F1026 Developing stem Medicago ... 35 1.8
 emb|AW686364|AW686364 NF037B05NR1F1000 Nodulated root Medicago t... 35 1.8
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 emb|AA660722|AA660722 00613 MtRHE Medicago truncatula cDNA 5', m... 34 3.5

- emb|AI054829|AI054829 coau0002E06 Cotton Boll Abscission Zone cD... 34 3.5
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 5 emb|AQ654502|AQ654502 Sheared DNA-25C14.TR Sheared DNA Trypanoso... 33 6.6
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 gb|L40389|YSAERG11X Candida glabrata ERG11 gene, complete cds. 33 6.6
 emb|X79365|CSMFPPB C.sativus MFP-b mRNA. 33 6.6
 gb|U05612|CSU05612 Colysis sintenensis chloroplast large subunit... 28 6.8
 10 emb|X02433|MIPSCOX2 Pea mitochondrial gene for cytochrome oxidas... 24 6.9
 emb|AQ654503|AQ654503 Sheared DNA-25C15.TR Sheared DNA Trypanoso... 33 9.0
 emb|AI163319|AI163319 A039P66U Hybrid aspen plasmid library Popu... 33 9.0
 emb|AQ641986|AQ641986 RPCI93-EcoRI-6N23.TJ RPCI93-EcoRI Trypanos... 33 9.0
 emb|AL034558|PFMAL3P2 Plasmodium falciparum MAL3P2, complete seq... 33 9.0
 15 emb|AQ649633|AQ649633 Sheared DNA-17K4.TF Sheared DNA Trypanosom... 33 9.0
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 emb|AQ940463|AQ940463 Sheared DNA-33A23.TR Sheared DNA Trypanoso... 33 9.0
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 25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af000657|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|af000657|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|af000657|/ncgi)
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emb|AW982334|AW982334 HVSMEg0002O20f Hordeum vulgare pre-anthesi... 86 1e-24
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60 emb|AI043565|AI043565 L30-578T3 Ice plant Lambda Uni-Zap XR expr... 75 3e-19
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40	gb U10150 BNU10150 Brassica napus Naeha calmodulin (bcm1) mRNA,...	38	0.030
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5 emb|AF206700|AF206700 Neurospora crassa heterokaryon incompatibi... 31 9.1
dbj|D15051|BLYIDS2NK Hordeum vulgare gene for ids2, complete cds. 31 9.1
gb|BE021558|BE021558 sm49e02.y1 Gm-c1028 Glycine max cDNA clone ... 31 9.1
emb|AW442607|AW442607 EST307537 tomato mixed elicitor, BTI Lycop... 31 9.1
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10 emb|AI780125|AI780125 EST261004 tomato susceptible, Cornell Lyco... 31 9.1

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15 (777 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

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35 emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 189 2e-47
emb|AI896756|AI896756 EST266199 tomato callus, TAMU Lycopersicon... 188 4e-47
emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 188 4e-47
emb|AI773854|AI773854 EST254954 tomato resistant, Cornell Lycop... 133 2e-44
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10	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac006587 /ncgi http://www.ncgr.org/cgi-bin/ff?ac006587 (504 letters)		
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	emb AL049184 PFMAL13P3 Plasmodium falciparum chromosome 13 strai...	35	0.56
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	gb T09806 T09806 0387m7 gmbPfHB3.1, G. Roman Reddy Plasmodium fa...	35	0.56
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	gb U36927 PYU36927 <i>Plasmodium yoelii</i> rhoptry protein gene, compl...	33	1.5
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	gb U49822 SDU49822 <i>Saccharomyces douglasii</i> mitochondrial tRNA-Se...	33	2.0
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	emb AW458882 AW458882 sh16a07.y1 Gm-cl016 <i>Glycine max</i> cDNA clone...	33	2.0
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15	emb AL096783 PFMAL13P9 <i>Plasmodium falciparum</i> chromosome 13 strai...	33	2.0
	gb M35612 YSCMTARSA Yeast (<i>S.cerevisiae</i>) mitochondrial autonomou...	33	2.0
	emb AL031744 PFMAL1P1 <i>Plasmodium falciparum</i> chromosome 1 strain ...	32	2.8
	emb AF093584 AF093584 <i>Plasmodium vivax</i> merozoite surface protein...	32	2.8
	emb AC006280 AC006280 <i>Plasmodium falciparum</i> chromosome 12 clone ...	32	2.8
20	emb AC004710 AC004710 <i>Plasmodium falciparum</i> chromosome 12, *** S...	32	2.8
	emb AE001410 AE001410 <i>Plasmodium falciparum</i> chromosome 2, sectio...	32	2.8
	emb X74069 SCALP1 <i>S.cerevisiae</i> APL1 gene for basic-amino-acid pe...	32	2.8
	emb AC005504 AC005504 <i>Plasmodium falciparum</i> chromosome 12, *** S...	32	2.8
	emb AW727908 AW727908 GA_Ea0028M15 <i>Gossypium arboreum</i> 7-10 dpa ...	32	2.8
25	emb AE001395 AE001395 <i>Plasmodium falciparum</i> chromosome 2, sectio...	32	2.8
	emb AF030694 AF030694 <i>Plasmodium falciparum</i> strain Dd2 heat shoc...	32	2.8
	emb AQ647469 AQ647469 RPCI93-EcoRI-6E20.TJ RPCI93-EcoRI Trypanos...	32	2.8
	emb Z38061 SC9168 <i>S.cerevisiae</i> chromosome IX cosmid 9168.	32	2.8
	emb AL110675 CNS018QK <i>Botrytis cinerea</i> strain T4 cDNA library un...	32	2.8
30	emb AL008970 PFMAL3P4 <i>Plasmodium falciparum</i> MAL3P4, complete seq...	31	2.9
	emb AW035978 AW035978 EST282837 tomato callus, TAMU <i>Lycopersicon</i> ...	32	3.8
	emb AF126285 AF126285 <i>Pleurotus ostreatus</i> linear mitochondrial p...	32	3.8
	emb AL049181 PFMAL13P4 <i>Plasmodium falciparum</i> chromosome 13 strai...	32	3.8
	emb AW691746 AW691746 NF043G06ST1F1000 Developing stem <i>Medicago</i> ...	32	3.8
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	emb AW030017 AW030017 EST273272 tomato callus, TAMU <i>Lycopersicon</i> ...	32	3.8
	emb AL049183 PFMAL13P6 <i>Plasmodium falciparum</i> chromosome 13 strai...	32	3.8
	emb AC018661 AC018661 <i>Leishmania major</i> chromosome 35 clone L3836...	32	3.8
	emb AQ909783 AQ909783 GSSTc08262 Trypanosome cruzi random genom...	32	3.8
40	emb AQ906056 AQ906056 GSSTc07178 Trypanosome cruzi random genom...	32	3.8
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	emb X16104 SBKAFGK1 <i>Sorghum</i> DNA for kafirin, pGK1.	32	3.8
	emb AW684444 AW684444 NF017A07NR1F1000 Nodulated root <i>Medicago</i> t...	32	3.8
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45	emb AL033503 CAC49C4 <i>C.albicans</i> cosmid Ca49C4.	32	3.8
	emb AW761381 AW761381 sl66g01.y1 Gm-cl027 <i>Glycine max</i> cDNA clone...	32	3.8
	emb AW220823 AW220823 EST297292 tomato fruit mature green, TAMU ...	32	3.8
	emb AC007863 AC007863 Trypanosoma brucei chromosome VI clone RPC...	32	3.8
	dbj D83006 D83006 <i>Saccharomyces cerevisiae</i> MNN4 gene, complete cds.	32	3.8
50	emb AA557046 AA557046 888 Loblolly pine N <i>Pinus taeda</i> cDNA clone...	32	3.8
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	emb AQ935320 AQ935320 CpG2407A CpIOWAgDNA1 <i>Cryptosporidium parvu</i> ...	31	5.2
	emb Z68144 SPAC3H1 <i>S. pombe</i> chromosome I cosmid c3H1.	31	5.2
	emb AE001422 AE001422 <i>Plasmodium falciparum</i> chromosome 2, sectio...	31	5.2
55	emb AE001401 AE001401 <i>Plasmodium falciparum</i> chromosome 2, sectio...	31	5.2
	emb AE001380 AE001380 <i>Plasmodium falciparum</i> chromosome 2, sectio...	31	5.2
	emb AC004157 AC004157 <i>Plasmodium falciparum</i> chromosome 12 clone ...	31	5.2
	emb AE001376 AE001376 <i>Plasmodium falciparum</i> chromosome 2, sectio...	31	5.2
	emb AQ941118 AQ941118 Sheared DNA-35E12.TF Sheared DNA Trypanoso...	31	5.2
60	emb AQ949411 AQ949411 Sheared DNA-38N10.TF Sheared DNA Trypanoso...	31	5.2

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(375 letters)

Database: plantfungal
10 661,018 sequences; 426,114,510 total letters

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	gb BE124622 BE124622	EST393657	GVN Medicago truncatula cDNA clon...	162 1e-39
	emb AI943438 AI943438	MF02E10	MF Mesembryanthemum crystallinum c...	158 2e-38
20	gb BE033541 BE033541	MF02E10	MF Mesembryanthemum crystallinum cD...	158 2e-38
	emb AW667752 AW667752	GA_Ea0010I06	Gossypium arboreum 7-10 dpa ...	155 1e-37
	emb AW747419 AW747419	WS1_68_E10.b1_A002	Water-stressed 1 (WS1) ...	155 2e-37
	emb AW981480 AW981480	EST392633	DSIL Medicago truncatula cDNA cl...	154 4e-37
	emb AW441269 AW441269	EST310665	tomato fruit red ripe, TAMU Lyco...	153 5e-37
25	emb AW223703 AW223703	EST300514	tomato fruit red ripe, TAMU Lyco...	153 5e-37
	emb AW034892 AW034892	EST279121	tomato callus, TAMU Lycopersicon...	153 5e-37
	emb AW224013 AW224013	EST300824	tomato fruit red ripe, TAMU Lyco...	153 5e-37
	emb AW907232 AW907232	EST343355	potato stolon, Cornell Universit...	153 7e-37
	emb AW747501 AW747501	WS1_68_E10.g1_A002	Water-stressed 1 (WS1) ...	152 9e-37
30	emb AW730496 AW730496	GA_Ea0026O23	Gossypium arboreum 7-10 dpa ...	152 9e-37
	emb AW760599 AW760599	sl52d09.y1	Gm-c1027 Glycine max cDNA clone...	151 2e-36
	emb AI960575 AI960575	sc86c01.y1	Gm-c1018 Glycine max cDNA clone...	151 2e-36
	emb AW706639 AW706639	sj62h07.y1	Gm-c1033 Glycine max cDNA clone...	151 2e-36
	emb AI166395 AI166395	xylem.est.231	Poplar xylem Lambda ZAPII li...	150 5e-36
35	emb AI443884 AI443884	sa44f06.y1	Gm-c1004 Glycine max cDNA clone...	149 6e-36
	emb AW568285 AW568285	si69g11.y1	Gm-r1030 Glycine max cDNA clone...	149 6e-36
	emb AW186193 AW186193	se64g04.y1	Gm-c1019 Glycine max cDNA clone...	149 6e-36
	emb AI855496 AI855496	sc16h05.y1	Gm-c1013 Glycine max cDNA clone...	149 1e-35
	gb BE020351 BE020351	sm43b05.y1	Gm-c1028 Glycine max cDNA clone ...	148 2e-35
40	emb AW132618 AW132618	se06f04.y1	Gm-c1013 Glycine max cDNA clone...	148 2e-35
	emb AI777814 AI777814	EST258693	tomato susceptible, Cornell Lyco...	146 8e-35
	emb AV408412 AV408412	AV408412	Lotus japonicus young plants (two...	141 2e-33
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	emb AW738874 AW738874	gb03e09.y1	Moss EST library PPN Physcomitr...	99 2e-20
	emb AW476911 AW476911	ga38h10.y1	Moss EST library PPU Physcomitr...	95 2e-19
50	emb AL049558 SPBC216	S.pombe chromosome II	cosmid c216.	67 2e-19
	emb AW335287 AW335287	S45D10	AGS-1 Pneumocystis carinii f. sp. c...	71 3e-19
	emb AI822525 AI822525	L0-1030T3	Ice plant Lambda Uni-Zap XR expr...	95 3e-19
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	emb AW933218 AW933218	EST359061	tomato fruit mature green, TAMU ...	90 5e-18
55	emb AW933878 AW933878	EST359721	tomato fruit mature green, TAMU ...	90 5e-18
	emb AW222361 AW222361	EST299172	tomato fruit red ripe, TAMU Lyco...	90 5e-18
	emb AW617209 AW617209	EST323620	L. hirsutum trichome, Cornell Un...	90 5e-18
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60	emb AW220746 AW220746	EST297215	tomato fruit mature green, TAMU ...	90 5e-18
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	emb AW775277 AW775277 EST334342 DSIL Medicago truncatula cDNA cl...	88	4e-17
	emb AW127596 AW127596 M110327 DSLC Medicago truncatula cDNA clon...	86	9e-17
	emb AI026521 AI026521 TENU0733 T. cruzi epimastigote normalized ...	73	1e-16
5	emb X59720 SCCHRIII S.cerevisiae chromosome III complete DNA seq...	85	2e-16
	gb T36700 T36700 EST101687 S. cerevisiae strain X2180-1A Sacchar...	79	1e-14
	emb AW650769 AW650769 EST329223 tomato germinating seedlings, TA...	79	1e-14
	emb AW739119 AW739119 gb26a12.y1 Moss EST library PPN Physcomitr...	79	1e-14
	emb AT000681 AT000681 AT000681 Brassica rapa guard cell Brassica...	62	4e-14
10	gb N81594 N81594 TgESTzy60e01.r1 TgRH Tachyzoite cDNA Toxoplasma...	55	1e-12
	emb AA740047 AA740047 812 PUF2 Pinus taeda cDNA clone 9275M 3'...	62	4e-12
	emb AW907238 AW907238 EST343361 potato stolon, Cornell Universit...	68	2e-11
	emb AA948748 AA948748 L0-267M13R Ice plant Lambda Uni-Zap XR exp...	66	1e-10
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15	emb AW351206 AW351206 GM210011A20E12R Gm-r1021 Glycine max cDNA ...	61	5e-09
	emb AI495735 AI495735 sb15f07.y1 Gm-c1004 Glycine max cDNA clone...	61	5e-09
	emb AW597401 AW597401 si92d06.y1 Gm-c1031 Glycine max cDNA clone...	60	9e-09
	emb AW094112 AW094112 EST287292 tomato mixed elicitor, BTI Lycop...	58	2e-08
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20	emb AW931744 AW931744 EST357587 tomato fruit mature green, TAMU ...	46	9e-05
	emb AW459770 AW459770 sh91h03.y1 Gm-c1016 Glycine max cDNA clone...	42	0.002
	emb AI483073 AI483073 EST242396 tomato shoot, Cornell Lycopersic...	35	0.19
	emb AW686356 AW686356 NF040G07NR1F1000 Nodulated root Medicago t...	35	0.36
	emb AV389829 AV389829 AV389829 Chlamydomonas reinhardtii C9 Chla...	34	0.49
25	emb Z71549 SCYNL273W S.cerevisiae chromosome XIV reading frame O...	34	0.68
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	emb AL136235 SPAC664 S.pombe chromosome I cosmid c664.	32	1.8
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	emb X83998 CPEAPB C.parasitica eapB gene.	32	2.4
	gb BE049708 BE049708 NXNV_142_E09_F Nsf Xylem Normal wood Vertic...	31	3.3
35	emb AW310022 AW310022 sf28e03.x1 Gm-c1028 Glycine max cDNA clone...	31	3.3
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40	emb AW497050 AW497050 ga53b08.y1 Moss EST library PPU Physcomitr...	31	3.3
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45	emb X90948 ANRNAHSP7 A.nodosum mRNA for HSP70 protein.	31	4.6
	emb AW509671 AW509671 ga62c03.y1 Moss EST library PPU Physcomitr...	31	4.6
	emb AW561529 AW561529 ga81h08.y1 Moss EST library PPU Physcomitr...	31	4.6
	emb AW738897 AW738897 gb03h02.y1 Moss EST library PPN Physcomitr...	31	4.6
	emb X79095 FTPDKG F.trinervia pdk gene for pyruvate, orthophospha...	30	6.3
50	emb Z99262 SPAC9E9 S.pombe chromosome I cosmid c9E9.	30	6.3
	emb X79192 FBPDK F.brownii pdk gene.	30	6.3
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(844 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E		(bits)	Value
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	emb AI489421 AI489421	EST247760	tomato ovary, TAMU Lycopersicon ...	336	1e-91
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	emb AI489189 AI489189	EST247528	tomato ovary, TAMU Lycopersicon ...	273	1e-72
	emb AI488043 AI488043	EST246365	tomato ovary, TAMU Lycopersicon ...	269	2e-71
	emb AW625207 AW625207	EST319114	tomato radicle, 5 d post-imbibit...	258	5e-68
	emb AW559910 AW559910	EST314958	DSIR Medicago truncatula cDNA cl...	258	5e-68
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	emb AW218466 AW218466	EST303649	tomato radicle, 5 d post-imbibit...	238	3e-62
	emb AW624963 AW624963	EST313792	tomato radicle, 5 d post-imbibit...	234	8e-61
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25	emb AA495616 AA495616	c425 Zhou and Ragan 1993	Gracilaria gracil...	118	3e-52
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	gb BE020624 BE020624	sm51d11.y1	Gm-cl028 Glycine max cDNA clone ...	175	4e-43
30	emb AW218418 AW218418	EST303601	tomato radicle, 5 d post-imbibit...	174	9e-43
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	emb AW098211 AW098211	ga07f10.y1	Moss EST library CPU Ceratodon ...	147	9e-35
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40	emb Z72939 SCYGR154C	S.cerevisiae chromosome VII	reading frame O...	51	2e-23
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	emb AW221318 AW221318	EST297787	tomato fruit mature green, TAMU ...	68	9e-11
	emb AQ875035 AQ875035	V120D9 mTn-3xHA/lacZ	Insertion Library, st...	67	2e-10
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55	emb AA787150 AA787150	m8a03a1.r1	Aspergillus nidulans 24hr asexu...	58	1e-07
	emb AQ492097 AQ492097	V111F10 mTn-3xHA/lacZ	Insertion Library Sa...	55	9e-07
	emb AA788014 AA788014	r4b01a1.fl	Aspergillus nidulans 24hr asexu...	35	4e-04
	emb AA787149 AA787149	m8a03a1.fl	Aspergillus nidulans 24hr asexu...	46	5e-04
	emb AC007865 AC007865	Trypanosoma brucei	chromosome II clone RPC...	38	0.12
60	emb AA788490 AA788490	l3a06a1.fl	Aspergillus nidulans 24hr asexu...	35	0.58
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 5 emb|X71362|HVDHN7 *H.vulgare* gene for dehydrin 7. 34 1.5
 emb|X88851|SCESTGENE *S.cerevisiae* DNA for hypothetical proteins a... 34 1.5
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 emb|AI988341|AI988341 sc99e11.y1 *Gm-c1020* Glycine max cDNA clone... 34 2.1
 emb|Y10224|CMAO1 *C.melo* aol gene, partial. 34 2.1
 10 emb|AI900471|AI900471 sc11b06.y1 *Gm-c1012* Glycine max cDNA clone... 34 2.1
 emb|AQ874584|AQ874584 V111B3 mTn-3xHA/lacZ Insertion Library, st... 34 2.1
 emb|AW279161|AW279161 sf67b09.y1 *Gm-c1013* Glycine max cDNA clone... 34 2.1
 emb|Z99531|SPAC19D5 *S.pombe* chromosome I cosmid c19D5. 33 2.8
 emb|AJ273736|AJ273736 *Metarhizium anisopliae* ARSEF 2575... 33 2.8
 15 emb|AW730699|AW730699 GA_Ea0027C11 *Gossypium arboreum* 7-10 dpa ... 33 3.9
 emb|AW982536|AW982536 HVSMEg0003I12f *Hordeum vulgare* pre-anthesi... 33 3.9
 emb|AJ229614|KLAJ9614 *Kluyveromyces lactis* DNA fragment for sequ... 33 3.9
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 emb|Z49624|SCYJR124C *S.cerevisiae* chromosome X reading frame ORF... 33 3.9
 20 emb|Z98547|PFMAL3P3 *Plasmodium falciparum* MAL3P3, complete seque... 25 5.2
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 emb|AZ214742|AZ214742 Sheared DNA-68E9.TR Sheared DNA Trypanosom... 32 5.3
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 emb|X68577|SC114 *S. cerevisiae* 11.4kb segment of chromosome II. 32 5.3
 25 gb|M31036|YSCACH1A *S.cerevisiae* acetyl-CoA hydrolase (ACH1) mRNA... 32 5.3
 emb|AJ243754|SAL243754 *Sinapis alba* chloroplast rpoB operon (rpo... 32 5.3
 emb|AL110506|SPBC577 *S.pombe* chromosome II cosmid c577. 26 5.9
 emb|AU010645|AU010645 AU010645 *Schizosaccharomyces pombe* late lo... 32 7.3
 emb|AI966191|AI966191 sc35a11.y1 *Gm-c1014* Glycine max cDNA clone... 32 7.3
 30 emb|AL022244|SPBC3B8 *S.pombe* chromosome II cosmid c3B8. 32 7.3
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- Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters
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- Score E
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- emb|AF053127|AF053127 *Malus domestica* leucine-rich receptor-like... 169 8e-99
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 emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 160 3e-83
 55 emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 154 8e-81
 emb|AI897516|AI897516 EST266959 tomato ovary, TAMU Lycopersicon ... 133 2e-73
 emb|AF053998|AF053998 *Lycopersicon esculentum* Hcr2-5D (Hcr2-5D) ... 143 2e-72
 emb|A67434|A67434 Sequence 7 from Patent WO9743429. 143 2e-72
 emb|AW650851|AW650851 EST329305 tomato germinating seedlings, TA... 123 4e-72
 60 emb|AF053995|AF053995 *Lycopersicon esculentum* Hcr2-0B (Hcr2-0B) ... 144 2e-71
 emb|AF053993|AF053993 *Lycopersicon esculentum* disease resistance... 145 4e-71

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	emb A67428 A67428 Sequence 1 from Patent WO9743429.	145 4e-71
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25	emb AW621923 AW621923 EST312721 tomato root during/after fruit s...	94 2e-43
	emb AW428824 AW428824 Ljimpest24-927-c5 Ljimp Lambda HybriZap ...	120 8e-43
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	85 2e-42
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	emb AW621706 AW621706 EST312504 tomato root during/after fruit s...	92 3e-41
30	emb AW668493 AW668493 GA_Ea0014C20 Gossypium arboreum 7-10 dpa ...	92 6e-41
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	emb AW929662 AW929662 EST338450 tomato flower buds 8 mm to pre-a...	92 8e-41
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	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	82 1e-40
35	emb Z73295 CRPK1 C.roseus mRNA for receptor-like protein kinase.	136 1e-40
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	emb AW010219 AW010219 ST03E03 Pine TriplEx shoot tip library Pin...	144 2e-40
	gb U20948 ITU20948 Ipomoea trifida receptor protein kinase (IRK1...	129 2e-40
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	emb AW092144 AW092144 EST285240 tomato mixed elicitor, BTI Lycop...	102 3e-40
	emb AW704459 AW704459 sk53c10.y1 Gm-c1019 Glycine max cDNA clone...	100 3e-40
	emb AW036762 AW036762 EST252151 tomato ovary, TAMU Lycopersicon ...	85 4e-40
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45	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	84 4e-39
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55	emb AW040672 AW040672 EST283536 tomato mixed elicitor, BTI Lycop...	102 4e-38
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60	emb AI771841 AI771841 EST252941 tomato ovary, TAMU Lycopersicon ...	85 3e-37
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- emb|AW756743|AW756743 sl26f10.y1 Gm-c1027 Glycine max cDNA clone... 92 4e-37
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 5 emb|AB030083|AB030083 Populus nigra PnLPK mRNA for lectin-like p... 121 6e-37
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 emb|AW746575|AW746575 WS1_54_G12.b1_A002 Water-stressed 1 (WS1) ... 150 8e-37
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 15 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 85 8e-36
 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 77 1e-35
 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 84 2e-35
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 20 emb|AW736597|AW736597 EST333089 KV3 Medicago truncatula cDNA clo... 91 4e-35
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 emb|AF166121|AF166121 Hordeum vulgare Cf2/Cf5 disease resistance... 103 2e-34
 emb|AW694942|AW694942 NF081G02ST1F1018 Developing stem Medicago ... 141 3e-34
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 82 3e-34
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- 35 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187|/ncgi)
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- 40 Database: plantfungal
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- 45 Score E
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- emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 820 0.0
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emb|AB024417|AB024417 Brassica oleracea SLG13 gene, partial cds. 498 e-178
15 dbj|D85206|D85206 Brassica oleracea DNA for S blycoprotein, part... 406 e-177
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20 emb|AB013719|AB013719 Brassica oleracea mRNA for SLG23Bol, compl... 404 e-175
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40 dbj|D85216|D85216 Brassica campestris DNA for S glycoprotein, pa... 409 e-171
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emb|X79432|BOSRK3 B.oleracea SRK3 gene. 396 e-171
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dbj|D85221|D85221 Brassica campestris DNA for S glycoprotein, pa... 348 e-170
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55 emb|Z21608|BNESLOGPA B.napus mRNA for endogenous S-locus glycopr... 477 e-168
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60 dbj|D85212|D85212 Brassica oleracea DNA for S glycoprotein, part... 244 e-164
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- emb|AB009677|AB009677 *Raphanus sativus* SLG(S1) gene for S glycop... 266 e-163
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 5 emb|Z19548|BNSLGP11 *B. napus* mRNA for S-locus glycoprotein type II. 286 e-163
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 emb|AF161333|AF161333 *Raphanus raphanistrum* subsp. *raphanistrum* ... 310 e-150
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 emb|X57673|BOSLR2RNA *B. oleracea* RNA for S-locus-related glycopr... 167 e-149
 emb|AB009873|AB009873 *Cheiranthus cheiri* gene for SLR1, partial ... 163 e-147
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 25 emb|X52089|BOSLRG *Brassica* gene for S locus related glycoprotein. 272 e-143

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 (2673 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| 45 emb A67434 A67434 Sequence 7 from Patent WO9743429. | 148 | 4e-74 | |
| emb AF053993 AF053993 <i>Lycopersicon esculentum</i> disease resistance... | 148 | 4e-74 | |
| emb A67429 A67429 Sequence 2 from Patent WO9743429. | 148 | 4e-74 | |
| emb A67428 A67428 Sequence 1 from Patent WO9743429. | 148 | 4e-74 | |
| emb AF053995 AF053995 <i>Lycopersicon esculentum</i> Hcr2-0B (Hcr2-0B) ... | 150 | 4e-74 | |
| 50 emb AF053997 AF053997 <i>Lycopersicon esculentum</i> Hcr2-5B (Hcr2-5B) ... | 146 | 1e-72 | |
| emb A67432 A67432 Sequence 5 from Patent WO9743429. | 146 | 1e-72 | |
| gb U42445 U42445 <i>Lycopersicon pimpinellifolium</i> leucine rich repe... | 150 | 3e-71 | |
| emb A57133 A57133 Sequence 4 from Patent WO9531564. | 150 | 3e-71 | |
| gb U42444 U42444 <i>Lycopersicon pimpinellifolium</i> leucine rich repe... | 150 | 8e-71 | |
| 55 emb A57130 A57130 Sequence 1 from Patent WO9531564. | 150 | 8e-71 | |
| emb AB029327 AB029327 <i>Nicotiana tabacum</i> mRNA for elicitor-induci... | 97 | 4e-65 | |
| emb AF053994 AF053994 <i>Lycopersicon esculentum</i> Hcr2-0A (Hcr2-0A) ... | 149 | 6e-37 | |
| emb AF119040 AF119040 <i>Lycopersicon esculentum</i> haplotype Northern... | 143 | 3e-36 | |
| emb AF053996 AF053996 <i>Lycopersicon pimpinellifolium</i> Hcr2-2A (Hcr... | 144 | 3e-35 | |
| 60 emb AF119041 AF119041 <i>Lycopersicon esculentum</i> haplotype Southern... | 139 | 2e-33 | |
| emb AJ002235 LHJ002235 <i>Lycopersicon hirsutum</i> Cf-4 resistance gen... | 139 | 3e-33 | |

- emb|AJ002236|LPJ002236 *Lycopersicon pimpinellifolium* Cf-9 resist... 140 4e-33
emb|AJ002237|LEJ002237 *Lycopersicon esculentum* haplotype of the ... 138 1e-32
emb|Y12640|LECF4A *L. esculentum* Cf-4A gene. 137 1e-32
emb|A58270|A58270 Sequence 1 from Patent WO9635790. 138 2e-31
5 gb|U15936|LPU15936 *Lycopersicon pimpinellifolium* Cf-9 precursor ... 138 2e-31
emb|AI778581|AI778581 EST259460 tomato susceptible, Cornell Lyco... 92 1e-29
emb|AW458587|AW458587 sh11a09.y1 Gm-c1016 Glycine max cDNA clone... 131 3e-29
emb|AW306725|AW306725 sf47e12.y1 Gm-c1009 Glycine max cDNA clone... 129 1e-28
emb|AF215729|AF215729 Glycine max RFLP clone A 45-10 sequence; a... 123 5e-27
10 emb|X81370|TAAWJL236 *T. aestivum* (subclone pAWJL236) AWJL236 gene. 115 8e-27
emb|AF140552|AF140552 *Lycopersicon esculentum* plant disease resi... 121 2e-26
emb|AI895949|AI895949 EST265392 tomato callus, TAMU *Lycopersicon*... 70 5e-25
emb|AW624314|AW624314 EST322175 tomato flower buds 3-8 mm, Corne... 113 5e-24
emb|X81369|TAAWJL218 *T. aestivum* (subclone pAWJL218) AWJL218 gene. 104 1e-23
15 emb|X81367|TAAWJL172 *T. aestivum* (subclone pAWJL172) AWJL172 gene. 99 7e-23
emb|X81368|TAAWJL175 *T. aestivum* (subclone pAWJL175) AWJL175 gene. 101 2e-22
emb|AW705275|AW705275 sk59a10.y1 Gm-c1019 Glycine max cDNA clone... 108 2e-22
emb|AF166121|AF166121 *Hordeum vulgare* Cf2/Cf5 disease resistance... 94 3e-22
emb|AI779817|AI779817 EST260696 tomato susceptible, Cornell Lyco... 100 1e-21
20 emb|AW888094|AW888094 NXNV_108_E11_F Nsf Xylem Normal wood Verti... 105 2e-21
emb|AQ917191|AQ917191 T233043b *Medicago truncatula* BAC library M... 93 1e-20
gb|U77888|INU77888 *Ipomoea nil* receptor-like protein kinase (inr... 79 2e-20
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25 emb|AW064561|AW064561 ST33A08 Pine TriPLEx shoot tip library Pin... 98 3e-19
emb|AI484441|AI484441 EST242451 tomato ovary, TAMU *Lycopersicon* ... 98 3e-19
emb|AW279193|AW279193 sf67g09.y1 Gm-c1013 Glycine max cDNA clone... 98 4e-19
emb|AI900597|AI900597 sc13d11.y1 Gm-c1013 Glycine max cDNA clone... 97 5e-19
emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 82 1e-18
30 emb|AW032163|AW032163 EST275617 tomato callus, TAMU *Lycopersicon*... 64 1e-18
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emb|AW650508|AW650508 EST328962 tomato germinating seedlings, TA... 91 1e-18
emb|AI488023|AI488023 EST246345 tomato ovary, TAMU *Lycopersicon* ... 91 1e-18
emb|AI896676|AI896676 EST266119 tomato callus, TAMU *Lycopersicon*... 91 1e-18
35 emb|AW307311|AW307311 sf55d03.y1 Gm-c1009 Glycine max cDNA clone... 66 2e-18
emb|AV415568|AV415568 AV415568 *Lotus japonicus* young plants (two... 85 2e-18
emb|AI895309|AI895309 EST264752 tomato callus, TAMU *Lycopersicon*... 95 2e-18
emb|AI727073|AI727073 BNLGHI7256 Six-day Cotton fiber *Gossypium* ... 95 2e-18
emb|AW306675|AW306675 se53h08.y1 Gm-c1017 Glycine max cDNA clone... 95 3e-18
40 emb|X79130|TSLRRR *Triticum* sp. (pAWJL3) leucine rich repeat regi... 84 4e-18
emb|AW031498|AW031498 EST274952 tomato callus, TAMU *Lycopersicon*... 94 5e-18
emb|AW775087|AW775087 EST334238 KV3 *Medicago truncatula* cDNA clo... 94 6e-18
emb|AW690301|AW690301 NF029C05ST1F1000 Developing stem *Medicago* ... 81 7e-18
emb|AW267958|AW267958 EST306300 DSIR *Medicago truncatula* cDNA cl... 80 7e-18
45 emb|AI895893|AI895893 EST265336 tomato callus, TAMU *Lycopersicon*... 61 9e-18
emb|AW647847|AW647847 EST326301 tomato germinating seedlings, TA... 91 1e-17
emb|AW929189|AW929189 EST337977 tomato flower buds 8 mm to pre-a... 92 2e-17
emb|AW689506|AW689506 NF021E06ST1F1000 Developing stem *Medicago* ... 92 2e-17
emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 82 2e-17
50 emb|AW929854|AW929854 EST354124 tomato flower buds 8 mm to pre-a... 91 4e-17
emb|AW929780|AW929780 EST354050 tomato flower buds 8 mm to pre-a... 91 4e-17
emb|AW031218|AW031218 EST274756 tomato callus, TAMU *Lycopersicon*... 91 4e-17
emb|AW033367|AW033367 EST276938 tomato callus, TAMU *Lycopersicon*... 89 1e-16
emb|AI443128|AI443128 sa84f10.y1 Gm-c1004 Glycine max cDNA clone... 89 1e-16
55 emb|AI896313|AI896313 EST265756 tomato callus, TAMU *Lycopersicon*... 60 1e-16
emb|AW735867|AW735867 EST336635 tomato flower buds 0-3 mm, Corne... 89 2e-16
emb|AW980804|AW980804 EST391957 GVN *Medicago truncatula* cDNA clo... 69 2e-16
emb|AI488443|AI488443 EST246782 tomato ovary, TAMU *Lycopersicon* ... 88 3e-16
emb|AW033129|AW033129 EST276688 tomato callus, TAMU *Lycopersicon*... 78 3e-16
60 emb|AW127035|AW127035 ga20c02.y1 Moss EST library PPU *Physcomitr*... 88 4e-16
emb|AI895669|AI895669 EST265112 tomato callus, TAMU *Lycopersicon*... 88 4e-16

- emb|AW618685|AW618685 EST320671 *L. pennellii* trichome, Cornell U... 88 4e-16
 emb|AI894989|AI894989 EST264432 tomato callus, TAMU Lycopersicon... 88 4e-16
 emb|AI782076|AI782076 EST262955 tomato susceptible, Cornell Lyco... 87 5e-16
 emb|AW648795|AW648795 EST327249 tomato germinating seedlings, TA... 87 5e-16
 5 emb|AW694942|AW694942 NF081G02ST1F1018 Developing stem Medicago ... 78 6e-16
 emb|AV415057|AV415057 AV415057 *Lotus japonicus* young plants (two... 87 7e-16
 emb|AW399097|AW399097 EST309597 *L. pennellii* trichome, Cornell U... 63 8e-16
 emb|AW761367|AW761367 sl66e07.y1 *Gm-c1027 Glycine max* cDNA clone... 86 1e-15
 emb|AW649208|AW649208 EST327662 tomato germinating seedlings, TA... 86 1e-15
 10 emb|AV428126|AV428126 AV428126 *Lotus japonicus* young plants (two... 85 2e-15
 emb|AW290705|AW290705 NXNV045C11F Nsf Xylem Normal wood Vertical... 85 2e-15
 emb|AI352869|AI352869 MB70-4A PZ204.BNlib *Brassica napus* cDNA cl... 85 2e-15
 emb|AA661049|AA661049 00946 MtRHE *Medicago truncatula* cDNA 5' si... 85 2e-15
 emb|AW455303|AW455303 EST311841 tomato root during/after fruit s... 85 3e-15
 15 emb|AW869870|AW869870 NXNV_122_E02_F Nsf Xylem Normal wood Verti... 85 3e-15
 emb|AW398651|AW398651 EST309151 *L. pennellii* trichome, Cornell U... 84 4e-15
 emb|AW398661|AW398661 EST309161 *L. pennellii* trichome, Cornell U... 84 4e-15
 emb|AF049920|AF049920 *Petunia x hybrida* PGPS/D4 (PGPS/D4) mRNA, ... 84 4e-15
 emb|AW624634|AW624634 EST322579 tomato flower buds 3-8 mm, Corne... 59 4e-15
 20 emb|AW618879|AW618879 EST320865 *L. pennellii* trichome, Cornell U... 62 4e-15
 gb|BE035885|BE035885 MO11F02 *Mesembryanthemum crystallinum* cD... 84 5e-15

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- 25 emb|cab51412.1| (al096882) acc synthase (atacs-6) [arabidopsis
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 /ncgi
 (1488 letters)

Database: plantfungal

- 30 661,018 sequences; 426,114,510 total letters

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| 35 | Sequences producing significant alignments: | | | |
| | emb X82273 BOACCS <i>B. oleracea</i> mRNA for ACC synthase. | 986 | 0.0 | |
| | emb X72676 BJMACC <i>B. juncea</i> mRNA for 1-Aminocyclopropane-1-carbo... | 875 | 0.0 | |
| | emb AF057563 AF057563 <i>Nicotiana glutinosa</i> 1-aminocyclopropane-1-... | 765 | 0.0 | |
| 40 | emb AJ005002 NTAJ5002 <i>Nicotiana tabacum</i> mRNA for 1-aminocyclopro... | 761 | 0.0 | |
| | emb AB034992 AB034992 <i>Malus domestica</i> MdACS-5A mRNA for 1-aminoc... | 754 | 0.0 | |
| | emb AB034993 AB034993 <i>Malus domestica</i> MdACS-5B mRNA for 1-aminoc... | 755 | 0.0 | |
| | gb U72389 LEU72389 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1-... | 756 | 0.0 | |
| | gb U72390 LEU72390 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1-... | 753 | 0.0 | |
| 45 | emb AB033503 AB033503 <i>Populus euramericana</i> peacs-2 mRNA for 1-am... | 741 | 0.0 | |
| | gb U68216 CPU68216 <i>Carica papaya</i> ACC synthase mRNA, complete cds. | 461 | 0.0 | |
| | emb AF061605 AF061605 <i>Nicotiana glutinosa</i> ACC synthase mRNA, com... | 742 | 0.0 | |
| | emb AB013100 AB013100 <i>Lycopersicon esculentum</i> LE-ACS6 mRNA for 1-... | 741 | 0.0 | |
| | emb AJ012551 CSI012551 <i>Citrus sinensis</i> mRNA for ACC synthase. | 449 | 0.0 | |
| 50 | emb AB013346 AB013346 <i>Lycopersicon esculentum</i> mRNA for 1-aminocy... | 739 | 0.0 | |
| | emb AB033502 AB033502 <i>Populus euphratica</i> peacs-1 mRNA for 1-amin... | 620 | 0.0 | |
| | gb U88971 PHU88971 <i>Pelargonium hortorum</i> 1-aminocyclopropane-1-ca... | 455 | 0.0 | |
| | emb Z11613 VRACCSYNM <i>V. radiata</i> mRNA for ACC synthase. | 456 | 0.0 | |
| | emb X98492 NTACCS <i>Nicotiana tabacum</i> mRNA for ACC-synthase (clone... | 455 | 0.0 | |
| 55 | emb X67100 GMCACCS1 <i>G. max</i> mRNA for ACC synthase. | 454 | 0.0 | |
| | emb Z18952 DCAMCRBSY <i>D. caryophyllus</i> mRNA for 1-aminocyclopropane... | 716 | 0.0 | |
| | emb AJ012696 CSI012696 <i>Citrus sinensis</i> mRNA for ACC synthase (AC... | 449 | 0.0 | |
| | emb AJ011095 CSI011095 <i>Citrus sinensis</i> mRNA for ACC synthase (ac... | 452 | 0.0 | |
| | emb Z18953 PHAMCRBSY <i>P. hybrida</i> mRNA for 1-aminocyclopropane 1-ca... | 450 | 0.0 | |
| 60 | emb AB006804 AB006804 <i>Cucumis sativus</i> CS-ACS2 mRNA for ACC synth... | 451 | 0.0 | |
| | emb AF080258 AF080258 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo... | 711 | 0.0 | |

- emb|AF016459|AF016459 *Pisum sativum* 1-aminocyclopropane-1-carbox... 445 0.0
emb|AF109927|AF109927 *Musa acuminata* 1-aminocyclopropane-1-carbo... 707 0.0
dbj|D30805|CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy... 705 0.0
5 emb|AB021906|AB021906 *Musa acuminata* MA-ACS1 mRNA for ACC syntha... 703 0.0
emb|AB006803|AB006803 *Cucumis sativus* CS-ACS1 mRNA for ACC synth... 703 0.0
emb|AF129508|AF129508 *Musa acuminata* 1-aminocyclopropane-1-carbo... 702 0.0
emb|X65982|NTXACCSYN *N.tabacum* mRNA for 1-aminocyclopropane-1-ca... 438 0.0
emb|AB031026|AB031026 *Prunus mume* PM-ACS1 mRNA for ACC synthase,... 434 0.0
10 emb|AB015625|AB015625 *Pyrus pyrifolia* pPPACS3 mRNA for 1-aminocy... 418 0.0
dbj|D01032|CUCACCW *Cucurbita maxima* mRNA for 1-aminocyclopropane... 695 0.0
dbj|E03724|E03724 cDNA encoding detriment induced type 1-aminocy... 695 0.0
gb|M58323|CUCACCSYN *Cucurbita pepo* 1-aminocyclopropane-1-carboxy... 692 0.0
emb|Y11357|CP1A1CS *C.papaya* mRNA for 1-aminocyclopropane-1-carbo... 430 0.0
emb|X62536|LEACC *L.esculentum* mRNA for ACC synthase. 327 0.0
15 emb|AF057562|AF057562 *Nicotiana glutinosa* 1-aminocyclopropane-1-... 437 0.0
emb|X59145|LEACC2MR *Lycopersicon esculentum* LE-ASCC2 mRNA (ptACC... 326 0.0
gb|U79999|MAU79999 *Musa acuminata* ACC synthase (acs3) mRNA, comp... 687 0.0
emb|Y15739|MAACSYNTH *Musa acuminata* mRNA for 1-aminocyclopropane... 687 0.0
gb|M34289|TOMACS *Tomato* 1-aminocyclopropane-1-carboxylate syntha... 327 0.0
20 gb|M63490|TOMACCS *Tomato* 1-aminocyclopropane-1-carboxylate synth... 682 0.0
emb|X59146|LEACC4MR *Lycopersicon esculentum* LE-ACC4 mRNA (ptACC4... 681 0.0
gb|U17229|PHU17229 *Pelargonium hortorum* clone pGAC-1 1-aminocycl... 438 0.0
gb|U17231|PHU17231 *Pelargonium hortorum* clone pGAC-2 1-aminocycl... 423 0.0
emb|AF038945|AF038945 *Rumex palustris* 1-aminocyclopropane-1-carb... 407 0.0
25 gb|L20634|POTACCSYN *Solanum tuberosum* 1-aminocyclopropane-1-carb... 403 0.0
emb|AJ276295|CSI276295 *Citrus sinensis* partial mRNA for ACC synt... 446 0.0
emb|AF239987|AF239987 *Prunus persica* ACC synthase ACS1 mRNA, par... 662 0.0
emb|AF178076|AF178076 *Carica papaya* 1-aminocyclopropane-1-carbox... 395 0.0
emb|X82265|CAACCI *C.annuum* mRNA for 1-aminocyclopropane-1-carboxyl... 639 0.0
30 gb|U70842|STU70842 *Solanum tuberosum* 1-aminocyclopropane-1-carbo... 637 0.0
emb|AF144746|AF144746 *Solanum melongena* 1-aminocyclopropane-1-ca... 636 0.0
emb|AJ012577|CPA012577 *Carica papaya* mRNA for 1-aminocyclopropan... 387 e-180
gb|U73815|MDU73815 *Malus domestica* ACC synthase (MdACS-2) mRNA, ... 623 e-178
dbj|D37937|D37937 *Cucumis melo* mRNA for 1-aminocyclopropane-1-ca... 380 e-177
35 emb|Z11562|VRACCSYN *V.radiata* mRNA for 1-aminocyclopropane-1-car... 375 e-176
emb|AF177769|AF177769 *Carica papaya* 1-aminocyclopropane-1-carbox... 369 e-175
emb|AF083814|AF083814 *Antirrhinum majus* ACC synthase 1 (ACS1) mR... 605 e-172
emb|AF178077|AF178077 *Carica papaya* 1-aminocyclopropane-1-carbox... 316 e-172
emb|AF239989|AF239989 *Prunus persica* ACC synthase ACS25 mRNA, pa... 597 e-170
40 gb|U22523|MIU22523 *Mangifera indica* 1-aminocyclopropane-carboxyl... 359 e-169
emb|X66605|DCACCS *D.caryophyllus* mRNA for 1-aminocyclopropane-1-... 396 e-168
gb|L31347|MAUACCSYN *Malus domestica* 1-aminocyclopropane-1-carbox... 378 e-168
emb|AB015624|AB015624 *Pyrus pyrifolia* mRNA for 1-aminocyclopropan... 377 e-168
emb|AF049137|AF049137 *Dianthus caryophyllus* 1-aminocyclopropane-... 338 e-167
45 emb|AF170705|AF170705 *Mangifera indica* 1-aminocyclopropane-1-car... 290 e-167
gb|U03294|MSU03294 *Malus sylvestris* 1-aminocyclopropane-1-carbox... 372 e-166
emb|Z77854|PSPACS1 *Phalaenopsis species* mRNA for 1-aminocyclopro... 513 e-166
emb|AJ277160|CPA277160 *Carica papaya* partial paccs1A gene for 1-... 266 e-165
gb|U73816|MDU73816 *Malus domestica* ACC synthase (MdACS-3) mRNA, ... 505 e-164
50 emb|AB007449|AB007449 *Actinidia deliciosa* mRNA for 1-aminocyclop... 355 e-164
emb|AB007639|AB007639 *Pyrus pyrifolia* mRNA for 1-aminocyclopropan... 502 e-164
dbj|D01033|CUCACCA *Cucurbita maxima* mRNA for 1-aminocyclopropane... 366 e-164
emb|X87112|PCPCACS1G *P.communis* mRNA for 1-aminocyclopropane-1-c... 363 e-163
gb|U17972|LEU17972 *Lycopersicon esculentum* 1-aminocyclopropane-1-... 362 e-163
55 emb|AB015495|AB015495 *Passiflora edulis* PE-ACS2 mRNA for ACC syn... 368 e-162
emb|AB006805|AB006805 *Cucumis sativus* CS-ACS3 mRNA for ACC synth... 360 e-160
emb|AB000679|AB000679 *Vigna radiata* mRNA for 1-aminocyclopropane... 365 e-158
gb|U34987|VRU34987 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 325 e-157
gb|M66619|DINCARACC *D.caryophyllus* 1-aminocyclopropane-1-carboxy... 496 e-156
60 gb|U34986|VRU34986 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 362 e-156
gb|U64031|DCU64031 *Dendrobium crumenatum* ACC synthase gene, comp... 259 e-154

emb|AF016458|AF016458 Pisum sativum 1-aminocyclopropane-1-carbox... 355 e-154
emb|Z27233|STACCAS1 S.tuberosum (STAC1) gene for amino cycloprop... 237 e-152
emb|Z27234|STACCAS2 S.tuberosum STACS2 gene for 1-Aminocycloprop... 232 e-152
5 emb|AF043122|AF043122 Lycopersicon esculentum ACC synthase (LE-A... 236 e-150
gb|U37774|CMU37774 Cucurbita maxima 1-aminocyclopropane-1-carbox... 234 e-150
gb|L34171|TOMACS3A Lycopersicon esculentum 1-aminocyclopropane-1... 235 e-149
gb|U18055|LEU18055 Lycopersicon esculentum 1-aminocyclopropane-1... 235 e-149
emb|AF151961|AF151961 Vigna radiata 1-aminocyclopropane-1-carbox... 232 e-146
10 emb|Z12135|VRACCSYN4 V.radiata gene for ACC synthase (pMAC-4). 376 e-145
gb|L07883|DORAMICARB Moth orchid 1-aminocyclopropane-1-carboxyla... 243 e-144
emb|AF074927|AF074927 Sinapis arvensis 1-aminocyclopropane-1-car... 330 e-142
emb|AF083815|AF083815 Antirrhinum majus ACC synthase 2 (ACS2) mR... 482 e-141
emb|AB021907|AB021907 Musa acuminata MA-ACS2 mRNA for ACC syntha... 310 e-140
emb|AB021908|AB021908 Musa acuminata MA-ACS3 mRNA for ACC syntha... 298 e-138
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http://www3.ncbi.nlm.nih.gov/htbin-
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(1950 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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			(bits) Value
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	emb AB006809 AB006809 Cucurbita sp. mRNA for PV72, complete cds.	606	0.0
	emb AW267745 AW267745 EST305873 DSIR Medicago truncatula cDNA cl...	350	e-124
35	emb AW931583 AW931583 EST357426 tomato fruit mature green, TAMU ...	165	e-112
	emb AW309187 AW309187 sg05d06.y1 Gm-c1019 Glycine max cDNA clone...	326	e-108
	emb AW622833 AW622833 EST306903 tomato flower buds 3-8 mm, Corne...	387	e-106
	emb AW774434 AW774434 EST333585 KV3 Medicago truncatula cDNA clo...	294	e-100
	emb AW689392 AW689392 NF018F12ST1F1000 Developing stem Medicago ...	338	e-100
40	gb BE054150 BE054150 GA_Ea0034H17f Gossypium arboreum 7-10 dpa ...	195	2e-99
	emb AI782787 AI782787 EST263666 tomato susceptible, Cornell Lyco...	332	6e-90
	emb AW737948 AW737948 EST339375 tomato flower buds, anthesis, Co...	225	1e-89
	emb AW615949 AW615949 EST325315 tomato flower buds 0-3 mm, Corne...	217	3e-86
	emb AW932529 AW932529 EST358372 tomato fruit mature green, TAMU ...	303	1e-83
45	emb AW685785 AW685785 NF030C07NR1F1000 Nodulated root Medicago t...	157	2e-81
	emb AW747297 AW747297 WS1_67_G06.b1_A002 Water-stressed 1 (WS1) ...	286	4e-76
	emb AI443067 AI443067 sa47a01.y1 Gm-c1004 Glycine max cDNA clone...	265	6e-76
	emb AI728635 AI728635 BNLGH11276 Six-day Cotton fiber Gossypium...	135	1e-75
	emb AI484571 AI484571 EST242801 tomato ovary, TAMU Lycopersicon ...	278	1e-73
50	emb AI727826 AI727826 BNLGH19195 Six-day Cotton fiber Gossypium ...	135	9e-71
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55	emb AW397829 AW397829 sg68h03.y1 Gm-c1007 Glycine max cDNA clone...	225	1e-57
	emb AW289687 AW289687 NXNV004E04F.Nsf Xylem Normal-wood Vertical...	182	7e-55
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60	emb AW623959 AW623959 EST321904 tomato flower buds 3-8 mm, Corne...	74	1e-49
	emb AW568619 AW568619 si60a11.y1 Gm-r1030 Glycine max cDNA clone...	165	2e-47

- emb|AI967865|AI967865 Ljimp14-100-f3 Ljimp Lambda HybriZap ... 180 5e-47
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emb|AW398931|AW398931 EST309431 L. pennellii trichome, Cornell U... 132 2e-45
5 emb|AW737369|AW737369 EST338892 tomato flower buds, anthesis, Co... 182 6e-45
emb|AW096632|AW096632 EST289812 tomato mixed elicitor, BTI Lycop... 81 7e-45
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10 emb|AW290400|AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical... 170 4e-41
gb|BE125908|BE125908 DG1_59_E01.b1_A002 Dark Grown 1 (DG1) Sorgh... 164 2e-39
emb|AI161766|AI161766 A006P54U Hybrid aspen plasmid library Popu... 76 3e-39
emb|AI162330|AI162330 A016P01U Hybrid aspen plasmid library Popu... 130 2e-37
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15 gb|L38113|L38113 BNAF0628E Mustard flower buds Brassica rapa cDN... 153 4e-36
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20 emb|AW906386|AW906386 EST342508 potato stolon, Cornell Universit... 78 2e-27
emb|AW126100|AW126100 N100297e rootphos(-) Medicago truncatula c... 73 9e-27
emb|AW620693|AW620693 sj08d10.y1 Gm-c1032 Glycine max cDNA clone... 77 1e-26
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emb|AW706755|AW706755 sk02f10.y1 Gm-c1023 Glycine max cDNA clone... 117 3e-25
25 emb|AW125944|AW125944 N100139e rootphos(-) Medicago truncatula c... 71 1e-23
emb|AW932524|AW932524 EST358367 tomato fruit mature green, TAMU ... 69 1e-22
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emb|AW093844|AW093844 EST287024 tomato mixed elicitor, BTI Lycop... 98 3e-19
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30 emb|AW119909|AW119909 sd54d08.y1 Gm-c1016 Glycine max cDNA clone... 88 2e-16
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35 emb|AW760128|AW760128 sl58d09.y1 Gm-c1027 Glycine max cDNA clone... 66 8e-14
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gb|C95899|C95899 C95899 Marchantia polymorpha immature sex organ... 38 0.31
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50 emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 35 1.5
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60 emb|AZ216543|AZ216543 Sheared DNA-116G5.TR Sheared DNA Trypanoso... 35 2.8
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- gb|U18916|SCE9781 *Saccharomyces cerevisiae* chromosome V cosmids ... 35 2.8
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 emb|AI822187|AI822187 L0-664T3 Ice plant Lambda Uni-Zap XR expre... 31 3.3
 emb|AI822671|AI822671 L0-1192T3 Ice plant Lambda Uni-Zap XR expr... 31 3.3
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- 25 emb|X97606|MSRNAAAA *M.sativa* mRNA translated from abscisic activ... 306 e-115
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 emb|AW774316|AW774316 EST333467 KV3 Medicago truncatula cDNA clo... 308 5e-83
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 30 emb|AW267789|AW267789 EST305917 DSIR Medicago truncatula cDNA cl... 169 4e-81
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 emb|AI794650|AI794650 sb67a05.y1 Gm-c1019 Glycine max cDNA clone... 286 2e-76
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 35 emb|AW399617|AW399617 EST310117 *L. pennellii* trichome, Cornell U... 281 5e-75
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 emb|AW756208|AW756208 sl17d10.y1 Gm-c1036 Glycine max cDNA clone... 264 5e-70
 emb|AW760494|AW760494 sl51a09.y1 Gm-c1027 Glycine max cDNA clone... 178 1e-69
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 40 emb|AJ223291|SRAJ3291 *Sesbania rostrata* mRNA for putative chalco... 115 2e-64
 emb|AW830327|AW830327 sm25f04.y1 Gm-c1028 Glycine max cDNA clone... 242 2e-63
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 45 gb|U13925|MSU13925 Medicago sativa Apollo clone CHR7 chalcone re... 117 6e-61
 emb|X57526|HVALREDR *H.vulgare* gene for aldose reductase-related ... 92 1e-60
 emb|X82367|MSCHR1B *M.sativa* mRNA for chalcone reductase (1115 bp). 116 1e-60
 emb|X82366|MSCHR1A *M.sativa* mRNA for chalcone reductase (1202 bp). 116 2e-60
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 50 gb|U13924|MSU13924 Medicago sativa Apollo clone CHR12 chalcone r... 114 8e-60
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 emb|AF108438|AF108438 *Papaver somniferum* putative NADPH-dependen... 154 1e-59
 gb|L12042|BMUSUSCUL *Bromus inermis* aldose reductase-related prot... 86 2e-59
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 55 emb|X59465|PSXYL1RE *P.stipitis* XYL1-gene for NAD(P)H-dependent X... 125 2e-58
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 60 emb|AB002106|AB002106 *Candida tropicalis* DNA for D-xylose reduct... 124 2e-57
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- dbj|D83718|GYCPKR *Glycyrrhiza echinata* mRNA for polyketide reduc... 111 6e-57
gb|U40706|PTU40706 *Pachysolen tannophilus* aldose reductase gene,... 123 8e-57
dbj|D86559|D86559 *Glycyrrhiza glabra* mRNA for polyketide reducta... 110 1e-56
5 dbj|D86558|D86558 *Glycyrrhiza glabra* mRNA for polyketide reducta... 110 1e-56
emb|AF074484|AF074484 *Candida tenuis* xylose reductase (xylr) gen... 127 2e-54
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emb|Z73100|SPAC26F1 *S.pombe* chromosome I cosmid c26F1. 92 1e-51
emb|AW730093|AW730093 GA_Ea0027M16 *Gossypium arboreum* 7-10 dpa ... 128 1e-51
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gb|U00059|YSCH8263 *Saccharomyces cerevisiae* chromosome VIII cosm... 116 2e-50
dbj|D11080|MAUS6PDH Apple S6PDH mRNA for NADP-dependent D-sorbit... 78 2e-49
15 emb|AF219625|AF219625 *Aspergillus niger* D-xylose reductase (xylA... 86 6e-49
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emb|AW773597|AW773597 EST332583 KV3 *Medicago truncatula* cDNA clo... 161 2e-48
emb|AF108433|AF108433 *Papaver somniferum* NADPH-dependent codeino... 85 2e-47
emb|AW982655|AW982655 HVSMEg0003N17f *Hordeum vulgare* pre-anthesi... 156 2e-47
20 emb|AL021815|SPBC8E4 *S.pombe* chromosome I cosmid c8E4. 84 3e-47
gb|J04483|LEIP10011E *Leishmania major* reductase (P100/11E) mRNA,... 83 5e-47
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emb|AW351113|AW351113 GM210010B20E10R Gm-r1021 *Glycine max* cDNA ... 122 2e-46
emb|AW267703|AW267703 EST305831 DSIR *Medicago truncatula* cDNA cl... 114 3e-46
25 emb|AL110661|CNS018Q6 *Botrytis cinerea* strain T4 cDNA library un... 108 2e-45
emb|AB014493|AB014493 *Gibberella zeae* gene for reductase, partia... 91 5e-45
emb|X94335|SC130KBXV *S.cerevisiae* 130kb DNA fragment from chromo... 57 2e-44
emb|X90518|SCXVORFS *S.cerevisiae* DNA of 51 Kb from chromosome XV... 57 2e-44
emb|Z75028|SCYOR120W *S.cerevisiae* chromosome XV reading frame OR... 57 2e-44
30 emb|X13228|SCGKY Yeast GCY gene (homologous to vertebrate eye le... 57 2e-44
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35 gb|BE036644|BE036644 MP03B08 MP *Mesembryanthemum crystallinum* cD... 80 9e-43
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40 gb|U21747|AFU21747 *Avena fatua* aldose reductase-related protein ... 91 4e-41
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45 emb|AW568008|AW568008 si56c03.y1 Gm-r1030 *Glycine max* cDNA clone... 166 3e-40
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50 emb|AW306925|AW306925 sf50e02.y1 Gm-c1009 *Glycine max* cDNA clone... 93 2e-38
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55 emb|AW728632|AW728632 GA_Ea0017G17 *Gossypium arboreum* 7-10 dpa ... 80 3e-36
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60 emb|AW756704|AW756704 sl26b12.y1 Gm-c1027 *Glycine max* cDNA clone... 79 2e-35
gb|U26463|SSU26463 *Sporidiobolus salmonicolor* NADPH-dependent al... 86 3e-35

emb|AW234076|AW234076 sf34a01.y1 Gm-c1028 Glycine max cDNA clone... 111 7e-35

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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35	emb X13754 SOPHTRAN Spinach mRNA for chloroplast phosphate trans...	186 8e-69	
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	emb AW399333 AW399333 EST309833 L. pennellii trichome, Cornell U...	175	8e-43
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	emb AW671381 AW671381 LG1_335_G10.b1_A002 Light Grown 1 (LG1) So...	173	3e-42
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	emb AW559735 AW559735 EST314727 DSIR Medicago truncatula cDNA cl...	167	3e-42
	gb BE034606 BE034606 MK02F02 MK Mesembryanthemum crystallinum cD...	170	2e-41
10	emb AW690541 AW690541 NF035G02ST1F1000 Developing stem Medicago ...	166	5e-41
	gb U13632 BOU13632 Brassica oleracea var. botrytis non-green pla...	166	2e-40
	emb A93887 A93887 Sequence 1 from Patent WO9725346.	166	2e-40
	emb AW782182 AW782182 sm02e11.y1 Gm-c1027 Glycine max cDNA clone...	166	3e-40
	gb U66402 NTU66402 Nicotiana tabacum plastid phosphate/phosphoen...	165	6e-40
15	emb AW666055 AW666055 sk31e07.y1 Gm-c1028 Glycine max cDNA clone...	160	2e-39
	emb AW776623 AW776623 EST335688 DSIL Medicago truncatula cDNA cl...	162	4e-39
	gb U66401 NTU66401 Nicotiana tabacum plastid phosphate/phosphoen...	162	4e-39
	emb AF173656 AF173656 Beta vulgaris clone GPTII109UNI glucose-6-...	161	1e-38
	emb AW736423 AW736423 EST332437 KV3 Medicago truncatula cDNA clo...	153	6e-38
20	emb AW038916 AW038916 EST280872 tomato mixed elicitor, BTI Lycop...	158	1e-37
	emb AW930290 AW930290 EST340747 tomato fruit mature green, TAMU ...	157	2e-37
	emb AV415709 AV415709 AV415709 Lotus japonicus young plants (two...	153	2e-36
	emb AW201212 AW201212 se99c01.y1 Gm-c1027 Glycine max cDNA clone...	93	3e-36
	emb AI736196 AI736196 sb24f10.y1 Gm-c1008 Glycine max cDNA clone...	151	8e-36
25	emb AV426398 AV426398 AV426398 Lotus japonicus young plants (two...	149	6e-35
	emb AV422882 AV422882 AV422882 Lotus japonicus young plants (two...	147	2e-34
	emb AF173660 AF173660 Beta vulgaris clone GPTII109UNI glucose-6-p...	146	4e-34
	emb AI822397 AI822397 L0-856T3 Ice plant Lambda Uni-Zap XR expre...	125	7e-34
	emb AW040008 AW040008 EST282499 tomato mixed elicitor, BTI Lycop...	144	1e-33
30	emb AW039997 AW039997 EST282488 tomato mixed elicitor, BTI Lycop...	144	1e-33
	gb BE059998 BE059998 sn39f10.y1 Gm-c1027 Glycine max cDNA clone ...	143	3e-33
	emb AW671168 AW671168 LG1_330_E06.b1_A002 Light Grown 1 (LG1) So...	142	5e-33
	emb AW667825 AW667825 GA_Ea0010N10 Gossypium arboreum 7-10 dpa ...	141	9e-33
	emb AW760961 AW760961 sl61c01.y1 Gm-c1027 Glycine max cDNA clone...	138	8e-32
35	emb AW832362 AW832362 sm08e01.y1 Gm-c1027 Glycine max cDNA clone...	138	8e-32
	emb AW781979 AW781979 sl99a06.y1 Gm-c1027 Glycine max cDNA clone...	138	8e-32
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	emb AW287694 AW287694 LG1_271_C05.b1_A002 Light Grown 1 (LG1) So...	135	8e-31
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40	emb AW564618 AW564618 LG1_297_G09.b1_A002 Light Grown 1 (LG1) So...	134	1e-30
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	emb AW888070 AW888070 NXNV_126_H09_F Nsf Xylem Normal wood Verti...	134	1e-30
	emb AW694653 AW694653 NF078G03ST1F1023 Developing stem Medicago ...	108	2e-30
	emb AV425340 AV425340 AV425340 Lotus japonicus young plants (two...	132	5e-30
45	emb AW030490 AW030490 EST273745 tomato callus, TAMU Lycopersicon...	132	7e-30
	emb AW738715 AW738715 EST340142 tomato flower buds, anthesis, Co...	132	7e-30
	emb AW040512 AW040512 EST283472 tomato mixed elicitor, BTI Lycop...	131	1e-29
	emb AW780617 AW780617 sl73c03.y1 Gm-c1027 Glycine max cDNA clone...	131	1e-29
	emb AW287232 AW287232 LG1_268_C02.b1_A002 Light Grown 1 (LG1) So...	130	2e-29
50	emb AV410940 AV410940 AV410940 Lotus japonicus young plants (two...	130	2e-29
	emb AW286886 AW286886 LG1_222_F11.b1_A002 Light Grown 1 (LG1) So...	129	3e-29
	emb AW399232 AW399232 EST309732 L. pennellii trichome, Cornell U...	129	5e-29
	emb AW287673 AW287673 LG1_271_A05.b1_A002 Light Grown 1 (LG1) So...	129	5e-29
	emb AV412063 AV412063 AV412063 Lotus japonicus young plants (two...	128	7e-29
	emb AV421682 AV421682 AV421682 Lotus japonicus young plants (two...	128	7e-29
55	emb AW759175 AW759175 sl38a01.y1 Gm-c1027 Glycine max cDNA clone...	128	7e-29
	emb AW672543 AW672543 LG1_360_B12.b1_A002 Light Grown 1 (LG1) So...	128	7e-29
	emb AW596590 AW596590 sj14c04.y1 Gm-c1032 Glycine max cDNA clone...	128	9e-29
	emb AW694511 AW694511 NF077A11ST1F1084 Developing stem Medicago ...	128	9e-29
60	emb AV415908 AV415908 AV415908 Lotus japonicus young plants (two...	127	2e-28

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(834 letters)

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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

15	gb U21848 BNU21848 Brassica napus chitinase class IV (LSC222) mR...	225	e-134
	emb X61488 BNCHITIN B.napus mRNA for chitinase.	156	7e-88
	gb U97521 VVU97521 Vitis vinifera class IV endochitinase (VvChi4...	173	3e-77
	gb U97522 VVU97522 Vitis vinifera class IV endochitinase (VvChi4...	174	2e-76
	emb X57187 PVCHITIN P.vulgaris mRNA for chitinase.	149	2e-74
20	emb AF112966 AF112966 Triticum aestivum chitinase IV precursor (...)	157	5e-70
	dbj D45181 D45181 Chenopodium amaranticolor mRNA for chitinase, ...	100	5e-67
	gb U52845 DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP...	114	7e-67
	gb U52846 DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP...	111	9e-66
	gb BE034166 BE034166 MG05H02 MG Mesembryanthemum crystallinum cD...	129	1e-65
25	gb U52847 DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP...	110	8e-65
	gb U52848 DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3...	111	2e-64
	gb BE034975 BE034975 ML07H10 ML Mesembryanthemum crystallinum cD...	125	2e-64
	gb BE034428 BE034428 MH04G02 MH Mesembryanthemum crystallinum cD...	123	2e-63
	gb BE034976 BE034976 ML07H11 ML Mesembryanthemum crystallinum cD...	120	6e-63
30	dbj D45183 D45183 Chenopodium amaranticolor mRNA for chitinase, ...	96	1e-62
	dbj D45184 D45184 Chenopodium amaranticolor mRNA for chitinase, ...	100	3e-62
	dbj D45182 D45182 Chenopodium amaranticolor mRNA for chitinase, ...	100	4e-60
	emb X75945 BVCH4RNA B.vulgaris Ch4 mRNA for chitinase.	92	6e-60
	emb A23392 A23392 B.vulgaris mRNA for chitinase 4 (B15).	92	6e-60
35	emb X88803 VURNACH14 V.unguiculata mRNA for chitinase class 4 (p...	118	3e-59
	emb A1897733 A1897733 EST267176 tomato ovary, TAMU Lycopersicon ...	110	1e-58
	gb BE034406 BE034406 MH04D10 MH Mesembryanthemum crystallinum cD...	105	2e-58
	gb L25826 BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds.	158	3e-58
	gb BE034497 BE034497 MH05H03 MH Mesembryanthemum crystallinum cD...	89	8e-58
	gb L42467 PIACHI Picea glauca chitinase (chi) mRNA, complete cds.	93	2e-57
40	emb AF090336 AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA...	166	2e-57
	emb A1897843 A1897843 EST267286 tomato ovary, TAMU Lycopersicon ...	103	1e-56
	emb AF112963 AF112963 Triticum aestivum chitinase II precursor (...)	149	9e-56
	gb BE035287 BE035287 MM04H04 MM Mesembryanthemum crystallinum cD...	162	4e-54
45	emb AW680953 AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S...	178	3e-52
	gb BE033502 BE033502 ME03F10-ME Mesembryanthemum crystallinum cD...	87	4e-50
	gb M94105 ALCCHITIN Allium sativum chitinase mRNA, 3' end.	100	6e-49
	emb A1898279 A1898279 EST267722 tomato ovary, TAMU Lycopersicon ...	83	1e-48
	gb U83592 MSU83592 Medicago sativa class I chitinase mRNA, compl...	109	1e-48
	gb U83591 MSU83591 Medicago sativa class I chitinase mRNA, compl...	109	1e-48
50	emb AW030814 AW030814 EST274069 tomato callus, TAMU Lycopersicon...	83	3e-48
	emb AW035013 AW035013 EST279284 tomato callus, TAMU Lycopersicon...	83	3e-48
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	gb BE034481 BE034481 MH05F02 MH Mesembryanthemum crystallinum cD...	162	5e-48
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55	emb A1485982 A1485982 EST244303 tomato ovary, TAMU Lycopersicon ...	83	1e-47
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60	emb X15494 STCHITIN Potato endochitinase gene (EC 3.2.1.14).	95	6e-47
	emb X07130 STCHIT Solanum tuberosum mRNA for endochitinase (EC 3...	95	6e-47

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 gb|S43926|S43926 CH5B=chitinase [*Phaseolus vulgaris*=beans, cv Sa... 106 5e-46
 emb|X88800|VURNACHI1 *V. unguiculata* mRNA for chitinase class I (p... 105 1e-45
 5 emb|AJ012821|CAR012821 *Cicer arietinum* mRNA for class I chitinase. 108 6e-45
 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem *Medicago* ... 78 8e-45
 emb|Y10373|MTCHITIN1 *M. truncatula* mRNA for chitinase. 109 8e-45
 emb|AW033122|AW033122 EST276681 tomato callus, TAMU *Lycopersicon*... 83 2e-44
 gb|M94106|ALCCHINTIA *Allium sativum* chitinase mRNA, 3' end. 102 3e-44
 10 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 170 3e-44
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 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 178 4e-44
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 95 5e-44
 gb|M15173|TOBECH Tobacco (*N. tabacum*) endochitinase mRNA, partial... 95 5e-44
 15 emb|AF061806|AF061806 *Elaeagnus umbellata* basic chitinase mRNA, ... 105 1e-43
 emb|Z54234|VVCHIT1MR *V. vinifera* mRNA for chitinase. 98 1e-43
 gb|S44869|S44869 basic chitinase [*Nicotiana tabacum*=tobacco, cv ... 95 2e-43
 emb|X16939|NTECHITR *Nicotiana tabacum* mRNA for endochitinase (EC... 95 2e-43
 emb|X76041|TACHIG *T. aestivum* (Chinese spring) chi gene for endoc... 93 4e-43
 20 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 97 6e-43
 emb|Z46948|SNCHJET15 *S. nigra* mRNA for chitinase, pathogenesis-re... 104 2e-42
 gb|U02605|STU02605 *Solanum tuberosum* chitinase (chtB1) mRNA, par... 95 3e-42
 gb|U02606|STU02606 *Solanum tuberosum* chitinase (chtB2) mRNA, par... 95 4e-42
 emb|Z46950|SNCHJET19 *S. nigra* mRNA chitinase class II, pathogenes... 104 6e-42
 25 gb|U78888|GHU78888 *Gossypium hirsutum* class I endochitinase mRNA... 102 1e-41
 gb|BE034450|BE034450 MH05B01 MH *Mesembryanthemum crystallinum* cD... 81 3e-41
 emb|Z15140|LECHI9 *L. esculentum* mRNA for chitinase. 95 3e-41
 gb|U02607|STU02607 *Solanum tuberosum* chitinase (chtB3) mRNA, par... 95 6e-41
 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 95 6e-41
 30 emb|AF034566|AF034566 *Gossypium hirsutum* class I chitinase mRNA,... 100 6e-41
 gb|BE033398|BE033398 ME01A01 ME *Mesembryanthemum crystallinum* cD... 165 7e-41
 gb|M25337|POPCHIB *Populus* sp. chitinase (win8) mRNA, complete cds. 89 8e-41
 gb|BE034267|BE034267 MH02D06 MH *Mesembryanthemum crystallinum* cD... 66 2e-40
 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU *Lycopersicon* ... 110 4e-40
 35 emb|AF000965|AF000965 *Poa pratensis* chitinase (Chi3) pseudogene ... 91 4e-40
 emb|X95610|CSHITIB *C. sativa* mRNA for chitinase Ib. 88 9e-40
 gb|U48687|CSU48687 *Castanea sativa* endochitinase mRNA, complete ... 88 9e-40
 emb|AW676775|AW676775 DG1_14_C09.g1_A002 Dark Grown 1 (DG1) Sorg... 161 2e-39
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 40 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 163 2e-39
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 45 emb|AW560048|AW560048 EST315096 DSIR *Medicago truncatula* cDNA cl... 109 7e-39
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 emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root *Medicago* t... 78 3e-38
 gb|U02287|HVVU02287 *Hordeum vulgare* cultivar NK1558 chitinase gen... 96 4e-38
 emb|AI897657|AI897657 EST267100 tomato ovary, TAMU *Lycopersicon* ... 101 1e-37
 50 emb|AF098302|AF098302 *Brassica juncea* chitinase mRNA, complete cds. 106 1e-37
 emb|AW746429|AW746429 WS1_53_G09.b1_A002 Water-stressed 1 (WS1) ... 97 4e-37
 emb|X74919|PVGEC9 *P. vulgaris* gene for endochitinase. 149 6e-37

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(1548 letters)

60 Database: plantfungal
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	emb AB001379 AB001379 Glycyrhiza echinata CYP81E1 mRNA for cyto...	323	e-137
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10	emb AB025016 AB025016 Lotus japonicus mRNA for cytochrome P450, ...	291	e-134
	emb AJ012581 CAR012581 Cicer arietinum mRNA for cytochrome P450.	324	e-134
	emb AJ000478 HTCYP81L Helianthus tuberosus mRNA for cytochrome P...	227	e-124
	emb AJ000477 HTCYP81C Helianthus tuberosus mRNA for cytochrome P...	227	e-124
	emb AJ239051 CAR239051 Cicer arietinum mRNA for cytochrome P450 ...	237	3e-82
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	emb AW185361 AW185361 se90e02.y1 Gm-c1027 Glycine max cDNA clone...	280	3e-74
	emb AW775904 AW775904 EST334969 DSIL Medicago truncatula cDNA cl...	228	1e-70
	emb AF082028 AF082028 Hemerocallis hybrid cultivar senescence-as...	189	2e-70
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20	emb AW307234 AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone...	258	1e-67
	emb AW733691 AW733691 sk83g07.y1 Gm-c1016 Glycine max cDNA clone...	253	3e-66
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25	emb AW329224 AW329224 N200436e rootphos(-) Medicago truncatula c...	224	1e-57
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	emb AI495626 AI495626 sb11c08.y1 Gm-c1004 Glycine max cDNA clone...	222	6e-57
	emb AW100311 AW100311 sd22g12.y2 Gm-c1012 Glycine max cDNA clone...	206	5e-56
	emb AW257188 AW257188 EST305325 KV2 Medicago truncatula cDNA clo...	177	6e-56
30	emb AI774414 AI774414 EST255514 tomato resistant, Cornell Lycopers...	144	5e-54
	emb AW171672 AW171672 N100566e rootphos(-) Medicago truncatula c...	212	7e-54
	emb AW932147 AW932147 EST357990 tomato fruit mature green, TAMU ...	211	1e-53
	emb AI731481 AI731481 BNLGHi9879 Six-day Cotton fiber Gossypium ...	168	3e-51
	emb AI731081 AI731081 BNLGHi8648 Six-day Cotton fiber Gossypium ...	200	2e-50
35	emb AI728374 AI728374 BNLGHi10609 Six-day Cotton fiber Gossypium...	163	9e-50
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	emb AF156976 AF156976 Gerbera hybrida flavone synthase II (CYP93...	100	8e-46
	dbj E13663 E13663 cDNA encoding cytochrome P450 which is induced...	104	1e-45
40	dbj D83968 SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)...	104	1e-45
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	emb AW695923 AW695923 NF100G02ST1F1018 Developing stem Medicago ...	170	9e-44
	emb AW684707 AW684707 NF020A02NR1F1000 Nodulated root Medicago t...	178	1e-43
	emb AB015762 AB015762 Nicotiana tabacum mRNA for cytochrome P450...	160	2e-43
45	emb AI973839 AI973839 sd11c06.y1 Gm-c1020 Glycine max cDNA clone...	104	2e-43
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	emb AW734404 AW734404 sk19f09.y1 Gm-c1028 Glycine max cDNA clone...	157	2e-43
	gb U29333 PSU29333 Pisum sativum novel wound-inducible cytochrom...	160	5e-43
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50	gb U72654 EGU72654 Eustoma grandiflorum flavonoid 3'-hydroxyla...	149	2e-42
	dbj D86351 D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,...	102	2e-42
	emb AW688601 AW688601 NF009D12ST1F1000 Developing stem Medicago ...	173	4e-42
	emb AW616170 AW616170 EST307209 L. hirsutum trichome, Cornell Un...	148	5e-42
	dbj D14589 D14589 Eustoma russellianum mRNA for flavonoid 3',5'-...	148	6e-42
55	emb AJ011862 CRO011862 Catharanthus roseus mRNA for flavonoid 3'...	155	6e-42
	emb Z22545 PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA.	148	8e-42
	dbj D14588 PETHF1 Petunia hybrida Hfl mRNA for flavonoid-3',5'-h...	148	8e-42
	emb AW616482 AW616482 EST322893 L. hirsutum trichome, Cornell Un...	148	1e-41
	emb AW617814 AW617814 EST324213 L. hirsutum trichome, Cornell Un...	148	1e-41
60	emb AW309826 AW309826 sf25c03.x1 Gm-c1028 Glycine max cDNA clone...	166	1e-41
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 emb|AF195800|AF195800 Medicago sativa isoflavone synthase 1 (ifs... 99 4e-41
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 emb|AI776121|AI776121 EST257209 tomato resistant, Cornell Lycop... 111 5e-41
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 10 emb|AF195810|AF195810 Trifolium pratense isoflavone synthase 1 (... 98 6e-41
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 emb|AW651341|AW651341 EST329795 tomato germinating seedlings, TA... 148 7e-41
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 20 emb|AI782402|AI782402 EST263281 tomato susceptible, Cornell Lyco... 144 2e-40
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 25 emb|AF195817|AF195817 Beta vulgaris isoflavone synthase 2 (ifs2)... 97 2e-40
 emb|AW687247|AW687247 NF007E11RT1F1086 Developing root Medicago ... 167 2e-40
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 30 emb|AW034115|AW034115 EST277610 tomato callus, TAMU Lycopersicon... 147 4e-40
 emb|AF081575|AF081575 Petunia x hybrida flavonoid 3',5'-hydroxyl... 142 5e-40
 emb|Z17369|HTTC4MMR H.tuberosus mRNA for trans-cinnamate 4-monoo... 143 5e-40
 emb|A74279|A74279 Sequence 1 from Patent WO9401564. 143 5e-40
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 35 emb|AW616066|AW616066 EST296823 L. hirsutum trichome, Cornell Un... 145 5e-40
 emb|AW728802|AW728802 GA_Ea0028I12 Gossypium arboreum 7-10 dpa ... 148 6e-40
 emb|AF195801|AF195801 Medicago sativa isoflavone synthase 2 (ifs... 98 7e-40
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 40 gb|L07634|PHVC4HYDRO Phaseolus aureus cinnamate 4-hydroxylase mR... 141 9e-40
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 emb|AJ243804|CAR243804 Cicer arietinum mRNA for cytochrome P450 ... 96 1e-39
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 45 emb|AF195816|AF195816 Beta vulgaris isoflavone synthase 1 (ifs1)... 97 1e-39

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 (2805 letters)

55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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- emb|AF109392|AF109392 Brassica napus ligand gated channel-like p... 142 3e-57
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gb|BE022401|BE022401 sm85d03.y1 Gm-c1015 Glycine max cDNA clone ... 55 3e-13
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gb|BE059628|BE059628 sn34g08.y1 Gm-c1016 Glycine max cDNA clone ... 58 5e-10
10 emb|AW928584|AW928584 EST337372 tomato flower buds 8 mm to pre-a... 66 1e-09
emb|AW622410|AW622410 EST313197 tomato root during/after fruit s... 40 3e-06
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emb|AW933376|AW933376 EST359219 tomato fruit mature green, TAMU ... 52 2e-05
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15 emb|AW925534|AW925534 HVSMEg0002H02 Hordeum vulgare pre-anthesis... 48 3e-04
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30 emb|AW224605|AW224605 EST303048 tomato root, plants pre-anthesis... 31 0.42
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35 emb|AW455351|AW455351 EST311889 tomato root during/after fruit s... 31 0.42
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50 emb|AW933175|AW933175 EST359018 tomato fruit mature green, TAMU ... 36 1.6
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 emb|AL122012|LMFL8342 Leishmania major Friedlin chromosome 23 co... 35 4.2
 emb|AW257203|AW257203 EST305340 KV2 Medicago truncatula cDNA clo... 35 4.2
 5 emb|AC005504|AC005504 Plasmodium falciparum chromosome 12, *** S... 35 4.2
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 10 emb|AC004710|AC004710 Plasmodium falciparum chromosome 12, *** S... 35 4.2
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 15 emb|AV406712|AV406712 AV406712 Lotus japonicus young plants (two... 34 5.7
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 20 gb|U08622|SPU08622 Schizosaccharomyces pombe cAMP-dependent prot... 34 5.7
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 emb|AW442327|AW442327 EST311723 tomato fruit red ripe, TAMU Lyco... 34 7.8
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 40 post/entrez/query?db=n&form=6&dopt=g&uid=gb|af071527|/ncgi
 http://www.ncgr.org/cgi-bin/ff?af071527
 (1926 letters)

Database: plantfungal

45 661,018 sequences; 426,114,510 total letters

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- emb|AI894928|AI894928 EST264371 tomato callus, TAMU Lycopersicon... 58 2e-07
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 55 emb|AI729861|AI729861 BNLGHi5428 Six-day Cotton fiber Gossypium ... 52 2e-05
 emb|AW035961|AW035961 EST282820 tomato callus, TAMU Lycopersicon... 51 3e-05
 emb|AV420300|AV420300 AV420300 Lotus japonicus young plants (two... 49 1e-04
 emb|AZ124241|AZ124241 T223105b Medicago truncatula BAC library M... 49 1e-04
 emb|AW694103|AW694103 NF072D04ST1F1041 Developing stem Medicago ... 48 3e-04
 60 emb|AI896054|AI896054 EST265497 tomato callus, TAMU Lycopersicon... 47 4e-04
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10	emb AQ638202 AQ638202 927P1-9H10.TP 927P1 Trypanosoma brucei gen...	41	0.033
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	emb X02390 ANTRPC1 Aspergillus nidulans trpC gene.	35	2.0
25	emb X52152 SCIME S. cerevisiae IME1 gene for Ime1, a meiosis ind...	35	2.0
	emb Z49595 SCYJR095W S.cerevisiae chromosome X reading frame ORF...	35	2.0
	gb L47610 PIAEMB4R Picea glauca EMB4 mRNA.	35	2.0
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30	gb M37188 YSCIME1 S.cerevisiae meiosis-inducing protein (IME1) g...	35	2.0
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 5 emb|AW924917|AW924917 WS1_73_B03.b1_A002 Water-stressed 1 (WS1) ... 33 9.9
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 10 emb|AW399343|AW399343 EST309843 *L. pennellii* trichome, Cornell U... 33 9.9
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 (1062 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

- 25 Searching.....done

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Sequences producing significant alignments: (bits) Value

- 30 emb|AI486803|AI486803 EST245125 tomato ovary, TAMU *Lycopersicon* ... 358 6e-98
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 35 gb|L42466|PIAEFE *Picea glauca* ethylene-forming enzyme (EFE) mRNA... 156 4e-75
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 emb|AW574101|AW574101 EST316692 *GVN Medicago truncatula* cDNA clo... 198 2e-67
 emb|AW268031|AW268031 EST306309 *DSIR Medicago truncatula* cDNA cl... 126 6e-65
 40 emb|AW775553|AW775553 EST334618 *DSIL Medicago truncatula* cDNA cl... 210 3e-63
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 emb|AW349732|AW349732 GM210006A11F12R *Gm-r1021 Glycine max* cDNA ... 228 6e-59
 gb|U97530|PAGU97530 *Prunus armeniaca* ethylene-forming-enzyme-like... 143 1e-58
 45 emb|AF082862|AF082862 *Pisum sativum* unknown mRNA, partial cds. 220 2e-56
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 55 gb|U54566|NGU54566 *Nicotiana glutinosa* 1-aminocyclopropane-1-car... 174 2e-52
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- emb|AB023786|AB023786 Ipomoea batatas ans I mRNA for anthocyanid... 111 4e-50
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 5 emb|A35021|A35021 L.esculentum pTOM13. 159 1e-49
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 40 emb|AW685110|AW685110.NF025C04NR1F1000 Nodulated root Medicago t... 158 1e-47
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 45 emb|Y10034|PP1AMCSYN R.palustris mRNA for 1-aminocyclopropane-1-... 159 2e-47
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 55 emb|Z46349|NTACCDEAM N.tabacum mRNA for 1-aminocyclopropane-1-ca... 150 8e-47
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- emb|AB010992|AB010992 Lycopersicon esculentum Le3OH-2 mRNA for 3... 133 2e-46
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 http://www.ncgr.org/cgi-bin/ff?al035527
 15 (1731 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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- 5 emb|AW201920|AW201920 sf08g07.y1 Gm-c1027 Glycine max cDNA clone... 105 4e-27
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- emb|AW234064|AW234064 sf33g09.y1 Gm-c1028 Glycine max cDNA clone... 93 1e-25
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- emb|AW398957|AW398957 EST309457 L. pennellii trichome, Cornell U... 87 5e-25
- emb|AW350656|AW350656 GM210008B20D6R Gm-r1021 Glycine max cDNA 3... 116 7e-25
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- emb|AW773596|AW773596 EST332582 KV3 Medicago truncatula cDNA clo... 89 2e-24
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- emb|AW756588|AW756588 sl24c08.y1 Gm-c1036 Glycine max cDNA clone... 75 5e-24
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- emb|AW929899|AW929899 EST354169 tomato flower buds 8 mm to pre-a... 73 3e-21
- 35 emb|AW563695|AW563695 LG1_248_G02.g1_A002 Light Grown 1 (LG1) So... 70 6e-21
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 10 http://www.ncgr.org/cgi-bin/ff?ac006580
 (828 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Score E
 Sequences producing significant alignments: (bits) Value

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25 emb|AJ010830|TSP010830 Triticum sp. mRNA for GRAB2 protein. 133 3e-44
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(1290 letters)

5

Database: plantfungal
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Searching.....done

10

Score E

Sequences producing significant alignments: (bits) Value

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emb|AW720283|AW720283 LjNEST20a9r Lotus japonicus nodule library... 295 4e-79
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gb|BE021080|BE021080 sm55b08.y1 Gm-c1028 Glycine max cDNA clone... 282 3e-75
20 emb|AW509358|AW509358 si22a10.y1 Gm-c1029 Glycine max cDNA clone... 272 3e-72
emb|AW622811|AW622811 EST306797 tomato flower buds 3-8 mm, Corne... 252 4e-66
emb|AV390505|AV390505 AV390505 Chlamydomonas reinhardtii C9 Chla... 147 4e-58
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25 emb|AI774300|AI774300 EST255316 tomato resistant, Cornell Lycopers... 210 1e-53
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50	emb AW216510 AW216510 EST295224 tomato callus, TAMU Lycopersicon...	34	3.4
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 (990 letters)

60 Database: plantfungal
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35	emb AI896567 AI896567	EST266010 tomato callus, TAMU Lycopersicon...	110	2e-41
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	emb AW707185 AW707185	sk10h04.y1 Gm-c1023 Glycine max cDNA clone...	82	9e-38
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45	emb AW226128 AW226128	ST77F07 Pine TriplEx shoot tip library Pin...	136	2e-31
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50	emb AF195243 AF195243	Chlamydomonas reinhardtii apospory-associa...	71	3e-27
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	emb AW668439 AW668439	GA_Ea0013P01 Gossypium arboreum 7-10 dpa ...	117	1e-25
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55	gb H75140 H75140	18 PtiFG1 Pinus taeda cDNA clone 0149e, mRNA se...	106	2e-23
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	emb AW678374 AW678374	WS1_15_D11.b1_A002 Water-stressed 1 (WS1) ...	70	5e-22
	emb AW678403 AW678403	WS1_15_D11.g1_A002 Water-stressed 1 (WS1) ...	70	5e-22
	emb AW678308 AW678308	WS1_14_G02.g1_A002 Water-stressed 1 (WS1) ...	62	3e-21
60	emb AQ946977 AQ946977	Sheared DNA-47C11.TF Sheared DNA Trypanoso...	92	8e-18
	emb AW707360 AW707360	832006H03.y1 C. reinhardtii CC-125 nutrien...	71	5e-17

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40	emb AI896247 AI896247 EST265690 tomato callus, TAMU Lycopersicon...	55	1e-06
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45	emb AW729558 AW729558 GA_Ea0025G01 Gossypium arboreum 7-10 dpa ...	51	2e-05
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55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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60 Score E
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- gb|BE052481|BE052481 GA_Ea0034B15f *Gossypium arboreum* 7-10 dpa ... 248 8e-65
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 emb|AV427652|AV427652 AV427652 *Lotus japonicus* young plants (two... 88 2e-16
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 10 emb|AW747181|AW747181 WS1_66_B09.b1_A002 Water-stressed 1 (WS1) ... 59 2e-09
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 gb|BE122206|BE122206 894018B07.x1 *C. reinhardtii* CC-1690, normal... 36 0.83
 emb|AW757802|AW757802 874003G04.x1 *C. reinhardtii* CC-1690, Lambd... 36 0.83
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 (711 letters)

- 5 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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55 Database: plantfungal
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5	emb AW688778 AW688778 NF011E05ST1F1000 Developing stem Medicago ...	244 1e-65
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10	emb AL023554 SPBC16G5 S.pombe chromosome II cosmid c16G5.	81 1e-31
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	emb X73297 SCSETRP4 S.cerevisiae spacer element.	29 0.002
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- gb|U18839|SCE9747 *Saccharomyces cerevisiae* chromosome V cosmids ... 33 8.1
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 (643 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

25

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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 50 emb|AW033868|AW033868 EST277439 tomato callus, TAMU *Lycopersicon*... 62 1e-18
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- emb|AW680050|AW680050 WS1_3_G12.g1_A002 Water-stressed 1 (WS1) S... 57 1e-15
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40 dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 50 1e-11
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- emb|AV426673|AV426673 AV426673 Lotus japonicus young plants (two... 48 4e-08
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5 emb|AW030314|AW030314 EST273569 tomato callus, TAMU Lycopersicon... 53 4e-07
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(643 letters)
- 15 Database: plantfungal
661,018 sequences; 426,114,510 total letters
- Searching.....done
- 20 Score E
Sequences producing significant alignments: (bits) Value
- gb|L46574|L46574 BNAF1975 Mustard flower buds Brassica rapa cDNA... 84 2e-29
emb|AB006600|AB006600 Petunia x hybrida mRNA for ZPT2-13, comple... 57 2e-25
25 emb|AB006599|AB006599 Petunia x hybrida mRNA for ZPT2-12, comple... 57 5e-23
emb|AI485362|AI485362 EST243683 tomato ovary, TAMU Lycopersicon ... 64 4e-22
emb|AI898309|AI898309 EST267752 tomato ovary, TAMU Lycopersicon ... 63 8e-22
emb|AI483886|AI483886 EST249757 tomato ovary, TAMU Lycopersicon ... 64 2e-21
emb|AB006604|AB006604 Petunia x hybrida mRNA for ZPT2-9, complet... 102 2e-21
30 emb|AW030869|AW030869 EST274159 tomato callus, TAMU Lycopersicon... 61 4e-21
emb|AI485555|AI485555 EST243876 tomato ovary, TAMU Lycopersicon ... 55 7e-21
emb|AB000451|AB000451 Petunia hybrida mRNA for PETHy;ZPT2-5, com... 62 2e-20
emb|AI486627|AI486627 EST244948 tomato ovary, TAMU Lycopersicon ... 55 2e-20
emb|AI486228|AI486228 EST244549 tomato ovary, TAMU Lycopersicon ... 55 2e-20
35 emb|AI771123|AI771123 EST252223 tomato ovary, TAMU Lycopersicon ... 55 6e-20
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45 emb|AI771824|AI771824 EST252924 tomato ovary, TAMU Lycopersicon ... 59 5e-18
emb|AW685937|AW685937 NF031H10NR1F1000 Nodulated root Medicago t... 59 9e-18
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50 emb|AV422177|AV422177 AV422177 Lotus japonicus young plants (two... 56 8e-17
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dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 56 3e-16
dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 56 3e-16
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55 emb|AW033574|AW033574 EST277145 tomato callus, TAMU Lycopersicon... 53 2e-15
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emb|AW034640|AW034640 EST278324 tomato callus, TAMU Lycopersicon... 53 2e-15
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60 emb|AW033257|AW033257 EST276828 tomato callus, TAMU Lycopersicon... 53 3e-15
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- emb|AW032357|AW032357 EST275811 tomato callus, TAMU Lycopersicon... 53 3e-15
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5 emb|AW030876|AW030876 EST274166 tomato callus, TAMU Lycopersicon... 53 4e-14
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dbj|D16416|WHTWZF1B Wheat mRNA for WZF1, complete cds. 47 3e-13
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15 emb|AW034622|AW034622 EST278306 tomato callus, TAMU Lycopersicon... 50 2e-12
gb|U76555|BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA... 52 2e-12
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emb|AW153229|AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone... 51 3e-12
emb|AW625323|AW625323 EST319146 tomato radicle, 5 d post-imbibit... 52 3e-12
20 emb|AW924443|AW924443 WS1_69_C08.g1_A002 Water-stressed 1 (WS1) ... 57 3e-12
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25 emb|AI988290|AI988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone... 50 5e-12
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emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 49 6e-12
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gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 48 8e-12
30 emb|AI988657|AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone... 49 8e-12
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dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 50 1e-11
emb|AW219517|AW219517 EST301915 tomato root during/after fruit s... 52 1e-11
gb|U76554|BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR... 52 2e-11
35 emb|AW729218|AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ... 48 2e-11
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45 emb|AW219736|AW219736 EST302218 tomato root during/after fruit s... 52 4e-11
dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene. 46 5e-11
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50 emb|AW216968|AW216968 EST295682 tomato callus, TAMU Lycopersicon... 53 4e-09
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emb|AI966679|AI966679 sc55a11.y1 Gm-c1015 Glycine max cDNA clone... 54 3e-08
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55 gb|BE125698|BE125698 DG1_54_B08.g1_A002 Dark Grown 1 (DG1) Sorgh... 57 1e-07
emb|AF119050|AF119050 Datisca glomerata zinc-finger protein 1 (z... 56 3e-07
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60 emb|AI960244|AI960244 sc80g07.y1 Gm-c1018 Glycine max cDNA clone... 54 9e-07
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(639 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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emb Y11607 MSMP2C M.sativa mRNA for protein phosphatase 2C.	164	7e-70	
emb AJ242803 SST242803 Sporobolus stapfianus partial mRNA for pu...	154	4e-61	
emb AI055336 AI055336 coau0003L08 Cotton Boll Abscission Zone cD...	163	7e-56	
emb AI488711 AI488711 EST247050 tomato ovary, TAMU Lycopersicon ...	158	5e-46	
emb AI489841 AI489841 EST248180 tomato ovary, TAMU Lycopersicon ...	173	1e-42	
emb AW832587 AW832587 sm14b05.y1 Gm-cl027 Glycine max cDNA clone...	119	5e-40	
emb AW676724 AW676724 DG1_13_B08.g1_A002 Dark Grown 1 (DG1) Sorg...	152	2e-36	
emb AW423616 AW423616 sh69d07.y1 Gm-cl015 Glycine max cDNA clone...	110	3e-36	
emb AW278110 AW278110 sf39h03.y1 Gm-cl009 Glycine max cDNA clone...	119	2e-35	
emb AW698103 AW698103 NXNV_066_C09_F Nsf Xylem Normal wood Verti...	120	2e-33	
emb AI489730 AI489730 EST248069 tomato ovary, TAMU Lycopersicon ...	62	3e-29	
emb AV428740 AV428740 AV428740 Lotus japonicus young plants (two...	59	2e-19	
emb AF092431 AF092431 Lotus japonicus nodule-enhanced protein ph...	64	1e-18	
emb AF092432 AF092432 Lotus japonicus protein phosphatase type 2...	73	8e-18	
emb AI731667 AI731667 BNLGH10427 Six-day Cotton fiber Gossypium...	80	4e-16	
emb AW458317 AW458317 sh86c05.y1 Gm-cl016 Glycine max cDNA clone...	77	7e-16	
emb AW035781 AW035781 EST281935 tomato callus, TAMU Lycopersicon...	84	1e-15	
emb AW647646 AW647646 EST307124 tomato germinating seedlings, TA...	84	1e-15	
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emb AW776573 AW776573 EST335638 DSIL Medicago truncatula cDNA cl...	78	2e-15	
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gb H07534 H07534 cbn054 BNL2 Brassica napus cDNA 5'/3', mRNA seq...	82	5e-15	
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emb AI812394 AI812394 1H12 Pine Lambda Zap Xylem library Pinus t...	75	1e-14	
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emb AA080599 AA080599 EST054 Sugarcane leaf roll Saccharum sp. c...	74	3e-14	
emb AW328993 AW328993 N200187e rootphos(-) Medicago truncatula c...	78	8e-14	
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emb AW223860 AW223860 EST300671 tomato fruit red ripe, TAMU Lyco...	69	1e-13	
emb AW930922 AW930922 EST356765 tomato fruit mature green, TAMU ...	69	1e-13	
emb AW126261 AW126261 N100368e rootphos(-) Medicago truncatula c...	71	3e-13	
emb AW217002 AW217002 EST295716 tomato callus, TAMU Lycopersicon...	75	6e-13	
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 emb|AW934653|AW934653 EST353545 tomato flower buds 0-3 mm, Corne... 69 3e-11
 emb|AW736469|AW736469 EST332483 KV3 Medicago truncatula cDNA clo... 69 3e-11
 emb|AI052979|AI052979 Mpc9 Ice plant seedlings, RT-PCR, pCRII M... 63 3e-11
 gb|BE049699|BE049699 NXNV_142_B11_F Nsf Xylem Normal wood Vertic... 63 3e-11
 emb|AW224147|AW224147 EST300958 tomato fruit red ripe, TAMU Lyco... 69 3e-11
 10 emb|AW623772|AW623772 EST321717 tomato flower buds 3-8 mm, Corne... 68 5e-11
 emb|AW929331|AW929331 EST338119 tomato flower buds 8 mm to pre-a... 68 5e-11
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 25 emb|AI167089|AI167089 xylem.est.857 Poplar xylem Lambda ZAPII li... 48 6e-10
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 35 emb|AW739238|AW739238 gb39a01.y1 Moss EST library PPN Physcomitr... 59 3e-08
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(1551 letters)

Database: plantfungal
5 661,018 sequences; 426,114,510 total letters

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15	emb AB027616 AB027616 Pisum sativum mRNA for apyrase, partial cd...	64	2e-29
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	emb AW621504 AW621504 EST312302 tomato.root.during/after fruits.....	62	7e-25
	emb AF156780 AF156780 Lotus japonicus nod factor binding lectin....	60	2e-23
	emb AW618513 AW618513 EST320499 L. pennellii trichome, Cornell U...	67	5e-22
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25	emb AW928903 AW928903 EST337691 tomato flower buds 8 mm to pre-a...	71	7e-22
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	emb AA660474 AA660474 00360 MtRHE Medicago truncatula cDNA 5' si...	65	7e-12
	emb AI441990 AI441990 sa82g03.y1 Gm-c1004 Glycine max cDNA clone...	60	2e-11
45	emb AW696828 AW696828 NF109D12ST1F1101 Developing stem Medicago ...	57	2e-11
	gb BE059022 BE059022 sn24b03.y1 Gm-c1016 Glycine max cDNA clone ...	53	4e-11
	emb AW306606 AW306606 se53a03.y1 Gm-c1017 Glycine max cDNA clone...	56	8e-11
	emb AI490444 AI490444 EST248770 tomato ovary, TAMU Lycopersicon ...	61	2e-10
	emb AW564791 AW564791 LG1_301_H10.b1_A002 Light Grown 1 (LG1) So...	51	2e-10
50	emb AI771846 AI771846 EST252946 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AI897295 AI897295 EST266654 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AI485852 AI485852 EST244173 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AI899079 AI899079 EST268522 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AW922880 AW922880 DG1_47_F10.b1_A002 Dark Grown 1 (DG1) Sorg...	48	4e-10
55	emb AI490499 AI490499 EST249033 tomato ovary, TAMU Lycopersicon ...	61	5e-10
	emb AI488302 AI488302 EST246624 tomato ovary, TAMU Lycopersicon ...	60	1e-09
	emb AV418181 AV418181 AV418181 Lotus japonicus young plants (two...	57	2e-09
	emb AW924275 AW924275 WS1_52_E03.b1_A002 Water-stressed 1 (WS1) ...	64	3e-09
	emb AW257004 AW257004 EST305141 KV2 Medicago truncatula cDNA clo...	48	8e-09
60	emb AI771696 AI771696 EST252796 tomato ovary, TAMU Lycopersicon ...	61	3e-08
	emb AW623313 AW623313 EST321258 tomato flower buds 3-8 mm, Come...	58	2e-07

- emb|AA231755|AA231755 CDO38.R cDNA from oat Avena sativa cDNA cl... 56 7e-07
 emb|AW736308|AW736308 EST332392 KV3 Medicago truncatula cDNA clo... 54 4e-06
 emb|AW563435|AW563435 LG1_214_E12.b1_A002 Light Grown 1 (LG1) So... 38 4e-05
 emb|AB010444|AB010444 Neospora caninum mRNA for NTPase, complete... 41 1e-04
 5 emb|AL160371|LMFLCHR15 Leishmania major Friedlin assembled chrom... 44 0.004
 emb|AF203695|AF203695 Saccharomyces cerevisiae golgi nucleoside ... 43 0.005
 gb|U18778|SCE9537 Saccharomyces cerevisiae chromosome V cosmid... 43 0.005
 emb|AZ124337|AZ124337 T223080b Medicago truncatula BAC library M... 41 0.026
 emb|AW225681|AW225681 ST70C07 Pine TriplEx shoot tip library Pin... 41 0.026
 10 emb|AW774350|AW774350 EST333501 KV3 Medicago truncatula cDNA clo... 41 0.026
 emb|AI974272|AI974272 T110271e KV0 Medicago truncatula cDNA clon... 40 0.035
 emb|AL049184|PFMAL13P3 Plasmodium falciparum chromosome 13 strai... 39 0.13
 emb|AI728079|AI728079 BNLGHI9928 Six-day Cotton fiber Gossypium ... 29 0.23
 emb|X61608|BNLHCB3A B.napus gene for LHCII Type III chlorophyll ... 37 0.33
 15 emb|AW671082|AW671082 LG1_284_C02.b1_A002 Light Grown 1 (LG1) So... 37 0.33
 emb|AZ124338|AZ124338 T223081b Medicago truncatula BAC library M... 36 0.85
 emb|AF188744|AF188744 Brassica napus high-affinity ammonium tran... 35 1.2
 dbj|D37795|D37795 Ipomoea nil Tpn1 gene. 35 1.2
 dbj|E08493|E08493 gDNA encoding transposable element, Tpn1 which ... 35 1.2
 20 emb|AL356192|NCB24B19 Neurospora crassa DNA linkage group II BAC... 30 1.3
 emb|AF106939|AF106939 Phanerochaete chrysosporium 1,4-benzoquino... 29 1.4
 emb|AL163492|LMFL787 Leishmania major Friedlin chromosome 19 cos... 35 1.5
 emb|AW234282|AW234282 sf23d03.y1 Gm-c1028 Glycine max cDNA clone... 35 1.6
 emb|AL116534|CNS01D9A Botrytis cinerea strain T4 cDNA library un... 35 1.6
 25 emb|AW428880|AW428880 Ljirmp25-999-b7 Ljirnp Lambda HybriZap ... 35 1.6
 gb|N60092|N60092 TgESTzy11d09.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.2
 emb|AW056764|AW056764 ST55E11 Pine TriplEx shoot tip library Pin... 35 2.2
 gb|N81562|N81562 TgESTzy59h03.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.2
 emb|AW286610|AW286610 LG1_335_A07.g1_A002 Light Grown 1 (LG1) So... 35 2.2
 30 emb|AQ656308|AQ656308 Sheared DNA-27M14.TR Sheared DNA Trypanoso... 35 2.2
 emb|AL162692|SPBP4H10 S.pombe chromosome II P1 clone p4H10. 34 3.0
 emb|AQ652731|AQ652731 Sheared DNA-18C6.TR Sheared DNA Trypanosom... 34 3.0
 emb|AF016222|AF016222 Schizosaccharomyces pombe Rsv1p (rsv1) gen... 34 3.0
 emb|AW350237|AW350237 GM210008A10B2R Gm-r1021 Glycine max cDNA 3... 34 4.1
 35 emb|AQ943814|AQ943814 Sheared DNA-34A9.TF Sheared DNA Trypanosom... 34 4.1
 emb|AW666160|AW666160 sk32h08.y1 Gm-c1028 Glycine max cDNA clone... 34 4.1
 emb|AL109736|SPCC18B5 S.pombe chromosome III cosmid c18B5. 27 4.6
 emb|AW441608|AW441608 EST311004 tomato fruit red ripe, TAMU Lyco... 33 5.7
 emb|AL035476|PFMAL4P3 Plasmodium falciparum chromosome 4 strain ... 33 5.7
 40 emb|AW398001|AW398001 sg71a06.y1 Gm-c1007 Glycine max cDNA clone... 33 5.7
 emb|AW933585|AW933585 EST359428 tomato fruit mature green, TAMU ... 33 5.7
 emb|AI069343|AI069343 mgae0006cG03f Magnaporthe grisea Appressor... 33 5.7
 emb|X62697|NCACU3 N.crassa acu-3 gene for isocitrate lyase. 26 5.7
 emb|AI488866|AI488866 EST247205 tomato ovary, TAMU Lycopersicon ... 31 6.2
 45 emb|Z79690|ANPFA A.niger pfkA gene. 26 7.3
 emb|X13508|HVGHRDSP Barley gene for storage protein gamma-hordein. 28 7.8
 gb|M36378|BLYGIHORDA Barley gamma-1 hordein storage protein gene... 28 7.8
 emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 33 7.8
 emb|AI900865|AI900865 sb95d08.y1 Gm-c1012 Glycine max cDNA clone... 33 7.8
 50 emb|AZ124341|AZ124341 T223084b Medicago truncatula BAC library M... 33 7.8

Query= AL035679.144_at 17653_at /id_source genbank /description
 emb|cab38823.1| (al035679) putative protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 55 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi)
<http://www.ncgr.org/cgi-bin/ff/al035679>
 (1455 letters)

- 60 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E	(bits)	Value
5	Sequences producing significant alignments:			
	emb AW091895 AW091895	EST285075	tomato mixed elicitor, BTI Lycop...	306 3e-82
	emb AW040183 AW040183	EST282682	tomato mixed elicitor, BTI Lycop...	306 3e-82
	emb AW776130 AW776130	EST335195	DSIL Medicago truncatula cDNA cl...	204 2e-51
10	emb AI897609 AI897609	EST267052	tomato ovary, TAMU Lycopersicon ...	182 4e-45
	emb AI055000 AI055000	coau0002L23	Cotton Boll Abscission Zone cD...	90 1e-42
	emb AI055639 AI055639	coau0004K19	Cotton Boll Abscission Zone cD...	107 2e-22
	emb AW693198 AW693198	NF061D12ST1F1000	Developing stem Medicago ...	66 6e-10
	emb AW684256 AW684256	NF014F09NR1F1000	Nodulated root Medicago t...	43 0.007
15	emb AW667681 AW667681	GA_Ea0010D15	Gossypium arboreum 7-10 dpa ...	43 0.007
	emb AW736130 AW736130	EST332126	KV3 Medicago truncatula cDNA clo...	39 0.12
	emb AW683515 AW683515	NF015C12LF1F1097	Developing leaf Medicago ...	36 0.21
	emb AI781902 AI781902	EST262781	tomato susceptible, Cornell Lyco...	36 0.57
	gb U12141 SCU12141	Saccharomyces cerevisiae	chromosome XIV left ...	35 0.73
20	emb AW277626 AW277626	sf84e07.y1	Gm-c1019 Glycine max cDNA clone...	36 0.79
	emb Z71330 SCYNL054W	S.cerevisiae	chromosome XIV reading frame O...	35 0.80
	emb AW692595 AW692595	NF057C11ST1F1000	Developing stem Medicago ...	35 1.1
	emb X54145 ANPECT	A.niger	gene for pectinesterase.	35 1.5
	emb A35008 A35008	A.niger	PE gene.	35 1.5
25	emb A34997 A34997	A.niger	pectinesterase coding sequence.	35 1.5
	emb AQ162316 AQ162316	mgxb0012I08r	CUGI Rice Blast BAC Library P...	34 2.8
	emb AF132029 AF132029	Hortonia floribunda	chloroplast atpB-rbcL ...	34 2.8
	emb AW567917 AW567917	si67c02.y1	Gm-r1030 Glycine max cDNA clone...	34 2.8
	emb AQ951657 AQ951657	Sheared DNA-48F5	TR Sheared DNA Trypanosom...	34 2.8
30	gb U81520 CIU81520	Cichorium intybus	sucrose: sucrose 1-fructosyl...	34 3.9
	emb AZ047925 AZ047925	LMAJFV1_lm68e11.x1	Leishmania major FV1 ra...	34 3.9
	emb AI730144 AI730144	BNLGH16313	Six-day Cotton fiber Gossypium ...	34 3.9
	emb AQ942723 AQ942723	Sheared DNA-42J12	TR Sheared DNA Trypanoso...	34 3.9
	gb U05812 HMU05812	Herpetomonas muscarum	ATCC 30261 kinetoplast ...	34 3.9
35	emb AW681095 AW681095	WS1_8_B09.g1_A002	Water-stressed 1 (WS1) S...	34 3.9
	emb AL049180 PFMAL13P1	Plasmodium falciparum	chromosome 13 strai...	27 4.9
	emb AW832107 AW832107	sm30e05.y1	Gm-c1028 Glycine max cDNA clone...	33 5.3
	gb N82224 N82224	TgESTzy37d01.r1	TgRH Tachyzoite cDNA Toxoplasma...	33 5.3
	emb A94222 A94222	Sequence 5 from Patent	EP0952222.	33 5.3
40	emb AA741851 AA741851	LmLv39p3/584B	Leishmania major promastigot...	33 5.3
	emb AW728096 AW728096	GA_Ea0029O02	Gossypium arboreum 7-10 dpa ...	33 7.3
	emb AW278032 AW278032	sf89g07.y1	Gm-c1019 Glycine max cDNA clone...	33 7.3
	gb N82117 N82117	TgESTzy36b06.r1	TgRH Tachyzoite cDNA Toxoplasma...	33 7.3
	emb AL355930 NCB208	Neurospora crassa	DNA linkage group II BAC c...	32 10.0
45	emb AW688738 AW688738	NF011A11ST1F1000	Developing stem Medicago ...	32 10.0
	emb AI781529 AI781529	EST262408	tomato susceptible, Cornell Lyco...	32 10.0
	emb AI397765 AI397765	NCC5A11T7	Conidial Neurospora crassa cDNA ...	32 10.0
	emb AF127239 AF127239	Nicotiana tabacum	cultivar Burley 21 argin...	32 10.0
	emb AW180260 AW180260	MgA0351fMgA	Library Mycosphaerella gramin...	32 10.0
50	emb AF127240 AF127240	Nicotiana tabacum	cultivar Xanthi arginine...	32 10.0
	gb BE055666 BE055666	GA_Ea0009H20f	Gossypium arboreum 7-10 dpa ...	32 10.0
	gb BE036548 BE036548	MP01C02	MP Mesembryanthemum crystallinum cD...	32 10.0
	emb AW038750 AW038750	EST280611	tomato mixed elicitor, BTI Lycop...	32 10.0
	emb AL133484 LMFL236	Leishmania major	Friedlin chromosome 19 cos...	32 10.0
55	gb BE123936 BE123936	EST394061	DSIL Medicago truncatula cDNA clo...	32 10.0

Example 4

Immediate Early Transcriptional Responses Controlled by a Salicylic Acid Dependent Local Resistance Pathway

- Salicylic Acid (SA) is an important mediator of local and systemic defense responses. In *Arabidopsis*, accumulation of SA is essential for local resistance against many pathogens including *Peronospora parasitica* (*Peronospora*) isolates. Furthermore, numerous defense-related genes can be activated by SA treatment. In addition to local resistance, SA-accumulation is required for systemic acquired resistance (SAR). In the SAR pathway, SA has been shown to act upstream of *NPRI*, which is also essential for SAR. Short application of the SA analog BTH (e.g., 4 hours) to plant tissue appears to simulate local defense responses to *Peronospora parasitica*, whereas sustained SA treatment (e.g., 48 hours) elicits SAR-related plant responses (Maleck et al., 2000).
- A previous cDNA microarray study identified a cluster of roughly 30 co-regulated genes that appear to be specifically involved in resistance of the *Arabidopsis* ecotype WS against the *Peronospora* isolate Noco2 (Maleck et al., 2000). These genes are strongly activated in response to infection with Noco2 (incompatible interaction) and 4 hours after BTH treatment. However, these genes were not markedly activated during a compatible interaction with the *Peronospora* isolate Emwa1 or an incompatible interaction with *Pseudomonas syringae* (DC3000 avrRpt2) bacteria. BTH treatment for 48 hours (that simulates SAR) even strongly repressed these genes. Thus, a rapid and transient SA peak may control Noco2 triggered defense genes.
- Resistance of the *Arabidopsis* ecotype Col-0 against the *Peronospora* isolate Emoy2 appears to be regulated by a similar pathway that also is dependent on accumulation of SA. Emoy2 resistance in Col-0 is controlled by the resistance gene *RPP4*. To further explore early SA-dependent gene regulatory events and to relate these to *Peronospora*-induced resistance responses, immediate-early target genes of SA were identified using Affymetrix chip experiments with the protein biosynthesis inhibitor cycloheximide (CHX). Genes of this category likely are linked to transcriptional regulators acting closely downstream of SA. Results from these "SA-chip" experiments were combined with those from a set of chip experiments examining expression

profiles triggered in the *Arabidopsis* ecotype Col-0 by the *Peronospora* isolate Emoy2 to identify clusters of co-regulated *RPP4* controlled SA-dependent immediate early genes.

Results

5 To identify genes controlled by the *RPP4* pathway, interactions between the *Peronospora* isolate Emoy2 and Col-0 wild type plants, the defense mutants *ndr1*, *npr1* and *pad4* as well as transgenic NahG plants were examined by chip experiments. The interactions between Emoy2 and Col-0, *ndr1* or *npr1* are incompatible (plant is disease resistant), whereas the interactions involving *pad4* and NahG are compatible (plant is susceptible, i.e., disease develops). For each interaction three different time points were analyzed: 0, 12 and 48 hours post infection with 50,000 Emoy2 spores/ml. Genes that were at one or more time points more strongly expressed in Col-0, *ndr1* and *npr1* as compared to *pad4* and NahG were considered as controlled by the *RPP4* pathway. Genes represented by 271 probe sets showed at least one 2-fold expression difference in comparison between Col-0 and *pad4* or NahG and were selected for further analysis.

To identify immediate early target genes of SA, Col-0 wt seedlings were pretreated with CHX or mock treated 15 minutes before spraying with 2 mM SA or water and harvested 2 hours later (Table 28).

Table 28

<u>Plants</u>	<u>Treatment</u>
Col-0	untreated (mock)
25 Col-0	+ SA
Col-0	+ SA + CHX
Col-0	+ CHX

271 probe sets were found to be upregulated in a *RPP4* pathway-specific manner (SEQ ID NOs: 400-684). Emoy2-induced upregulation of these genes is compromised in *pad4* and *NahG* plants. These *RPP4* controlled genes were further analyzed concerning their responses to SA, CHX and SA + CHX. The 271 probe sets were subcategorized by K-means clustering over the SA/CHX data set. Nine K-means clusters comprised three subgraphs. For each of these subgraphs, the first data point represented the untreated control value, the second data point represented the response to combined SA/CHX treatment, the third

data point represented CHX treatment alone and the fourth data point represented SA treatment alone. K-means clustering defined two categories of RPP4 controlled CHX/SA-responsive genes: immediate early genes (SA-responsive, not CHX affected) and super-induced genes (additive effects of SA and CHX).

Two K-means clusters represent *RPP4*-controlled SA-induced immediate early genes (Table 29; SEQ ID NOs: 150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615 and 526). *RPP4*-controlled upregulation of these genes is SA dependent and SA induction is not compromised by CHX, which blocks or reduces protein biosynthesis. Thus, all essential regulators that mediate SA-responsiveness of these genes must be already preformed and, hence, are likely to act closely downstream of SA. This set of 15 genes includes seven potential regulator genes that may be involved in the control of secondary response genes (which require protein biosynthesis) or other late responses.

Table 29

12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase
14978_at	gb AAB64024.1 (AC002333) putative glucosyltransferase
15479_at	emb CAB39671.1 (AL049483) putative protein
15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1
16061_s_at	gb AAB97145.1 (AF000977) MEK1
16109_s_at	gb AAC05342.1 (AC002521) putative protein kinase
16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2
16603_s_at	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase
17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel
17930_s_at	emb CAA07352.1 (AJ006960) peroxidase
18966_at	gb AAC95196.1 (AC004561) putative glutathione S-transferase
20429_s_at	emb CAB10219.1 (Z97336) hypothetical protein - weak similarity to NF-kappa-B
20685_at	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein
13702_s_at	emb CAA19683.1 (AL024486) putative protein
14704_s_at	gb AAD15461.1 (AC006067) unknown protein

To further subcategorize these genes and to more precisely define a cluster of strictly co-regulated genes, the set of 15 genes was analyzed by K-means clustering over the *RPP4* data set (Emoy2 infections). This allows to use *RPP4* triggered expression timing as an additional criterion for subclustering. Normalized absolute expression levels at 0, 12 and 48 hpi in Emoy2 infected

Col-0 (w.t.), *ndr1*, *npr1*, *pad4* and *NahG* plants are displayed. Genes that share a pronounced almost linear and sustained expression increase were chosen for further analysis. These 5 genes (Table 30, which show a pronounced Emoy2-induced SA-dependent but *npr1*-independent linear expression increase and which encode potential regulators) are upregulated by the *RPP4* pathway, respond to Emoy2 recognition with a steep, sustained, almost linear expression increase. This pronounced "upregulation" is SA dependent and independent of *de novo* protein biosynthesis. Transcription factors that mediate this response must be present when SA is perceived and may act closely downstream of SA.

The mechanism that switches these genes on may involve posttranslational modifications of such preformed transcription factors.

Table 30

15	12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase
	15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1
	16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2
	17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel
20	20429_s_at	emb CAB10219.1 (Z97336) hypothetical protein - weak similarity to NF-kappa-B

To identify the potential binding sites of such key transcription factors, the promoters of these five genes were searched for conserved compact sequence motifs (Table 31; SEQ ID NOs: 757-764; SEQ ID NO:765 is a consensus sequence). Using the program "AlignACE", a strikingly conserved motif was found that is present in all five promoters. This motif resembles the described consensus binding site of WRKY transcription factors, W box. However, the W box core motif, TGAC, is followed by an "A". The permutation TGACA has never been associated with WRKY binding. In addition to this, four more positions are highly conserved. This motif may be the specific binding site of an unconventional WRKY transcription factor or a factor of a novel so far unknown type. Yeast one hybrid screens can reveal the identity of this factor.

Table 31

	W box-like Motif		
35	MAP Score: 4.4		
	ACAGTGACA 0 391 1	(12345)	SEQ ID NO:757
	ACAGTGACA 1 236 1	(16140)	SEQ ID NO:758

	ACAGTGACA 1 317 1	(16140)	SEQ ID NO:759
	ACAGTGACA 2 281 1	(15616)	SEQ ID NO:760
	ACAGTAACA 3 84 1	(17498)	SEQ ID NO:761
	AAAGTAACA 3 1557 0	(17498)	SEQ ID NO:762
5	AAAGTGACA 4 1840 0	(20429)	SEQ ID NO:763
	AAAGTGACA 4 2131 0	(20429)	SEQ ID NO:764

ACAGTGACA	SEQ ID NO:765
-----------	---------------

A

10	Expt. Frequency:	0.02/1kb
	Obs. in SOMc7:	0.06/1kb
	Obs. in this cluster:	0.50/1kb

15 One K-means cluster of the 271 RPP4 controlled probe sets represents RPP4-controlled SA/CHX super-induced genes (Table 32; SEQ ID NOs: 214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551). RPP4-controlled upregulation of these genes is SA-dependent; these genes are weakly inducible upon both SA and CHX treatment alone. The response to

20 combined treatment with SA and CHX is stronger than the response to either single treatment. Induction of genes in response to CHX alone has been described before and has been attributed to hypothetical proteins that are rapidly turned over and either repress transcription of the respective gene or control degradation of the respective mRNA. Block of synthesis of such hypothetical

25 proteins may lead to increased mRNA levels by either increased transcription or reduced mRNA degradation. Like the set of immediate early SA responsive genes shown before, genes of this set also appear not to require *de novo* protein biosynthesis for their response to SA. In contrast to the previous gene set, however, the observed CHX-induced up-regulation may point to a de-repression

30 mechanism.

Table 32

	12505_s_at	gb AAC63643.1 (AC005309) putative CONSTANS-like B-box zinc finger protein
35	13656_at	gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function
	14116_at	gb AAC26243.1 (AF077407) contains similarity to sugar transporters
	14170_at	gb AAF29406.1 AC022354_5 (AC022354) unknown protein
40	14223_at	emb CAA19683.1 (AL024486) putative protein

- 14248_at gb|AAD31062.1|AC007357_11 (AC007357) Strong similarity to
gb|X97864 cytochrome P450
- 14608_at gb|AAD31074.1|AC007357_23 (AC007357) Similar to
gb|AF038007 FIC1, member of the PF|00122 E1-E2 ATPase
family.
- 5 14614_at gb|AAC16958.1| (AC004165) putative glucosyltransferase
15646_s_at gb|AAC37474.1| (L42212) serine acetyltransferase
16054_s_at emb|CAA74639.1| (Y14251) glutathione S-transferase
16105_s_at gb|AAC31756.1| (U68017) heat shock transcription factor 4
- 10 16968_at emb|CAA17559.1| (AL021961) glucosyltransferase -like protein
18235_at gb|AAB61480.1| (AC000348) T7N9.4
18567_at gb|AAC34217.1| (AC004411) putative alcohol dehydrogenase
18591_at emb|CAA52772.1| (X74756) ATAF2
19845_g_at emb|CAB37510.1| (AL035540) monooxygenase 2 (MO2)
- 15 20017_at gb|AAC16079.1| (AC004521) unknown protein

To further subcategorize these genes based on *RPP4* triggered expression timing, the set of 17 SA/CHX super induced genes was K-means clustered over the *RPP4* (Emoy2) data set (Table 33; SEQ ID NOs: 214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551). A group of five

20 genes was identified that consistently respond quickly ("fast", within 12 hpi) and that have elevated expression ground states in the *npr1* mutant. The fast response is SA dependent (is abolished or attenuated in *pad4* and *NahG*). The elevated expression ground states in *npr1* together with the observed CHX inducibility may point to an *NPR1*-dependent repression mechanism. Since

25 *NPR1* has been shown previously to act closely at the level of transcriptional regulation, a *NPR1* dependent repressor may shut expression of these genes down. Upon CHX treatment this hypothetical repressor is not synthesized anymore and expression of these genes is elevated. This repressor may also participate in *RPP4* triggered activation of these genes and allow Emoy2-

30 induced de-repression.

Table 33

- 18591_at emb|CAA52772.1| (X74756) ATAF2
- 14248_at gb|AAD31062.1|AC007357_11 (AC007357) Strong similarity to
gb|X97864 cytochrome P450
- 35 14614_at gb|AAC16958.1| (AC004165) putative glucosyltransferase
15646_s_at gb|AAC37474.1| (L42212) serine acetyltransferase
16105_s_at gb|AAC31756.1| (U68017) heat shock transcription factor 4

To identify binding sites of activating or repressing factors responsible for the co-regulation of this small cluster, the promoters of these genes were searched for conserved compact motifs with "AlignACE" (Table 34; SEQ ID NOs: 766-772, SEQ ID NO:773 is a consensus sequence). One strictly conserved octameric motif was found, which, however, is absent in one of the promoters. Yeast one hybrid screens can identify factors binding to this motif.

Table 34

Motif 15		
10	MAP Score: 1.23758	
	AATCGAAT 0 40 0	(18591) SEQ ID NO:766
	AATCGAAT 0 1741 1	(18591) SEQ ID NO:767
	AATCGAAT 1 386 1	(PAD3, 14248) SEQ ID NO:768
	AATCGAAT 2 334 1	(14614) SEQ ID NO:769
15	AATCGAAT 2 660 1	(14614) SEQ ID NO:770
	AATCGAAT 2 2105 1	(14614) SEQ ID NO:771
	AATCGAAT 3 1570 1	(15646) SEQ ID NO:772

	AATCGAAT	SEQ ID NO:773
20	expt.: 0.08/kb	
	obs.: 0.70/kb	
	SOMc7: 0.06/kb	
	Random20: 0.00/kb	
25	SOMc3: 0.10/kb	
	SOMc1: 0.10/kb	

As described hereinbelow, sets of genes specifically controlled by the *RPP7* and *RPP8* pathways were defined. Similarly a set of *RPP4* pathway controlled genes was defined (see Figure 4). Figure 4 shows a "Venn diagram" including only the transcription factor genes of these *RPP4*, *RPP7* and *RPP8* controlled genes. Three transcription factor genes were found to be specifically upregulated by each of the three *Peronospora* defense pathways: AtERF1, HSF4, ATAF2. Furthermore, ERF transcription factors appear to play an important role in controlling defense responses directed against *Peronospora* in general. Table 35 gives four potential target genes of ERF transcription factors. These genes contain ERF binding motifs in their promoters.

Table 35

40 Genes with potential ERF binding sites (GCCGCC or GCCGAC):

thioredoxin (13189) RPP7/RPP8 and (weakly) RPP4 controlled
 C2H2 zinc finger (15665) RPP7/RPP4 and (weakly) RPP8 controlled
 SigA binding protein (14148) RPP7/RPP4 controlled
 HSP70 (13284) RPP7/RPP8 controlled

5

These genes are specifically controlled by at least two different *Peronospora* defense pathways and show an almost linear increase of transcript levels during incompatible Hiks1 interactions (K-means clusters 3+5).

6 potential ERF binding sites in K-means cluster 3+5: 0.5 motifs /

10 1kb Expected: 0.1 motif / 1kb; Enrichment in K-means cluster 3+5: 5-fold

SEQ ID NO:789

MPTSATAVAPSTGSGVQKKDQDWRAILSPEQFRVLREKGTENRGKGEYT
 KLFDDGIYSCAGCATPLYKSTTKFDSGCGWPSFFDAIPGAIKQTD MFSGN
 15 AADGSIVTSGLDYILISINEKLKAYT

SEQ ID NO:790

1 tgcattcttt tgaggggttt aattttctgc atagctttgt ctaatctctt agagctcaat
 61 aagagaagat ggatgttcca cgccagctt tcaaatgttt tgatgacgat ggccggctta
 20 121 aacgttcagg gacggttgg accgcgagtgc cgcataatcat aaccgccgtg attggatctg
 181 gtgttctatc gcttgcgtgg gctataggtc aactcgggtg gatcgaggt cctacagtga
 241 tgttgtgttt ctctttgtc acttactact ctccacgct tcttagcgac tgctacagaa
 301 ccggagatcc tgtctctggg aagagaaact atacttcat ggacgctgc cgatcaatcc
 361 taggtggctt taggttcaag atttgtgggc tgattcagta ttgaatctg ttgggtatca
 25 421 cggtcgggta cacaatcgca gcatctataa gtatgatggc gatcaagagg tccaactgtt
 481 tccacgagag cggagggaaa aaccggtgc acatgtcgag caatccatac atgatcatgt
 541 ttgtgtgac cgagatcttg ctctctcaga tcaaagattt tgaccagatt tgggtggctt
 601 ccattgtgcg tgctatcatg tcttccatct actctgcaat cggtttagct ctcggaatca
 661 tcaagtgcg ggcaaatgga gttgtcaagg gaagtctcac cggaattagc atcgccgcag
 30 721 tgactcagac ccaaaaaata tggagaacct ttcaagcact tggagacatt gcctttgctt
 781 attcatactc tgttgttctt attgaaattc aggacactgt aagatctcca ccagcagaat
 841 caaaaacgat gaagatcgcc acaagaatca gcatcgctgt tacaacgaca ttttcatgc
 901 tatgtggttg tatgggctat gcggccttcg gagataaagc accgggaaac ctcttaaccg
 961 gttttggttt ctacaatccg tttggctcc ttgacgtggc taacgctgcc atagtatcc
 35 1021 acctgtagg agcttatcaa gtctttgctc agcccatctt cgcctttatt gagaacaac
 1081 tggccgctag gttcccgac agtgacttgg tgaccaagga atacgaaac cgaatccctg
 1141 gttttaggtc accgtacaaa gtcaacgttt tcagagcagt ttaccgaagc gggtttggtg
 1201 ttttgaccac tgtgatatcc atgcttatgc cgttttcaa cgacgtcgta gggattttag
 1261 gtgcgttagg gttttggcct ttgacgggtt actttccggt ggagatgtat ataagacaga
 40 1321 ggaaggttga gagatggagt atgaagtggg ttgtctgca gatgttgagc tgtggttgtt
 1381 tgatgatcac gttgtgcgcc ggagttggct ccatcgccgg agtaatgcta gaccttaagg
 1441 tttacaagcc gtcaagact acttactaaa caaacatga tgatagatga agaagaagaa
 1501 ggiggtggag aaaaaaaca aaagatataa attttaatga tgattttcat tggggaaatg
 1561 tgaataatgt aaaagtctt cgtttcgtat aattttatc ttgcgtaatt tatatacat

45

SEQ ID NO:791

MVKNLKVDP LAKVTASTTSMV KILSSLFITDDSYVLVSAKENKNQSEAE
 PSYYETLETYQGLPCPYGGYYGYYPGLDGSVGEAKDNGYYGYGTEVQ
 YPVMQGENGSVIYLM PGFQSYDASQTYMPINPVGVSSQALHSPMYAAQ
 GYYQNQFGYADVSSPTYLWDPVGD RYVYGVASYTPPLKQNISSSSHNH
 5 NNYYSKSKNSFTGHGMGDRPKTPRKASQNSYAPPPLLNQEKGR IAYPM
 DPVKKKSGALNRDETEKAKARTKENGTS MNDLANGQDHITNGECESCS
 LDAEGNERSNGVGSVIRRDQYNLPSFQTKYEEAIFV IKSYSSEDDIHKSIK
 YNVWSSTLNGNKKLDSA YQESQKKAADKSGKCPVFLFFSVNASGQFCG
 VAEMIGRVDYEKSMEFWQQDKWTGYFPVKWHI IKDVPNPQLRHILEN
 10 NENKPVTNSRDTQEVRLPQGNEVLNIFKNYAAKTSILDDDFDYENREKV
 MVQKKLRFPFVLKKKEEDLVADFKT MEMSNTVEEGNTELTGTVS

SEQ ID NO:792

1 cgatcacgga tctggcttgg ttcatacaaa accgccgttg ccgcggcacg ggcctacgat
 15 61 accgctgtgt ttacttacg tggctcttcg gcgagactca attccctga agaggtcttt
 121 aaggatggaa acggcgggtga aggccttagga ggagatatgt ctccgacgtt gatacggaag
 181 aaggcggctg aggtgggagc tagagtcgac gcagagttgc ggtagagaa taggatgggt
 241 gagaacttag acatgaataa gttgccggag gcatatggat tgaatttat agtttgtag
 301 ttataggtt ggagattgcc cggagacaga gtcaaacaga gttctctga ctcatatgag
 20 361 gcataatata gttaatatag taattttgt ttgagcata gtaattatgt cataacc

SEQ ID NO:793

1 gggcaatgat taticgttcg ccggaaccag aagcaaaat ttggtagat agggatccca
 61 taaaaacttc tticgaggaa tgggctaaac ccggtcattt ctcaagaaca atagctaagg
 25 121 gacctgatac taccacttgg atctggaacc tacatgctga tgctcacgat ttgatagtc
 181 ataccagtga ttggaggaa atctctcga aagtatttag tggccatttc ggccaactct
 241 ctatcatctt tcttggctg agtggcatgt attccatgg tgctcgttt tccaattatg
 301 aagcatggct gactgacact actcacattg gacctagtgc tcagggtggt tggccaatag
 361 tgggccaaga aatcctgaat ggagtagtgg gcggaggcct ccgaggaata caaataacct
 30 421 caggctttt tcagatttgg cgagcatccg gaataactag tgaattacaa ctttattgta
 481 ccgcaattgg cgcattggtc ttcgcagcct taatgcttt tgctggttgg ttccattatc
 541 acaaagcagc tccaaaattg gcttgggtcc aagatgtaga atctatgttg aatcaccatt
 601 tagcagggct actaggactt gggcccttt cttgggcagg acatcaagta catgtatctt
 661 atccgattaa ccaatttcta aacgtggag tagatcctaa agaaataccg ctctctcatg
 35 721 aatttatctt gaatcgggat ctttggctc aactttatcc aagttttgct gaaggagcaa
 781 ctccctttt taccttaaat tggtaaaaat actcggaatt tcttacttt cgtggcggat
 841 tagatccagt gactgggggt ctatggttaa ccgatatagc acatcatcat ttacgtatcg
 901 caattctttt tctaatacgc ggtcatatgt ataggacaa ctgggggtatt ggtcatgta
 961 taaaagatat tttagaggct cataaaggct catttacagg ccaaggccat aaaggcctat
 40 1021 atgaaattct aacaacatca ttgcc

SEQ ID NO:794

MEGSSSSSSSLISKSDAELEEM LDRMLTRLALCDDSKLES LVSNNLPLTISS
 LSSQSPVVRNKAMCVDFIFQVLEILSHV NKR VKHQHEIGLPLLALWKLY
 45 TDPA AAPMVRNFAIVYVEMAFERAPAKVIGECHASKISDDVSAKYRSLIT
 SQDKDLFLDFCLHMLLYQPSSQGGGSSPGLSVFQVNR IIGKQALKGDTLT
 RRKLPSNTFLTKNYHFLKINQFLKQLGILNVIGNMDLPGESVYPLYIAAS
 VDRVGM DLLVKIHSSQEPVAKRGEELLKKIASGTNLDDPKLINRFLFLFN
 GTTG TENVAPEHNVAPGNISLKMKLMSGFCRSIAAANSFPATLQCIFGC
 50 MYDILFLNLTFREKTEMAVRLFDALKLETQSLRSTIQEAIVSLAAAYKD

SPENILRDLEVLLANSLAEQNEARFCALRWATSLYNSSHCHPSLYICMLS
 AADPKLDIREIALEGLFLKEEGRSIVSNHDKYPKFIEMLEYILKQQPKLL
 DSSEMRSQKLLFPSQVYLVMIKFLVKCFELEMESNTQAVGTEFLDSAQ
 KMCSLLEHSLAFEGSAELHACASKALVSVGSYLPPEMVELYFSRKIVWLR
 5 SLLSHTDLSTRESVSRLLGMASCALSDAESCSLLSELISSISQPQKLRFEAQ
 HGGLCAVGFVSAHCLHRIPTVSKAVTQNAV KYLVEVVNLETAPLASVA
 MEALGHIGICGALPFLVNDSSPGTQVLEILQERLSKLLSGDDIKSVQKIAL
 SLGHICSNETSSSHLKIALDLLFSLRSKAEIILFAAGEALSFLWGGVPVT
 ADMILKTNYSLSLTDSDNFMKEVKSLSVDVKTDEEDSRTTTTRETITGKLF
 10 DTLTYSSRKEERCAGTVWMLSLTMYCGQQPSIQLMLPKIQEAFSHLLGD
 QNELTQELASQGMSIHYELGDASMKKSLVDALVNTLTGTSKRKRAIKLV
 EESEVFQEGTIGESPSGGKISTYKELCNLANEMGQPDLIYKFMDLANHQA
 SLNSKRGAAFGFSKIAKQAGDALRPHLRLLIPRLIRYQYDPDKNVQDAM
 AHIWKALIQDPKKA VDEHLNHIFDDL VQCGSRLWRSREASCLALADIQ
 15 GRKFDQVKEHLKKLWIAAFRAMDDIKETVRNAGDKLCRAVTSLTIRICD
 VTLTELADAKQAMDIVLPFLSEGIMSKVNSVRKASIGVVMKLAKFYSK
 HEINQFELLASFELNVLLGNIYDPLSDFVLFVTVLCRLHAANIGIETEKLE
 NLRISISKGSPMWETDLDCINIVDIESLEQLIPRLTQLVRGGVGLNTRVGV
 ASFISLLVQKVGSEIKPFTGMLLRLLFPVAKEEKSSAAKRAFSSACGIVLK
 20 YSSPSQAQSLIETAALHSGDRSSQIACASLFKSFSSTAADIMSSHQSAIVP
 AIFISRFEDKQISSLFEEVWEDITSGERVTLQLFLQEIYNHICESITSSSRFK
 LSFSLGKDALLDALGALSVACHEAITKEDPTTPTTILSLICSACKKKLKKY
 RESAFSCLEKVIAFGDPKFFHAVFPMLYEMCNTASIKTNTQVQAASDAV
 KTESENGEDGHVPLEKIMECVKSCIQVATIDDILSAKADLIHVLIISLSPGF
 25 LWTVKMSGISCVGKLCRSRFP SLWTDSDMDDLSPSDATKVFHELHSLVPK
 LLECIHTVKIAQFHVAASQC LLELIELYSTISSLHPVEVDFKA EVVSLLELE
 KSEEAKSLLRKS RDALANLPSLN

SEQ ID NO:795

30 MDKETEILSRLAANHLHLAQFEPLKATLLALRVNRPDLALTILQTIVSNA
 GRFDNVLWSRSCPSPLLSFLSTIELLRFENPTSPWGFDSSETLSLRADFLI
 MVQVLIDRVTERIKEDEESEDENSGLGNCRLRVLQGVLELGVERLKFVVD
 TSSSEGSNKIEEDAVVSLRSIVLDYSDVFDALCCNIQRQLAGCESYGTCL
 VEEVQGEEQRKEMNEATCIGSPELDNINVFALIQRNVQLAQLDAMKTKL
 35 DEGDERGAADRIRYLHLDYGVKENYHAYLKAALLSRVMEKKDEYGDS
 WHMVRQNLLFMYKEALSSNCGDLVQMIQGIQDDMLLPHSQLHLSLDNE
 QIPLPLECFRRYLVDLKTERNIEDKSSPMSRAINSCLRDMYHYARISGSHV
 LECVMCAALSSVKKEKLQEANDVLTLPRLRPLVASMGWDLLPGKTAT
 RRKLMRLLWTSDSQALRLEESSLYGNQTDLELASFAACVNSGKSWTP
 40 KASFLMHGNVSSAHDDAEVDPFVENLVLERLSAQSPRLRVLFDVVPGIKF
 QDAISLISMQPIASTAEAWKRIEDIELMHMRYALEAIVLALGAMEEAMK
 DETDASHRVVFYHLKDLTNHLEAIKNVPRKIMMVNIVISLLHIDDIRLSST
 QSASSACFSEKSNTPLDPLGTEGEKEIVISFTKQLLDVLRRLNLPSPHPIE
 QECQLDGNYSTDGRQALEWRVSMAKRFIEDCEWRLSVMQHLLPLSERQ
 45 WGLKEVLSILRAAPEKLLNLCMQRAKYDIGEEAVNRFALSAEDKATLEL
 AEWVDNAFKGTLVEDVMSRTAEGAAAVQDLDFHSLGSQLSPLAMVLLF
 AQSQVMLSEIYPGGAPKVGFTYWDQVHEVAIISVLRRLKRLQEFLEQDD
 PQILQASFGDTIISCTESHRRQGQKDRALAMLHQMIEDAHRGKRQFLSG
 KLHNLARALADEKPEVDVLKGDGSDMAVEKDGVGLGLKYTKQSPGS
 50 ANRAVDGNPVSHETEDKGKKSFGPLSNKTSTYLSQFILYTAAGDIVDGT

DTTHDFNFFSLVYEWPKDLLTRLVFDRSSTDAAAKVAEVMSADVFHEVI
 SACVPPVYPPRSGHWACIPVIPTTPCSHSEGKVLSPSIEAKPNCYVRSSA
 TPGVPLYPLQLDVIRHLVKISPVRVLACVFGGSILYNGSDSISSSLNDEF
 PSSPDADRLFYEFLDQSERYP TNLNRWIQM QTNLHRVSEFV VTPKQKPD
 5 DTRIKPDERTGIKRLL EHDSDSES DTEETFSKNNIQPALTDGSARDGGSFE
 NGVCRTDPTVFLSFDWENEVPYEKAVNRLIDEGKLM DALALSDRFLRN
 GASDWLLQLLIKSREENPSTSGRSQGYGGQSNWSWQYCLRLKDKQLAAT
 LALKCCIGDKLCRSTATYFRQMIAIAGKRLSFFLLFEIMFGSWYARCVTL
 10 KNLNGKQVEAECKEDPEGLALRLAGKGAVSAALEVAESAGLSIDLRLREL
 QGRQLVKLLTTDPLNGGGPAEASRFLSSLQDSADALPVVMGAMQLLPD
 LRSKQLLILKEFPALRDNNVIMAYAAKAISVTIIPPPREPRITVSASRLRQK
 SRAGPAVKASFTSSLSNFQREARRAFSWAPRNAENRTTSKD VYRKRNKS
 GLGASERAAWEAMTGIQEDQGSSYSADGQDRLPSVSIAEEWMLTGDKT
 KDEGVRASHKYESTPDILFKALLSLCSDDELVSARSAMDLCISQMKNVLS
 15 SKQLSEGASVETIGRAYHATEAFVQGLSYAKSLLRKLLGTTESTNNNGE
 RSRDVDDISSDAGSSSVGSQSTDEPSDVL SLTEIWLGRAELLQSLGSGIS
 TSLDDIADQLSSECLRDRLISDERYSMAVYMCKKCKIDVFPVWKA WGL
 ALLRMERYAQARVKFKQAFQLKGEDIPDVIQEIINTIEGGPPVDVSIVRS
 MYDHLAKSAPTILDDSLSADSYLNVLHMPSTFPRSESRRSLESEKNSSV
 20 PGSDFEDGPRSNLDTTRYSECTNYLQEHARQNLLGFMFRHGHFKDACM
 LFFPQSGLPPLQTSSVGAVSTSSSPQRTDPLATEYGTIESLCEFCVGYGAI
 SSLEEVITERLESAKNQDQAINQYIAGALTRICAFFEINRHFNYLYKFLVL
 KKDYVTSGYCCIQLFMNSTTQEDAVRHLEHAKKYWSLTILGVQAHFEE
 ALTARHRGSDSKLVTKGVRGKSAAEKLSEETLVKLSSRVKMQIDVVK
 25 SFSDSEGAPWKHSLFGNPNDSETSRRRCEIVETLVEKNFDLAYSVIYEFK
 LSAVDIYAGVATSLADRKKGSQ LTEL FKNIKGTIQDDDWDQVLNIADTG
 KARSVWLIFCEMLQVLGAAINIYANKHKERPDR LIDMLTSSHRKVLACV
 VCGRLKSAFQIASKSGSVADVQYVAHQALHANSHTVLD MCKQWLAKY
 30 M

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- 30 All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the

details described herein may be varied considerably without departing from the basic principles of the invention.

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 or the complement of the open reading frame, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
2. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which is substantially similar to an *Arabidopsis* nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
3. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
4. The isolated polynucleotide of claim 1, 2, or 3 which is DNA.
5. The isolated polynucleotide of claim 1, 2, or 3 which is RNA.
6. The isolated polynucleotide of claim 1 wherein the nucleotide sequence encodes a polypeptide having at least 90% amino acid sequence identity to the *Arabidopsis* polypeptide encoded by the open reading frame.
7. The isolated polynucleotide of claim 1 wherein the nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.

8. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a dicot.
9. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a monocot.
10. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a cereal plant.
11. An isolated polypeptide encoded by the polynucleotide of claim 1, 2, or 3.
12. An expression cassette comprising the polynucleotide of claim 1, 2, or 3 operably linked to suitable regulatory sequences.
13. The expression cassette of claim 12 wherein the polynucleotide is linked to a promoter for expression in a plant.
14. A recombinant vector comprising the polynucleotide of claim 1, 2, or 3.
15. A host cell comprising the expression cassette of claim 12.
16. A host cell comprising the polynucleotide of claim 1, 2, or 3.
17. The host cell of claim 15 or 16 which is selected from the group consisting of yeast, bacteria and plant.
18. A transformed plant, the genome of which is augmented with the polynucleotide of claim 1, 2, or 3 or a polynucleotide which comprises one of SEQ ID NOs: 1-684 and 789-795 which is expressed in an amount which confers resistance or tolerance to the plant to pathogen infection.

19. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene corresponding to the polynucleotide of claim 1, 2, or 3 or a gene corresponding to one of SEQ ID NOs: 1-684 and 789-795.
20. The plant of claim 19 which is altered by T-DNA insertion, transposon insertion, or targeted DNA insertion.
21. The plant of claim 19 in which expression is inhibited by transcription or post-transcriptional mechanisms.
22. The plant of claim 18 or 19 which is a monocot.
23. The plant of claim 18 or 19 which is a dicot.
24. The plant of claim 18 or 19 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
25. A method of expressing a polynucleotide in a cell, comprising:
introducing the polynucleotide of claim 1, 2, or 3 into a cell so as to express the open reading frame.
26. The method of claim 25 wherein the cell is a plant cell.
27. The method of claim 25 wherein the cell is a monocot cell.
28. The method of claim 25 wherein the cell is a dicot cell.
29. A composition comprising the polynucleotide of claim 1, 2, or 3 or comprising the polypeptide of claim 11.

30. A method to identify an open reading frame in the genome of a plant cell, the expression of which is altered by oomycete infection of the cell, comprising:
- a) contacting a plurality of isolated nucleic acid samples on a solid substrate with a probe comprising plant nucleic acid corresponding to RNA isolated from plant cells infected with an oomycete, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
 - b) comparing complex formation in a) to complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising plant nucleic acid corresponding to RNA from uninfected plant cells or from mutant plant cells which have a response to pathogen infection that is different than the plant cells in a), so as to identify which samples corresponding to genes having an open reading frame, the expression of which is altered in response to oomycete infection, wherein the genes comprise orthologs of *Arabidopsis* genes comprising one of SEQ ID NOs: 1-684 and 789-795.
31. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is induced in response to infection.
32. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is decreased in response to infection.
33. The method of claim 30 wherein the probe comprises nucleic acid from a dicot.
34. The method of claim 30 wherein the probe comprises nucleic acid from a monocot.

35. An isolated polynucleotide comprising an open reading frame of a gene identified by the method of claim 30.
36. A method to confer resistance or tolerance to a plant to a pathogen, comprising:
 - a) contacting plant cells with an expression cassette comprising a polynucleotide encoding a polypeptide that is substantially similar to a polypeptide encoded by a nucleic acid sequence comprising an open reading frame comprising one of SEQ ID NOs: 1-684 and 789-795 so as to yield transformed plant cells; and
 - b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the polynucleotide in the cells of the plant in an amount effective to confer resistance or tolerance to the plant to the pathogen relative to a corresponding plant which does not comprise the expression cassette.
37. The method of claim 36 wherein the polynucleotide hybridizes under moderate hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
38. The method of claim 36 wherein the polynucleotide hybridizes under stringent hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
39. A transformed plant prepared by the method of claim 36.
40. A seed of the plant of claim 39.
41. A progeny plant of the plant of claim 39.
42. A method for identifying a plant cell infected with a pathogen, comprising:

- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence substantially similar to one or more of SEQ ID NOs:1-184, 301-494 or 500-803, or a portion thereof so as to yield an amplified product; and
 - b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the product is indicative of pathogen infection.
43. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence is from a gene encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising at least one of SEQ ID NOs: 685-788.
44. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, which nucleotide sequence hybridizes under high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788 or which nucleotide sequence hybridizes under very high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788.
45. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, wherein the plant nucleotide sequence comprises SEQ ID NO: 710, SEQ ID NO: 711, SEQ ID NO: 714, SEQ ID NO: 715, SEQ ID NO: 764 or SEQ ID NO: 773.
46. The isolated polynucleotide of claim 43, 44, 45 or 46 wherein the nucleotide sequence which directs transcription is 25 to 2000 nucleotides in length.

47. A recombinant vector comprising the polynucleotide of claim 43, 44, 45 or 46.
48. The vector of claim 47 which is a plasmid.
49. An expression cassette comprising the polynucleotide of claim 43, 44, 45 or 46 operatively linked to an open reading frame.
50. The expression cassette of claim 49 operably linked to other suitable regulatory sequences.
51. A host cell comprising the expression cassette of claim 49.
52. A transformed plant, the genome of which is augmented with the expression cassette of claim 49.
53. A plant cell containing the expression cassette of claim 49.
54. A transformed plant comprising transformed plant cells, the transformed plant cells containing the expression cassette of claim 49.
55. The transformed plant of claim 54 wherein the plant is a dicot.
56. The cell of claim 53 which is a dicot cell.
57. The transformed plant of claim 54 wherein the plant is a monocot.
58. The cell of claim 53 which is a monocot cell.
59. The transformed plant of claim 54 which is a cereal plant.
60. A method of augmenting a plant genome, comprising:
 - a) contacting plant cells with the expression cassette of claim 49 so as to yield transformed plant cells; and

- b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.
61. A transformed plant prepared by the method of claim 60.
62. A seed of the plant of claim 61.
63. A progeny plant of the plant of claim 61.
64. A method of using a plant promoter, comprising: introducing the expression cassette of claim 49 to a plant cell and detecting the expression of the product of the open reading frame.
65. A recombinant vector comprising the expression cassette of claim 49.
66. A plant cell comprising the vector of claim 65.
67. A transformed plant, the cells of which comprise the vector of claim 65.
68. The plant of claim 52, 54, 61 or 67 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
69. The expression cassette of claim 49 wherein the open reading frame is in an antisense orientation.
70. The expression cassette of claim 49 wherein the open reading frame is in a sense orientation.
71. A transformed plant, the genome of which is augmented with a polynucleotide which is substantially similar to any one of SEQ ID NOs:

1-684 and 789-795 and which is expressed in an amount which inhibits or prevents pathogen infection.

72. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene comprising a polynucleotide substantially similar to any one of SEQ ID NOs: 1-684 and 789-795.
73. The plant of claim 71 or 72 wherein the polynucleotide is substantially similar to SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 32, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 792, SEQ ID NO: 57, SEQ ID NO: 68, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 102, SEQ ID NO: 111, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 682, SEQ ID NO: 129, SEQ ID NO: 137, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 157, SEQ ID NO: 161, SEQ ID NO: 165, SEQ ID NO: 170, SEQ ID NO: 174, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 184, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 197, SEQ ID NO: 208 or SEQ ID NO: 211.
74. The method of claim 36 wherein the polynucleotide is substantially similar to SEQ ID NO: 308, SEQ ID NO: 300, SEQ ID NO: 272, SEQ ID NO: 362, SEQ ID NO: 265, SEQ ID NO: 241, SEQ ID NO: 261, SEQ ID NO: 380, SEQ ID NO: 228, SEQ ID NO: 658, SEQ ID NO: 243, SEQ ID NO: 254, SEQ ID NO: 216, SEQ ID NO: 225, or one of SEQ ID NOs: 400-684.
75. The expression cassette of claim 12 wherein the polynucleotide is in antisense orientation.
76. The expression cassette of claim 12 wherein the polynucleotide is in sense orientation.

77. A method for identifying a plant cell infected with a pathogen, comprising:
- a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by an open reading comprising sequences selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 so as to form a complex; and
 - b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.
78. A method for identifying a plant cell infected with a pathogen, comprising:
- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with a probe comprising at least a portion of a polynucleotide that is substantially similar to any one of SEQ ID NOs: 1-684 and 789-795 under conditions effective to form a specific complex between the probe and the nucleic acid; and
 - b) detecting and determining the presence or amount of complex formation wherein the presence or amount of complex formation is indicative of pathogen infection.
79. A computer-readable medium having stored thereon a data structure comprising:
- a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a nucleotide molecule selected from the group consisting of SEQ ID NOs: 1-791 or the complement thereof; and
 - b) a module receiving the nucleic acid molecule which compares the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

80. The computer readable medium of claim 79 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
81. A computer-readable medium having stored thereon computer executable instructions for performing a method comprising:
- a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-791 or the complement thereof; and
 - b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.
82. The computer readable medium of claim 81 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
83. The method of claim 42, 60, 77 or 78 wherein the cells are dicot cells.
84. The method of claim 42, 60, 77 or 78 wherein the cells are monocot cells.
85. The method of claim 42, 60, 77 or 78 wherein the cells are maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat cells.

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RPP-DEPENDENT DEFENSE PATHWAYS

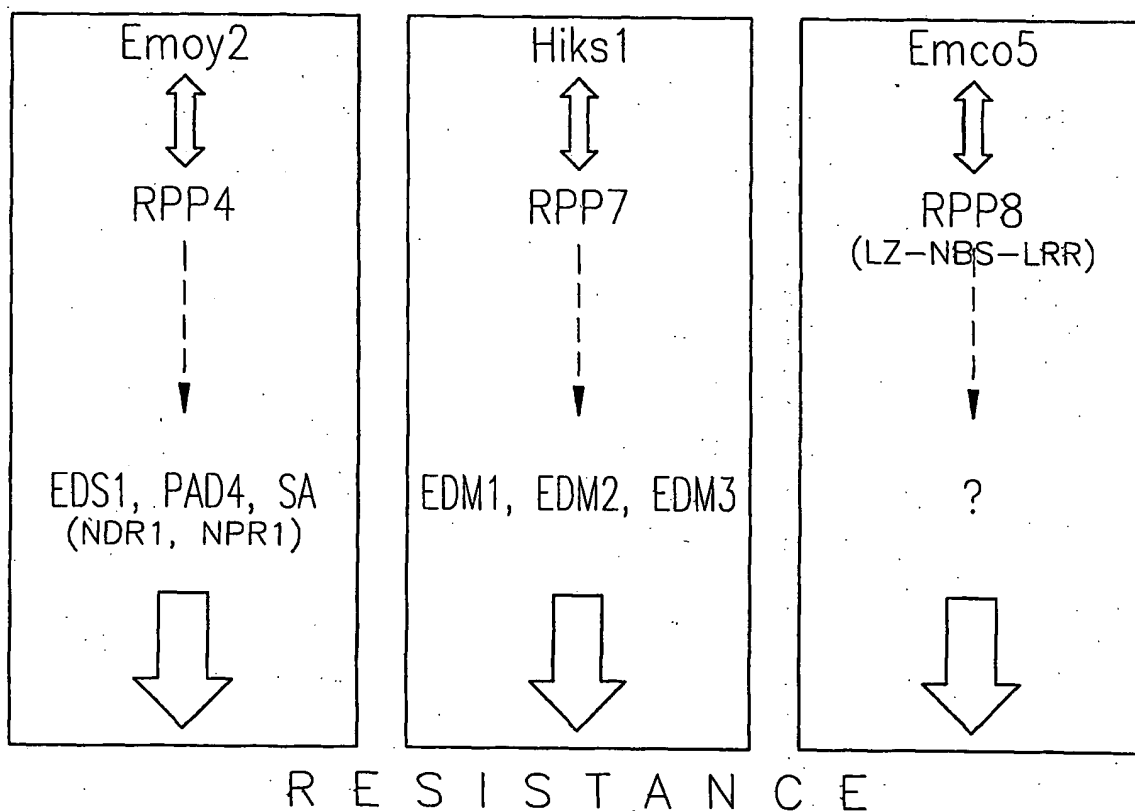


FIG. 1

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motifs:

Motif 1/ MAP Score: 6.87857

CAACAATGAC

TT TT

Motif 2 MAP Score: 2.22382

GATGGGNCNAA

TT A

C

Known stress-responsive cis-elements:

ttgacc, ttgact, ggtcaa and agtcaa W box

ttgaca and tgtcaa W box-like

tgacg and cgtca TGA-bZIP binding site

acgt bZIP binding site core

cacgtg G Box

gccgcc and ggccgc GCC box

| Subcluster A
17014 ribonuclease RNS1SEQ ID NO:
774

tagaattgaaaaagggtaatgtgaaaagggattctcaacaattattcaagataaaaat
 tgtataggtgttaataataatgtgtaaaagagaagacgatgtgaagtattaaaagaaa
 aaaaaaatggatgttgtatataagtaaccattgtagatagtttaagcaagaaaaattga
 tgttgcattggaaattaaaaaatttcaataaaattagaaaagcaactctaaatcattac
 ttattttattattttcaagaagttataaagtattaaacaattcgTTGACAaataagttt
 gatcgacattgtgtgacaaaattttaaacacatcattaataacaacgaggacaaatacag
 ttcagatatcgtctactattaaacacttcttctataggagcaaagaaaaattgtcggc
 aacgaactggggaccaataatattccgagtttgagttcaaactgagtaattttattttg
 agaaaatttgccaagttaacttataattctgggttACGTgtagtaattttattaagttgt
 tataggaaaatgagaaaataactaagacacatccaagaaagtttcacacgaaatttactt
 acaaaaagattgtttatttaataacttccgtatatagatatataaatatttaacacatta
 attataaagttcaagataattgattatctatctttttttgtcatctgaaattattatcg
 ctcaaacgaagtaattctgaggaaagttgtttacaaactagttattttcattattgtcta
 cttatataatagaattaaaaaaaattattgcttaatgcaatttagtttttagataaaatc

FIG. 2A

3/12

attaaacttaatagattatataagtttagatatcaataattgggcttgcttaaaaacata
aatataaaatattattgggcccgttACGTgcatacaaaaacgaaccttctaacaacaagt
gtgaACGTtacgacttcaaaattaaaaaaaaaacacaacaaactatgtccacACGTAatct
catatgattcagattccaaggagaacaaaattaaaaacaaatctcgtaaacatacatac
acttcacataaaaacaaaagggtacagtatataccataaatctccgagattcttttgatgt
atctgtccatttcattattacacaaactaggaaactgatatctctctattcacattect
ctgattctatttctctttatatatattcaccatttaaccatctcaatcttataaccctc
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14609 putative cytochrome P450

SEQ ID NO:

775

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taacaaacaatgatataaagaatatttcattaaataaaaagatattcttaactgaat
ttatttattaatttggtatatacttattaccgaaataaaggattgtttatttcttacaac
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16649 putative S-adenosyl-L-methionine:trans-caffeoyl-
Coenzyme A 3-O-methyltransferase (function:disease SEQ ID NO:
resistance) (promoter up to next ORF) 776

catgtctcttgagtcctcggtggtgtgcaaatgttcggttggtataaacgagagatgt
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taaggactaacacaccaattgatcttatccatgacttttcaaccatgggactagaaaat
caattatctagacagctacttgatgcgaatatattaacggtttatgtttcttaaggatttt

FIG. 2B

SUBSTITUTE SHEET (RULE 26)

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ttttctctcttaagggtgcatacaaatggttgaaatatgcaagcaggcgaacagtttgca
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17653 (similarity to DNA damage inducible)
(promoter up to next ORF)

SEQ ID NO:
777

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attatgtaatttcgcagaaagagaaaaagaaaaacacgtggtgattagagagtagtataaa
gatagttggttgggttctgttttttctgtatctcgaggcgccaaaaacaacaacaaaa
aaaacttcagagcggtgatcagattcaccgatttttctcaaaatg

FIG. 2C

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12778 Lipase/Acylhydrolase with GDSL-motif family SEQ ID NO:
(promoter up to next ORF) 780

catcatttagagagagggagaaacagaactgtgaaaagagaagaagattgcttttgtgc
cttagctcgtagaccgattcggttatatttatattgcaagtactacaatttggcaatgaa
aataatagttcattttactatacaaaataaacgtgtagcgcgaggttcattttactat
acacctatttaacgcactagcaaacgattatcgatcaattatattatagttcgccta
atcacgtctgacgcattactggtttctcttctactttatttttaattctcaacaaaata
tctattgttactacgagtaccaagaaagatcgtgcttttttttttttgggttcaacaaca
acttacaattacacaagagtctgaatacacataagctttaacccaatccggcaatatag
aatacaatttgggatcataattcagaaaagaaagagattccctagcaattctatctgcc
acacaattcccttctcatcgggtaaaagtcactttaacctcttcgaagtgtgaaaaga
tcgtgcatttagaggcaagaagtagaattaaacatacaaatccacggaaatataggggt
gtaaatggtaacactaaaccagattcagtaatttctgcagtaaccatttgcataaaaact
aaattttgctgactagccaaattcaacaaaaaaatttcaacaccaacatatacgtagat
atgtttatttctgctaaaacttttggataatttacgagtacacaactcgaattaaaata
tttttaatatcaaaatacatatcaaatagatatttttaataagtcagattatactgat
acgatatatgaataatatagatacataaaatatcactaccagaatagacaagagacgaa
tatgttcggataattatagataatttggataataattttaataacgtttagataaactta
aatcaattattaaaattttgcaaaaacaactcatacctatgctaagatattctttaaaa
gataaattatagtaatttctttaatcatcctcatcatattattgattaaattacttgaa
aacaattaaaaaaaacaattaacaatctatattttatcatcatgttaatttttgaaatt
attttcttaatagtgttttgacaaagattttcgtaattattttacatatttttaatagt
tcaaatttaataagaaagaataactcaattttgcggttgacacaatcttaatatagtag

|| Subcluster B

20245 glutathione-conjugate transporter
AtMRP4

SEQ ID NO:
781

atttttctaataagacttttcttattctcatagactcttcttattcatctttcttaact
aattcgaccaactcagtggagacaaatctcacacgaccctttccactttttggtaact
ttattattaatttattagtaggtgtagttcctttcttctctgctgatctTGTC AAC
aaaataactaaatttttccctaagcggctgtttatatattattaacaaagggttccgcgtg
tctcttgtttaactagtagactaaaaacaaatcgtaaaactcgattttctcaaccaaat
tagaagatactacggcatgtaattagctaataataaaagattcgaattttcgttccaat
ggatttgccttttcttttgcacaaaaccaagaatttgccttctcttggcagtagtttagc
tagacaacgcataatagctatatattttgtgtacactGGTCAAggtcgtggatACGTCAT
taataatattatttccaataagtcctattaaaacatttaaaacactttgagttttaaaac
aaacttagtgtaaagaaaaataaaaatagcagacagtttacgggtaagactagatgagcca
tatatgattgagtgcataaaacatcttttttctttcttttttgaaaaagcgaaactaa
aagattattagttgttggaatcagcttagcgtaattcttcgagaaaaatgactctaattgc
taaaatactgatttaataatctaatgttTTGACCCAAcagacttttttttttttt
ctatcctctaataatatataatcatatagtagtaattatttagtagataatatgattaa
cACGTgaatagcaaagtttctatcatttttattcaaaaaagattcataagtaataaaa
tgatAGTCAActtttctttttctttttgtgtttggccttttgtTGACGCGTCAttgttg

FIG. 2E

SUBSTITUTE SHEET (RULE 26)

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tacaccaccagtcacactattgtgggatgtgataatcggtaccttttaaatgtcaggagc
ttctttcttacattttccacttcaaacaaaccgataattcagaggaattttctcttctc
ctctctctctcttttttatatttttctactgggaaaaatg

17051 CTF2B involved in hydroxylation
and oxidation of an aromatic ring

SEQ ID NO:
782

catagccgcggtccaagaggaGGTCAAgtaggattcacttttctataatcaatattaaat
tgtagtcacaaaattcaagaaacttatatagaccttattttatttttgaaatcaatag
ttgtcggtgaaaagtatcttggggatatttagatttagcatatgAGTCAATGTTGgggtc
cttaagagttgaggctacaaatttataactcagaaaaagtgtatatgccctttaatttt
tggcctattgggtcttttatggCGTCAactccaatttcagtttgaaaagaaaGTCAAta
actaacaatggttcttTTGACTttgaaatcttagaagtttegacttacctatttctac
aagtgttaaatagcactgttattcaaaatcttatatttggttaattgtgcttaatatatt
ttaaaatttaataacttcattaaaaatccaatgttattcaaaactaaattacttttgaaa
tatgtgtatatgaagtcatttgaaatgaaatctcataaagtttcataagtaaatatta
gaataaaaacccaaggtaattgtatagattttgaaatccacacaataatatcgaattgt
aaaatctagagaattcaatttcaattcatgaaggagtgtaataatcatggatttttaa
agttagttgattgaatataaaagtaggaaagatgtgggattcatgtggtgggttggtccc
atctccatgatctctagtgaatttcagctTGACGcaactttcgtaaagatcttacttca
ttgtgtgttggtgttgagcctcactggattgggtgtgtcggttttttagttcactcagag
ttaagagtcctcgagtaagactctatcactatttaaataattaatgtaattgagttatg
ataattcaaatggatctccttcattccatagttgcatTTGACAtttttatataaaactt
gctgatttatctaagtcacaaatttgagtccttggtaatattcagtttcaatcatcaggag
atgtctaataagattaaaaattaaagatagaaatgtctaattggattgaaatatataaagt
gactcagccaaaaacatgttaactgaaaatcttgtataaaatggagattctctgataac

19640 putative glutathione S-transferase

SEQ ID NO:
783

aatgtagttttttctggttttgtggagttaatcactaccttttagcttggatttatagc
cttatgggtgttgatgggtcttgtgataaaacgacgacgaactttgccgttttatatgggc
ggcagtgatgtgaaatgcgaagagtctagaaggaaacagatgTTGACTttacaacata
tttataACGTtccctttataatttttttttatctcttttttagtaagtgagatgtgtc
ctaattcctaaccttgcccttatccctggagcatgtgtaccTTGACTtgatccattcatt
ttctgaagacaaccccatgcttCGTCAagaatttcttctgcttccccaattatacccat
cactttatcggtgttcttcataattgatccattttgtctgtgtatgaaacatcaacagc
tttaaaaccattttgtcattctcggttggttatattgacgcccgaagaaaacaaacactct
atagtcctgagctataaaaaaagaattagtagtaattctgttatttgatgttccttttggc
atatattaaaaatggttggttataataggcggttggttttccggttctccatctacga
acttggttgctgaattttccttccaacaatggttataaagtatcggatgaattttctatgg
ttacaagactcaccacctcagatactaaaaatataactaaagaaatttggttatattgtg
ccgcaacaaatagaccacatgtccggtgtactttcctctgtttacacaacttcttACG
TgtcgaaatacatgttcacatttaatacatagttgtgggtttattaagaaggatgggtTTG

FIG. 2F

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ACTaaattatagctttttatctactttttctttcatatgaaaactccaggtttatgaacca
atttcttatgatttgtaagaaattgaatactactacattttaaagtgtttataataatta
aTTGACAttagaatttagtaaaaacactaattgttcatacaaatgtttcatttattgtt
catacaaaactattataacaagattacacaaacatatagttaacatctactgatcgaaga
gtatcattgttctctcttaggctgatttgattctttctacaactttcttcatatg

14248 PAD3_at member of the PF|00067
Cytochrome P450 family

SEQ ID NO:
784

gttctggtcgaaggatttgtcccgaatgccaatggcgattgctagtgtggaactagca
ttgatgaatttgctttattttttgattggagatgcctgatgggactaaagggtgaaga
cattgatatggaagaagctggtaatatctctatTGTCAGaaaatacctcttcaacttg
tgccgtgttcaACGTtattgatgagcaataataagctcgataacatggaaagtgtatg
aagcaaaaaacataagattcttttagattttgttgtgttatataagaaagaaatgttcca
ataataaatcaagaaagaataacttttgttcatttacttaaaaaactagatcataatcaa
cacggattaagatctttttcattcaacaaaattctaaattttgttttttaagtaaaaa
atgttatagcataaatgttcagatttttatgtcgtatttatattgaattaaatataggac
aaagaaaaataagatacagaacaaagagaaattttgatccaaaaaaaagaaagaga
aataagatctagaacaaaaacgatacattcagattgattattgaaatcaaataatcgaa
tttataattgaatttgatggaatttataatgtattttttgtcatggaaataataaagt
tgtaatatagtaggcacgatcgaatctggagcttcaatttttttaactaattgtta
tggaagatgctggaatgatctctttttacaagaaagctcctctcattcttgttccggtt
aaacaccattaaagacatcggcacacaaaaattcaaacaccggttgaagattgtttgcta
tactttatttttatcaataataagttgcggtacttggttaactgtatACGTacttctat
ttcttatagttgtgcgataattaccacaagtccaaaaaagtaaaatatgaatttgataa
agcagtgtaaacctgagattttcaagatttgggcctaaaccattagagaatgctACGT
agagaaccattgggcccataaacttattttattcccgcgaagcctgagtggattcgaac
cactaccacaaaaagtaagagtttgggttatttgattttaatcattcactttgaattat
tatagacaccggacagtgaacttatgataaagagatttttaacctttaaaactaaaacac
taaaatacataatccaaagaagacggaacaaaaacaaaaacagagccaggaataatg

17500 athcallga_s_at calmodulin-like protein
(promoter up to next ORF)

SEQ ID NO:
785

catcaaactaatttggttattcttgagattaggaatgtgtgttcacctaaaagctagta
attgattactaaaatgtaatgcatgcaacaagaagagtcaatcgaattttatagagata
agtcataataaaatgattaattatcgctagaggaagctgcgatgaaattttcttacagctt
ttgtctttttacccatcctaattcatttaattctctgagcctacgccatcacacatatctaaa
agcaccttcttcgaaattcccttgaggacaaaacatggacctctttttgttcacttg
gattttctcggaatgacttgcatgtcttcttactatattttatgtatcccttcattc
tatactttttcgaaattctaatttaactctacatataatcccactcccaccagctaaag
tttagacatgacaagtattttatcaaattgctccttcaattcaaactactgaattattgtt
tggaataagtactttttggagacgtaagctatattttccaatccgaaatgaatgaaccaa
atgtccatagttctgttttttttctcctaaagtgaatatattaagagacactaaatt
ctagaaaaatatgtttaaaataataatcagtaattgtccaaaaaatgtgaataactta

FIG. 2G

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aatcaaaatcaggatacgaattgtcacaagaaacaaactttcctagataatgtatatatttt
atattattatcatattatgtatgcacttaagacatctccatccatgagaaacctacaaa
gtttttcaaacaaaaaaatattaatattatattataatttgattattttttattaaaaa
agtattttttgttaaaaaattaaaccaatagtaagatgagaattgtcatgatgggttgta
caaagtatctcagagtatctcagagtttctcacttgagaaactttctacactctctctc
cttcattttttattattttttatttttttaattgtgagaaattcttatgagataccacaa
tagagatgggtcttataaaatttatcaacatgggtgaatctctcatgttatatatagaggtg
atttaaaggctaaatagaataacacactacagcatataaaactcaatgatatg

18928 putative endochitinase (promoter up to next repeat region) SEQ ID NO: 786

cattttgtgtatggaggggtgttgtgtgaagaaatgaagaagggtgtgttgatgtatttat
agtgtaaatttggtctattcaaattgaaatattgatcagtggttagacatctttcacgat
tattgattggctttttctgagtc aaagtcaatgccactttgtaccacttaacaaaagtc
aatgacacagttttttctcttgctgttatgagaaattccatgtcgggtcatagatcagat
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tcataaaaacttgattgagataatcaagtttagattagttcaaacgtttgagatttttc
tattgaatagttccaagtttttgtaattagctcaaacgatattgttagctaataatagc
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tttataaatcaaaatcaacaaaattagaaaaatccaactcaattattgcaatttccaa
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cctggtctagagactctagaaccatcggagctcaagtgaaaaacgacgcggttaagctg
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tcctccgttggtgtttcaggacgacgcaaaaggggaaaaaaaattgaattctttctctcca
agcgaaactagggtttcgaaagtctctgtctcatcaaagcttcgaaaaggtagatttat
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ttaccttatattttaccgaaccagtgcccttatattctatcacattcgaagttattgggt
tctgggtacttatattgcttattgttctatgactacgatataattatcccaaagatttg
ttcttttctccgaatttggttagaaatggatataactcaaattctgaacatgcccgaa
gaatcct

14614 putative glucosyltransferase (promoter up to next repeat region) SEQ ID NO: 787

ttaatttatccacacctcaacgaaaatttccggttggtgctaacgaattcaggctgtg
aagttaaaagaaaaataacaaaattatagcttcacataagcgatcgatcttcaaactct
acacatgacagaagcaaataactaaattaaatagcgtaaattttgtaataataactagaa
aacctaaaaaccaaattgtaaaaaaccttatgggaaaaaatgtgataaagcacctaaacc
atagaataacttaaaatttcaattttccaatcaagggtatgatataaaaaccatggaaaa
caaattctcagccatatttctatctgaccgagtcctttttcaaaataatatatagacggt
agagtccttatatagtaaaaacatttttttaaaactaatttatcttctcatatgaaaatg
aatgcaataaaaaatgaccatataatgctgtaatgatattcaaggaagagatatcacaac
aaggctcgaagaaatatacaatatctgaaagtcgactatatgggtccactttccaaattag

FIG. 2H

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agatggaaagaagaaacgattatgcagcaaaccattgatcggacgaagaagaataaa
tatggaggccattactatagtagttggccttgaaatattttgggtccgagaaataataa
ataaacagttatggcttttcggatttggttgctttcaattttctcaaatggttgacaa
gtgttattacactcacctaaaacaggatcattccaatttcttgggctcagagtctgtac
tttcttcttctttaaaccaaggtcttataagtattctctaaaccaagtcactaaacaat
aattgggtcttgggtctggttcaaacttggtcaatggttgccacatagccattagccaca
caaaacaaaaattgtcttgcttttatatggaatgaagaaaaatcgaattttgtaccat
ttttgactttaaagtcacactcgccgtatacggcacaccaaatagacaaaaacatttga
ccaccaactttgctttaatgttaaaacttttttttgcacccactactctcttcttca
ctcctcaagtcacagtgaccaaatacacacacttcacaagaacaacctatg

||| Additional genes showing early and transient RPP-triggered expression

13176 Contains Myb DNA-binding domain
repeat signatures

SEQ ID NO:
788

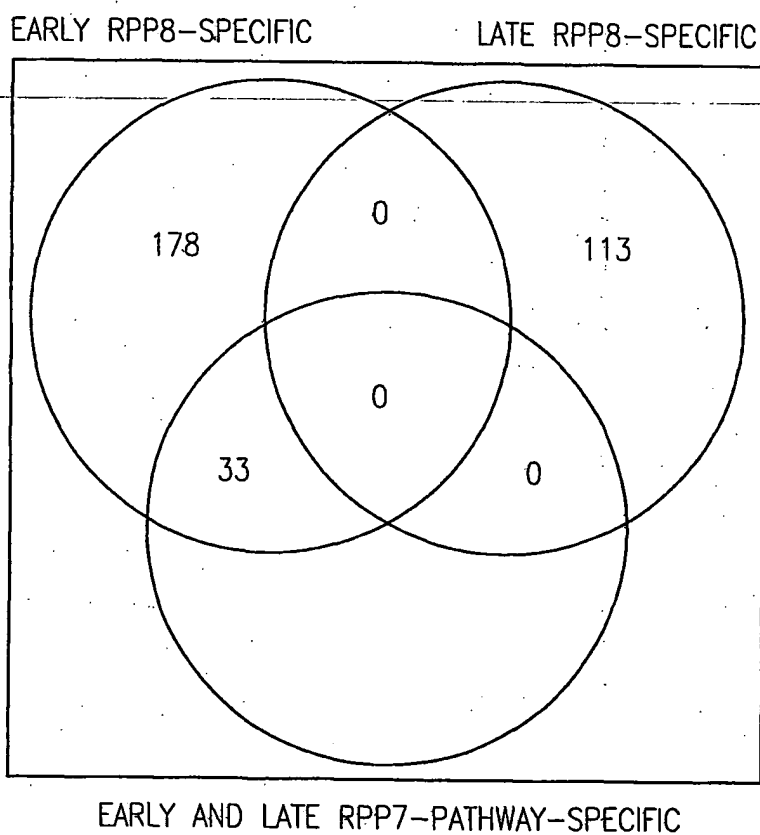
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agagatataccttcgccatCGTCAAttggcccaaagaacaaaatgtacatactttacaag
aggaatcaatattaaagtgtatataaccaatgacaaaggctccaataatatcttcttgt
cgttaattggagatcttctgaacatgacagtgagggtatacaatgggctagttccaata
tcaccaaatacaaccccaagtgtctgcaaagcaagtatgagtttctttcctataaccagt
gtcctgaaaaaacacattaccaagttcaacaactcaatcagatcgaaaagtaaacaca
tgaagaagaagaagaacattcacacacaaatgctaacctcgatttcggttttctgagtt
ccaggaatctcaagagcatctacatcgaaagAGTCAAcggcagggttagtgcaatcaa
acgctgctccacattgtcatcctcctcatcggaatccatttcggggtgattatgctcat
catatccatcatcgctcgtaatcttcattaacctcataatcatctttctcatcgacacc
catcgcgacaaTGACGTcgttgaatcgctctccgcaaaactcctcatcaatctcagaccc
atcgctccactgctttcttcttcACGTgaaacatcaatcaccggttgaaaacactga
agatctcgagattgtgattcagattcgatctctgatccaaggaaacaggattggaatt
ggtgtttttgagagattgagagatggaagagagagattgatctacatacactggagagg
acctggcacgaatgagaaagaagcttacACGTgtccaatcatgattggattcgagactc
acggtttaaggaaaaacaaaccagaccaaattaggcttaaccgctaaaaaacgggttc
tcgttttgaaagattgagagagacgatctacaaaggaggacaggaccggcaggaatga
gaagaagcttacACGTgtccaatcaggattgaacgatttaatacaagcttaaccgtatgt
aaaccggatttttagctgggtccacaagtAGTCAAatataagattttttaatAGTCAAata
attttcatagggcggaagttcaagatgagttactacactcatcaaagctcacaaaaaga
gaagagaagagacgaggatcaatcaccattctcatg

FIG. 21

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26 *Peronospora* (Hiks1 and Emco5) induced
RPP7, EDM1,2,3 and RPP8-Dependent genes

**FIG. 3**

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RPP4-pathway, RPP7-pathway and
RPP8-up-regulated transcription factor genes

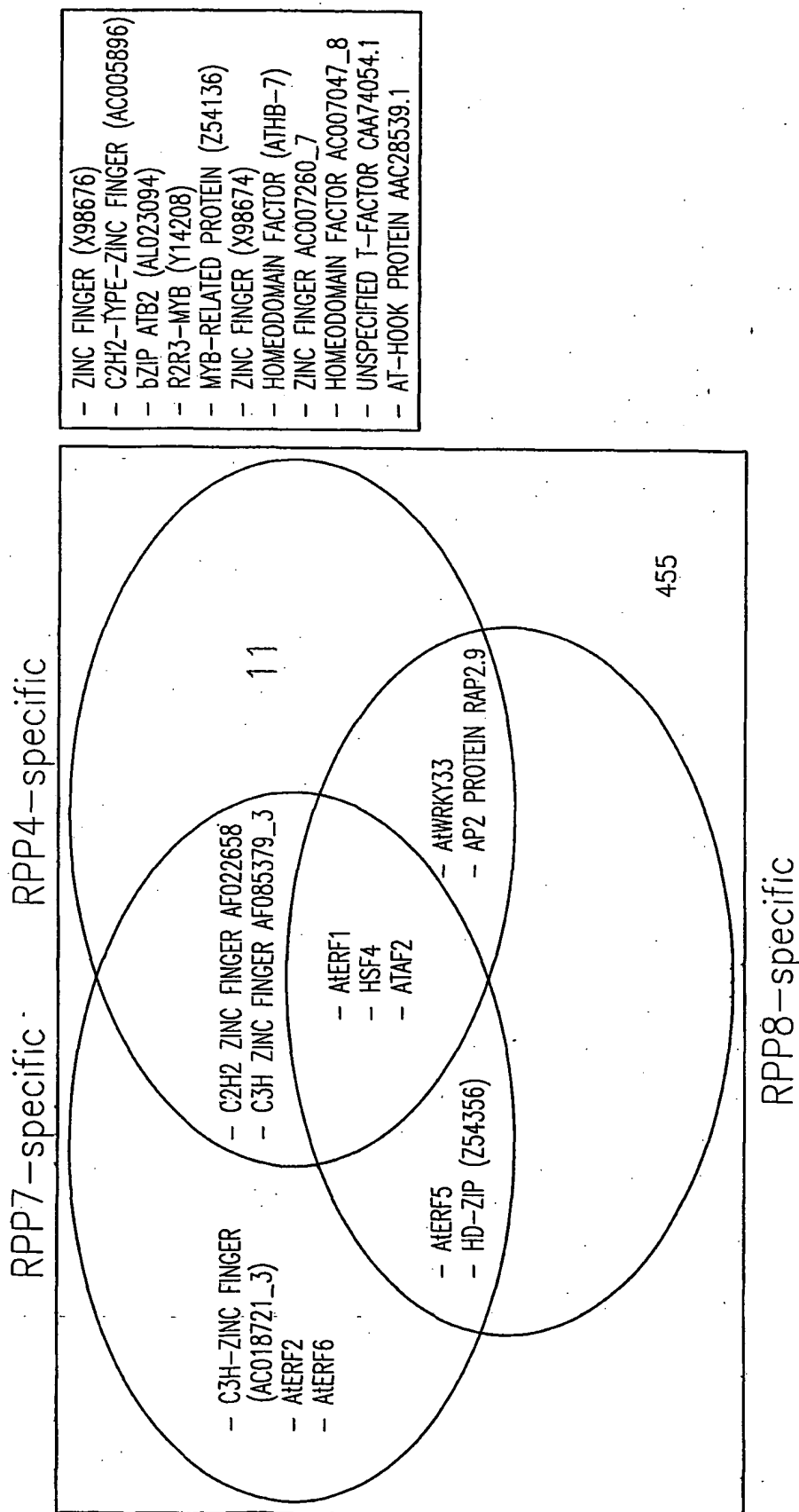


FIG. 4